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J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antildiotypic until-dics; evidence that Ab A; Reference number: PL0080; MUID:89094248; PMID:249205(A;Accession: PL0082 A;Molecule type: mRNA A
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ALIGNMENTS

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Database

| | C;Superfamily: immunoglobulin V region; immunoglobulin homelogy C;Keywords: immunoglobulin F;16-89/Domain: immunoglobulin homology <imm></imm> |
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| 09959) | A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-107 <fel> A;Residues: 1-107 <fel> A;Residues: 1-107 <fel> A;Roser-ferences: EMBL:M90690 A;Ote: sequence extracted from NCBI backbone (NCBIN:10995%, NCBIP:109959) A;Note: sequence extracted from NCBI backbone (NCBIN:10995%, NCBIP:109959)</fel></fel></fel> |
| | J. Biol. Chem. 267, 15552-15558, 1992 J. Biol. Chem. 267, 15552-15558, 1992 A;Title: Chimeric L6 anti-tumor antibody. Genomic construction, expression, A;Reference number: A42848; MUID:92348410; PMID:1639754 A;Accession: A42848 |
| an-2000 | Ig light chain V region - mouse (fragment) NyAlternate names: L6 anti-tumor antibody C:Species: Mus musculus (house mouse) C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000 C:Accession: A42848; S33902 C:Accession: A42848; S33902 |
| | Db 61 FSGSGSGTSYSLTISRVEAEDAATYYCHUMSSNEFIEGGGIALEJA ivii RESULT 2 A42848 |
| | QY 61 FSGSGSTSYSLTISRVEAEDAATYYCOOMSSNPPTFGGGTMLEIK 1044 |
| 1R 60 | QY 1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR |
| Gaps | Query Match 94.1%; Score 523; DB 2: Length 106; Best Local Similarity 94.3%; Pred. No. 9.2e-38; Matches 100; Conservative 3; Mismatches 3; Indels 0; |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 7; Page 128; 150pp; English
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                            Treating post-thromboembolic administering anti-factor IX activator
        Example 7:
                                                                                                                                              15-MAY-2000; 2000US-0571434.
                                                                                                                                                                                      22 - NOV - 2001
                                                                                                                                                                                                         WO200187339-A1
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Chimeric - Homo sa
                                                                                                                                                                                                                                                                   Human; mouse; BC2; animal post-thromboembolic induced ischaemia; thrombolytic agent; anti-factor IX antibody; plasminogen activator; thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic; vasotropic; cardiant; anti-respiratory syncytial virus;
                                                                                                                                                                                                                                                                                                                                                                 AAU81002;
                                                                                                                                                                                                                                                                                                                                                                                    AAU81002 standard;
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                                                                                                                                                                                                                                                                                                                        Mouse-human light chain polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thrombosis; therapy; Factor IX; anticoagulant; memoclonal antibody; humanised antibody; antibody engineering; light determining region; myocardial interction; angina; atrial fibrillation; stroke; kidney damage: pulmonary embolism; deep vein the pulmonary embolism; deep vein the discontinuous stroke; and the damage of the pulmonary embolism; deep vein the discontinuous stroke; and the damage of the damage 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method for treating in initial post-thremboembolic induced ischaemia or reduction is required dose of a thrombolytic agent in treatment of an animal post-thromboembolic induced ischaemia, comprising administering an anti-factor. It is intibody or its fragment, optionally in combination with a plasminumen activator or thromboembolic-induced ischaemia, for providing thromboembolic surely in an animal, and for reducing a required has of a thrombolytic agent. Sequences AAU80972-AAU81004 represent antibalies and vector polypeptides used in the method of the invention.
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17-JAN-1996;
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                                                                                                          SMITHKLINE BEECHAM CORP.
UNIV VERMONT & STATE AGRIC COLLEGE.
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tel AH, Sylvester DR:
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WPI; 1997-385117/35

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

Š protein protein search, using S W model

Run 9 :: November 27, 2002, 07:25:20 ; Search time 2.25869 Seconds (without alignments) 638.431 Million cell updates/sec

Title: Perfect score: US-09-893-615-1 15

Sequence: WRMYFSHRHAHLRSP 15

Scoring table: OLIGO

Searched: 283224 seqs, 96134422 residues Gapop 60.0 , Gapext 60.0

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Maximum Winimum DB BC seq length: 0 length: 2000000000

Post-processing: Listing first 45 summaries

pir2:*
pir3:*
pir4:*

Database

PIR_73:*

score d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

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| A55367 | AI1168 | T15228 | G69547 | T38520 | D70554 | A99323 | AB3589 | T28824 | G83032 | S25656 | E83153 | S34993 | D70828 | T08254 | AC2084 | AB0200 | D83261 | T22156 | F72515 | S39402 | T27345 | G83448 | S07776 | C81139 | \mathbf{r} | T19824 | A71447 | A40996 | ID | |
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| phosphatase cobC - | | probable histone B | ס | hypothetical conse | | hypothetical prote | protocatechuate 3, | | hypothetical prote | T-cell surface gly | conserved hypothet | nitrite reductase | hypothetical prote | probable transposa | phosphonate metabo | conserved hypothet | trar | | hypothetical prote | | hypothetical prote | | oxoglutarate dehyd | probable oxoglutar | 2-oxoglutarate deh | | hypothetical prote | phenylalanine 4-mo | Description | |

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probable transcrip RING-H2 zinc finge hypothetical zinc-probable glyoxalas probable ABC trans hypothetical prote probable RING zinc probable MADS-box hypothetical prote hypothetical prote probable transcrip hypothetical prote hypothetical prote T-cell surface gly nypothetical prote ypothetical prote

ALIGNMENTS

C;Species: Chromobacterium violaceum
C;Date: 03-Aug-1992 #sequence_revision 03-Aug-1992 #text_change 31-Mar-2000
C;Accession: A40996; B40996
R;Ontshi, A.; Liotta, L.J.; Benkovic, S.J.
J. Biol. Chem. 266, 18454-18459, 1991
A;Title: Cloning and expression of Chromobacterium violaceum phenylalanine hydroxylasi
A;Reference number: A40996; MUID:92011593; PMID:1655752 A; Experimental source: C; Keywords: biopterin; A;MoLecule type: DNA
A;Residues: 1-296 <ONI>
A;Residues: 1-296 <ONI>
A;Cross-references: GB:M55915; NID:g144481; PIDN:AAA23115.1; PID:g144482
A;Accession: B40996 phenylalanine 4-monooxygenase (EC 1.14.16.1) - Chromobacterium violaceum N; Alternate names: phenylalaninase; phenylalanine 4-hydroxylase A; Molecule type: protein A; Residues: 1-20 < ONS> A; Accession: A40996 A40996 Matches Query Match Best Local Similarity 6; Conserv 40.0%; So illarity 100.0%; For Conservative 0; strain ATCC 12540 oxidoreductase b; Score 6; DB 2
b; Pred. No. 12;
0; Mismatches DB 2; Length 296; 0.. lndėls 0, Gaps 0

8 RHAHLR 13

밁 192 RHAHLR 197

hypothetical protein - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear A; Variety: columbia cress)

C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998 C;Accession: A71447

R; Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; D. P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Gavanagh, T.; Hempel, S.; Kotter, P.; Entlan, K.D.; Rieger, M.; Schaeffer, M.; Grunk, B.; Nature 391, 485-488, 1998

A; Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; C.; Chalwatzis, Rechman, A.; Puigdomen

A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis A;Reference number: A71400; MUID:98121113; PMID:9461215 A;Accession: A71447

A; Molecule type: DNA A; Residues: 1-352 <BEV> A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Cross-references: GB:Z97344; NID:g2245126; PID:e327078; PID:g2245129

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RESULT
C81139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein C38D4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
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                                                                                                                                             A;Gene: odhA
C;Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin
                                                                                                                                                                                                                                                A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus A;Reference number: A89758; MUID:21311952; PMID:11418146 A;Accession: E89918
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A; Residues: 1-910 < KUR>
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A; Residues: 1-556 <WIL>
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631 FSHRHA

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R:Schulze, E.; Westphal, A.H.; Hanemaaijer, R.; de Kok, A. Eur. J. Biochem. 187, 229-234, 1990
A;Title: The 2-oxoglutarate dd4hydrogenase complex from Azotobacter vinelandil. A;Reference number: S07776, MUID:90126823; PMID:2404759
A;Accession: S07776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oxoglutarate dehydrogenase (lipoamide) (EC 1.2.4.2) - Azotobacter vinelandii N;Alternate names: 2-oxogluturate dehydrogenase complex chain El C;Species: Azotobacter vinelandii C;Species: Azotobacter vinelandii C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 15-Oct-1999 C;Accession: S07776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: sucA; NMB0955; NMA1149
C;Superfamily: oxoglutarate de
C;Keywords: oxidoreductase
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A; Molecule type: DNA
A; Residues: 1-942 <PAR>
A; Cross references: GB: AL162755; GB: AL157959; NID: g7379742;
A; Cross references: Serogroup A, Strain Z2491
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A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuol A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain A; Reference number: A81000; MUID:20175755; PMID:10710307
                                                                                                                                         A;Gene: sucA C;Superfamily: oxoglutarate dehydrogenase (lipoamide); thiamin pyrophosphate-binding C;Keywords: oxidoreductase; thiamin pyrophosphate; tricarboxylic acid cycle F;359-405/Domain: thiamin pyrophosphate-binding domain homology <TPB>
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A;Residues: 1-942 <TET>
A;Cross-references: GB:AE002446; GB:AE002098; NID:g7226195; PIDN:AAF41361.1; PID:g722
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Feb-2001
C;Accession: C81139; H81881
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C;Genetics:
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A; Residues: 1-943 <SCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Experimental source: serogroup B, Strain R;Parkhill, J.; Achtman, M.; James, K.D.; B; Holroyd, S.; Jagels, K.; Leather, S.; Mou Nature 404, 502-506, 2000
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A; Accession: C81139
A; Status: preliminary
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                                                                             40.0%;
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C:Accession: G83448

R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Wa adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: G83448

A:Accession: G83448
                                              J. Mol. Biol. 234, 508-512, 1993
A;Title: Nucleotide sequence analysis of fc A;Reference number: S39400; MUID:94047099; A;Accession: S39402
                                                                                                                                                                                                               RESULT
S39402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein Y70C5A.2 - Ca
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_rev
C;Accession: T27345
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C;Superfamily:
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C;Species: Bradyrhizobium japonicum
C;Date: 07-Oct-1994 #sequence_revision 26-May-1995 #text_change
C;Accession: S39402
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A;Introns: 21/2; 71/1; 144/3; 246/1; 283/1; 319/2; 559/3; 636/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-1037 <WIL>
A;Cross-references: EMBL:299282; PIDN:CAB16532.1; CESP:Y70C5A.2
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
A; Molecule
A; Residues:
                               A; Status: preliminary; nucleic acid sequence
                                                                                                                     R; van Soom, C.; Browaeys, J.; Verreth, C.; Vanderleyden, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: clone Y70C5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, A; Reference number: Z20349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-943 <STO>
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 type:
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                  DNA
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llarity 100.0%; Pred. N
Conservative 0; Misma
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                                                                   analysis of four genes, hupC,
MUID:94047099; PMID:8230232
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awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki DNA Res. 6, 83-101, 199
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: F72515
                                                                                                                                                                                                                                                                                                                                C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision
C:Accession: F72515
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                                                                                                 C;Superfamily:
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                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-101 <KAW>
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                                Matches
                                                 Query Match
Best Local
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Pred. No.
                                  red. No. 62
Mismatches
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                                                 DB 2;
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h, Y.; Yamaz
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R:Sulston, J. submitted to the EMBL Data Library, submitted to the EMBL Data Library, submitted to the EMBL Data Library, A;Introns: 17/1; 41/1; 97/1 C;Superfamily: Caenorhabditis elegans hypothetical A; Map position: X A; Introns: 17/1; 41/1; A;Status: preliminary; translated A;Molecule type: DNA A;Residues: 1-142 <WIL> hypothetical protein F44A6.4 - Caenorha C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision C;Accession: T22156 A; Gene: CESP:F44A6.4 A;Cross-references: EMBL:Z50858; PIDN:CAA90724.1; GSPDB:GN00028; CESP:F44A6.4 A;Experimental source: clone F44A6 A; Reference number: A; Accession: T22156 T22156 RESULT 11 Matches Genetics: Query Match Local Similarity hes 5; Conserv **HRHAH 11** Conservative 100.0%; 33.38; Caenorhabditis elegans 0; Score 5; Pred. No. from August 1995 Mismatches GB/EMBL/DDBJ 15-Oct-1999 DB 2; protein F44A6 #text_change 18-Feb-2000 0 Length 142; Indels 0 Gaps 0

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conserved hypothetical protein YPO1639 [imported] - Yersinia pestis (strain CO92) C;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB0200
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, in M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: D83261
R; Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                            RESULT
AC2084
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C; Superfamily:
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A; Reference number: A82950;
A; Accession: D83261
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                                R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.;
DNA Res. 8, 205-213, 2001
                                                                                A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change C;Accession: AC2084
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A; Residues: 1-148 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-147 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Genome sequence of Yersinia pestis, the causative agent of plague A;Reference number: AB0001; MUID:21470413; PMID:11586360
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                                                                                                                                       C; Species:
                                                                                                                                                      phosphonate metabolism protein [imported] - Nostoc
                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: YP01639
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              A; Title: Complete
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                                                                                                                                                                                                                                                                                                                                    33.3%;
Sequence of the Filamentous Nitrogen-fixing Cyanobacterium 7; MUID:21595285; PMID:11759840
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L.L.; Coulter,
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; Takazawa, I
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r, S.N.; Folger, K.R.; Kas,
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; Yasuda, N
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124 RHAHL

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8 RHAHL

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A; Accession: AC2084
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-151 <KUR>
A; Cross-references: GB:BA000019; PIDN:BAB73924.1;
A; Experimental source: strain PCC 7120
C; Genetics:
A; Gene: phnG
                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: T08254; T08389
R;Ng, W.V.; Ciufo, S.A.; Smith, T.M.; Bumgarner, R.E.; Baskin, Genome Res. 8, 1131-1141, 1998
A;Title: Snapshot of a large dynamic replicon in a halophilic A;Reference number: Z16408; MUID:99063795; PMID:9847077
A;Accession: T08254
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Halobacterium sp.
A;Variety: strain NRC-1
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Jan-2000
C;Accession: T08254; T08389
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T08254
                                                                                                                                                         A;Genetics: COP2
C;Genetics: <COP1>
                                                                                                                                                                                         A;Cross-references: EMBL:AF016485; NID:g2822278; A;Experimental source: strain NRC-1
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A; Molecule type: DNA
A; Residues: 1-176 < DAS>
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A;Experimental source: strain
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A; Residues: 1-176 < NGW>
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                                                                                                                         A; Genome: plasmid
                                                                                                                                             A; Gene: HALOSP: H0455
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91 SHRHA 95
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element: insertion sequence ISH5
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Y906_MYCTU

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Y823_MYCLE

GSPF_AERHY

UXUA_HAEIN

SYT8_MOUSE

O22A_DROME

O22B_DROME
ARKA_ARATH
VGLG_HSVEB
VGLX_HSVEK
PYRC_DEIRA
PYRC_THEAQ
YEYZ_YEAST
GLMU_BUCAI
TRPZ_ARATH
TRPZ_ARATH
KG3A_HUMAN
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GL2M_ARATH
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9 drosophila
0 drosophila
8 arabidopsis
7 equine herp
4 equine herp
3 deinococcus
1 thermus aqu
6 saccharomyc
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| TBX2_HUMAN | TBX2_MOUSE | YQOA_CAEEL | NOG1_YEAST | NOG1_SCHPO | V70K_TYMVA | V70K_TYMV | PUR6_YEAST | CIP4_HUMAN | SYN_TREPA | GALT_BACHD | FIXL_RHIME |
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| Q13207 | Q60707 | Q09299 | Q02892 | 094659 | P20131 | P10357 | P21264 | Q15642 | 083618 | Q9kdv2 | P10955 |
| homo sapien | mus musculu | caenorhabdi | saccharomyc | schizosacch | turnip yell | turnip yell | saccharomyc | homo sapien | treponema p | bacillus ha | rhizobium m |

ALIGNMENTS

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| st annotation update) |
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| 100). |
| Azotobacter vinelandii. Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae; |
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| 1 |
| 2404759; |
| 2-oxoglutarate dehydrogenase complex from Azotobacter |
| vinelandii. 1. Molecular cloning and sequence analysis of the gene |
| 234/1990) |
| |
| MEDLINE=90126825; PubMed=2404760; |
| rocessor complex from Protobactor |
| landii. 2. Molecular cloning and sequence analysis of the gene |
| the succinyitransferase component."; Biochem. 187:235-239(1990). |
| ASE COMPLEX CA |
| CONTAINS MULTIPLE COPIES OF 3 ENZYMATIC COMPONENTS: 2-OXOGLUTARATE |
| DEHYDROGENASE (E1), DIHYDROLIPOAMIDE SUCCINYLTRANSFERASE (E2) AND |
| NSE (E3). 2-oxoqlutarate + lipoamide = S- |
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| . PIROPHOSPHATE. |
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| European Bioinformatics Institute. There are no restrictions on its |
| itutions as long as its content is in no way |
| agreement (See http://www.isb-sib.ch |
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| Dehydrogenase_E1. |
| ifallsketorase. |
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Glycolysis; Oxidoreductase; Flavoprotein; Thiamine pyrophosphate. SEQUENCE 943 AA; 105687 MW; D3F35356D454EZA1 CRC64;

Length 943;

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RESULT 2

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                     Rhizobium sp. (strain NGR234).
Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodom; PD003112; hupe_hypc; 1.
TIGRRAMS; TIGRO0074; hypc_hupe; 1.
PROSITE; PS01097; hupe_hypc; FALSE_NEG.
SEQUENCE 98 AA; 10633 MW; A9BD353F9D4240F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001109; HupF_HypC.
Pfam; PF01455; HupF_HypC; 1.
ProDom; PD003112; HupF_HypC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bradyrhizobium japonicum.";
J. Mol. Biol. 234:508-512(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          van Soom C., Browaeys J., Verreth C., Vanderleyden J
"Nucleotide sequence analysis of four genes, hupC, hu
hupG, downstream of the hydrogenase structural genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=94047099; Pubmed=8230232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bradyrhizobium japonicum.
Bacteria; Proteobacteria; alpha subdivision;
Bradyrhizobium group; Bradyrhizobium.
                                                                                                             Hypothetical
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01-NOV-1995
16-OCT-2001
                                                                                                                                                     between the Swiss Institute of Bloinformat the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                         JOSE J.;
Thesis (1994), University of Saarlandes, Gel-1- FUNCTION: PROBABLY FACILITATES NICKEL II
-1- SIMILARITY: BELONGS TO THE UREF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein;
TRANSMEM 108 120
SEQUENCE 162 AA; 1
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MEDLINE=97305956; PubMed=9163424;
Freiberg C.A., Fellay R., Bairoch
                                                                                          EMBL; Z35136; CAA84508.1; InterPro; IPR002639; UreF. Pfam; PF01730; UreF; 1.
                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation {}^{\bullet}
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Bacteria; Firmicutes; I
                                                      SEQUENCE
                                                                  Nickel.
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(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
ssory protein ureF.
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RESULT 6
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01-APR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
T-cell surface glycoprotein CD8 alpha chain precursor (T-lymphocyte differentiation antigen T8/LEU-2).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin domain; Trans
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    FRDA_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Structure of CD8 alpha and beta chains of the orangutan: patterns of mRNA splicing encoding hingeless polypeptides.
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CD8A_HUMAN
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Best Local (
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15-JUL-1999 (Rel. 3
15-JUL-1999 (Rel. 3
15-JUN-2002 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD8A_HUMAN P01732;
                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
T-cell surface glycoprotein CD8 alpha chain
differentiation antigen T8/Leu-2).
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                                                                                                                                             diffications (Human).
Homo sapiens (Human).
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Motazoa; Chordata;
SEQUENCE FROM N.A. MEDLINE-85099337; Puk Littman D.R., Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U95736; AAB67778.1; -. HSSP; Q16595; 1DLX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom; PD006646; Frataxin_like; PROSITE; PS01344; FRATAXIN_1; 1. PROSITE; PS50810; FRATAXIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1096879; Frda.
InterPro; IPR001794; Frataxin.
InterPro; IPR002908; Frataxin_like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Studies of human, mouse and yeast homologues indicate a mitochondrial function for frataxin.";
Nat. Genet. 16:345-351(1997).
-i- FUNCTION: PROBABLY INVOLVED IN IRON HOMEOSTASIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koenig M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Koutnikova H., Campuzano V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND CHARACTERIZATION MEDLINE-97385237; Pubmed-9241270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frataxin, mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01491;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Mitochondrial.
PTM: PROCESSED BY MITOCHONDRIAL PROCESSING PEPTIDASE (MPP).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F01491; Frataxin_Cyay; 1. PR00904; FRATAXIN.
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207,
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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38, Last sequence update;
41, Last annotation updat
ndrial precursor (Fxn).
                                     PubMed=3871356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22924 MW;
       Maddon P.J.,
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); Pred. No. 44;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRATAXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MITOCHONDRION (BY SIMILARITY).
                                                                                                                                                                              Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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chain pu
       Chess
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                                                                                                                                                                              Vertebrata; Euteleostomi;
i; Hominidae; Homo.
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       <u>.</u>
                                                                                                                                                                                                                                                                                                                                                         precursor
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       Axel
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                                                                                                                                                                                                                                                                                                                                                             (T-lymphocyte
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RT CD8 at 2.64 resolution.";

RT CD8 at 2.64 resolution.";

CC -1- FUNCTION: IDENTIFIES CYTOTOXIC/SUPPRESSOR T-CELLS THAT INTERACT
CC WITH MIG CLASS I BEARING TARGETS. CD8 IS THOUGHT TO PLAY A ROLE IN
CC THE PROCESS OF T-CELL MEDIATED KILLING. CD8 ALPHA CHAINS BINDS TO
CC CLASS I MHC MOLECULES ALPHA 3 DOMAINS.
CC -1- SUBUNIT: IN GENERAL HETERODIMER OF AN ALPHA AND A BETA CHAIN
CC LINKED BY TWO DISULFIDE BONDS. CAN ALSO FORM HOMODIMERS.
C1- SUBURITI: IN GENERAL HETERODIMER OF AN ALPHA AND A BETA CHAIN
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC OF CD8 ALPHA TRANSCRIPTS INVOLVE EXCISION OF THE TRANSMEMBRANE OR
CC OF CD8 ALPHA TRANSCRIPTS INVOLVE EXCISION OF THE TRANSMEMBRANE OR
CC C-1- PTM: ALL OF THE FIVE MOST CARBOXYL-TERMINAL CYSTEINES ARE USED TO
CC WHILE THE FOUR AMINO-TERMINAL CYSTEINES AND HIGHER MULTIMERS,
CC WHILE THE FOUR AMINO-TERMINAL CYSTEINES ARE NOT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as non-profit institutions as non-profit institutions as not removed.

modified and this statement is not removed.

entities requires a license agreement (See | 100 pt | 
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SEQUENCE FROM N.A.
MEDLINE-85124610; PubMed-3918796;
MEDLINE-85124610; Sizer K.C., Vollmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trne isolation and sequence defining functional classes Cell 40:237-246(1985).
                                                                             EMBL;
EMBL;
EMBL;
PIR;
                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-89215302; PubMed-2496167;
Norment A.M., Lonberg N., Lacy E., Littman D.R.;
"Alternatively spliced mRNA encodes a secreted form alpha. Characterization of the human CD8 alpha gene.
J. Immunol. 142:3312-3319(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Structure and 2/T8).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90035142; pubMed-2509342;
Nakayama K.-I., Tokito S., Okumura K.,
"Structure and expression of the gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-86103103; PubMed-3936473;
Parnes J.R., Sizer K.C., Sukhatme V.P.,
"Structure of Leu-2/TB as deduced from t
Behring Inst. Mitt. 77:48-55(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunoglobulin and T cell receptor variable Cell 40:591-597(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenetics 30:393-397(1989).
BL; M26315; AAA79217.1; JUL; M26313; AAA79217.1; JUL; M26313; AAA79217.1; JUL; M12824; AAA61133.1; JUL; M12828; AAA61133.1; JUL; M12828; AAB64637.1; JUL; M27161; AAA59674.1; JUL; AAA694637.1; JUL; AAA69464637.1; JUL; AAA69464637.1; JUL; AAA69464637.1; JUL; AAA69464637.1; JUL; AAA69464637.1; JUL; AAA
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JOINED.
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encoding C
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                                                                                                                                                                                                                                                                                                                                                                                                               http://www.isb-sib.ch/announce/
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Best Local
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InterPro; IPR003596; I
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1
                                       Gregor J., David
                                                       SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch
Blattner F.R., Plunkett G. Glasner J.
Riley M., Collado-Vides J., Glasner J.
                                                                                                                                      p75682; Q9R2D5;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Hypothetical protein yagE.
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STRAIN-K12 / W311(
Takemoto K., Mori
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                        SEQUENCE
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PDB; 1CD8; 3
                             "The complete genome sequence Science 277:1453-1474(1997).
                                                                                                    NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunoglobulin domain;
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5; Conserv
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                                                  Davis N.W., Kirkpatrick
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ilarity 100.0%;
Conservative (
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183
204
        W3110;
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Murayama
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                                                                                                                  gamma subdivision;
                                                                                                                                                      sequence update)
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
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                                   Escherichia coli K-12.";
                                                  н. А.,
Kataoka
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A., Goeden M.A., R
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Mayhew G.F.,
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RANGE OF THE COLUMN TERMS 
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                                                                                                                                                                                                             Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Create 15-JUL-1998 (Rel. 36, Last s 16-OCT-2001 (Rel. 40, Last a Hypothetical protein MTH531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S. Mizono T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K.; "Systematic sequencing of the Escherica coli genome: analysis of tl 4.0 - 6.0 min (189,987 - 281,416bp) region."; Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanobacterium thermoautotrophicum.
Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-Delta H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      026631;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-98037514; PubMed-9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-187420;
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                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBI outstation - European Bioinformatics Institute. There are no restrictions on the by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                      SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
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Last annotation update)
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(See http://www.isb-sib.ch/announce,
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AC 024495; 024494; 022857;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hydroxyacylglutathione hydrolase, mitochondrial precursor (EC 3.1.2.6; GLyoxalase II) (Glx II).
GN GLX2-1 OR AT2643430 OR T1024.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
C Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
C C Spermatophyta; Brassicales; Brassicaceae. Arabidons; Rosidae;
C NCBT TRACHORDON, STANDARD, Arabidons; Rosidae;
C NCBT TRACHORDON, STANDARD, S
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                                                                                           SEQUENCE FROM N.A.

STRAIN-CV. COLUMBLA;

STRAIN-CV. COLUMBLA;

Shinozaki K., Davis R.W., Ecker J.R., Theologis A.:

Shinozaki K., Davis R.W., Ecker J.R., Theologis A.:

Shinozaki K., Davis R.W., Ecker J.R., Theologis A.:

SSP consortium (Salk/Stanford/PGEC).";

SSP consortium (Salk/Stanford/PGEC).";

SUBmitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: THIOLESTERASE THAT CATALYZES THE HYDROLYSIS OF S-

LACTOYL-GLUTAPHIONE TO FORM GLUTATHIONE AND D-LACTIC ACID.

-I- CATALYTIC ACTIVITY: (S)-(2-hydroxyacyl)glutathione + H(2)O

glutathione + a 2-hydroxy acid anion.

-I- COEACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20083487; PubMed-10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M., Venter T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant
[2]
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InterPro; IPR000205; NAD_binding.
Pfam; PF01225; Mur_ligase; 1.
Hypothetical protein; Ligase; ATP-binding; Complete proteome.
NP_BIND 112 118 ATP (POTENTIAL).
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MEDLINE-98009983; PubMed-9349270;
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                                                                                                                                                                                                                                                                                                                                                                                                                Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maiti M.K., Krishnasamy S., Owen H.A., Makaroff C
"Molecular characterization of glyoxalase II from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              "Sequence and thaliana.":
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                  PATHWAY: Glyoxal pathway.
SUBCELLULAR LOCATION: MITOCHONDRIAL.
SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Biol.
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Matches
STRAIN-Mistar;
STRAIN-89053978; PubMed-3263966;
Kido H., Yokogoshi Y., Katunuma N.;
Kido H., Yokogoshi Y., Katunuma Found
"Kunitz-type protease inhibitor found
"Kunitz-type protease inhibitor found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDINE-22182014; PubMed-1371936; MEDINE-22182014; PubMed-1371936; Lindqvist A., Bratt T., Altieri M., Kaster "Rat alpha 1-microglobulin: co-expression chain of inter-alpha-trypsin inhibitor."; Biochim. Biophys. Acta 1130:63-67(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          METAL
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMBP_RAT STANDARD; PRT; 349 AA.
Q64240; Q63336; P19603;
Q1-FEB-1991 (Rel. 17, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
Q1-VIN-2002 (Rel. 41, Last annotation update)
AMBP protein precursor (Contains: Alpha-1-microglobulin; 1
trypsin inhibitor light chain (ITI-LC) (Bikunin) (HI-30);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 141-195 FROM N.A. MEDLINE-87033744; PubMed-2429963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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                                                                                                                                                                                                 SEQUENCE OF 283-343,
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L; U90928; AAC49866.1; -.
L; AC002335; AAB64315.2; -.
L; AY091278; AAM14217.1; -.
L; AY063806; AAL36162.1; -.
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%; Pred. No. 67;
0; Mismatches
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D -> H (IN REF. 1; ARC49866).
MM; 2EDC21B4902419C5 CRC64;
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BY SIMILARITY. ALPHA-1-MICROGLOBULIN INTER-ALPHA-TRYPSIN II

INHIBITOR

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"MAST Cell protease inhibitor light chain.";

Inter-alpha-trypsin inhibitor light chain.";

RI J. Biol. Chem. 269:3818-3822(1994).

C. H. FUNCTION: ALPHA-I-MICROGLOBULIN OCCURS IN MANY PHYSIOLOGICAL FLUIDS INCLUDING PLASMA, URINE, AND CEREBROSPINAL FLUID. IT COMPLEXES NOT ONLY AS A FREE MONOMER BUT ALSO IN COMPLEXES WITH IGA COMPLEXES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; S87544; AAB2178
EMBL; J02600; AAA4159
PIR; A31890; A31890.
HSSP; P02760; 1BIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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Itoh H., Ide H.,
                                                                                                                                                                                                                  PROSITE; PS00280; BPTI_KUNITZ_1; PROSITE; PS50279; BPTI_KUNITZ_2; PROSITE; PS00213; LIPOCALIN; 1.
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ProDom; PD000222; Kunitz_BPT.
SMART; SM00131; KU; 2.
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InterPro; IPR002345; Lipocalin.
InterPro; IPR002566; Lipocal_cytFABP.
InterPro; IPR000566; Lipocal_cytFABP.
InterPro; IPR000561; Lipocalin; 1.
IPF000661; Lipocalin; 1.
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SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Synthesized in the liver and
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AAA41596.1; -.
                                                                                                                                                                                                        Plasma;
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                                                                                                                                                                                                                                                                                            2; Kunitz_BPTI; KU; 2.
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A COLE S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Ha A Cole S.T., Brosch R., Gas S., Barry C.E. III, Tekaia F., A Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., A Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holr A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L A Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., A Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
Tecomplete genome sequence.";
L Nature 393:537-544(1998).
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STRAIN-CDC 1551 / Oshkosh;

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,

Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., Hickey E.,

Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,

Fleischmann J., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg

Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg

Belcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein Rv0906 precursor.
RV0906 OR MT0929 OR MTCY31.34.
                           laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
-!- SIMILARITY: TO K.PNEUMONIAE ROMA.
                                                                                                                                                                     Bishai W.;
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BY SIMILARITY.
CHANGED (GLCNAC. . .) (POTENTIAL).
INHIBITORY SITE (P1) (CTYMOTRYPSIN, ELASTASE) (BY SIMILARITY).

INHIBITORY SITE (P1) (TRYPSIN) (BY SIMILARITY).

G -> A (IN REF. 2).
W -> L (IN REF. 3).
G -> N (IN REF. 3).
                                                                                                                                Mycobacterium
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E -> W (IN REF: 3).
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RESULT 13
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RX. MEDLINE-98044033; PubMed-9384377;
RX KUDSTF., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S.,
RA Borniss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borniss R., Bourschi C.V., Caldwell B., Cappano V., Carter N.M.,
RA Brouillet S., Bruschi C.V., Caldwell B., Cappano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kurita K., Lapidus A., Lardnois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
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Perego M., Hanstein C., Welsh K.,
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Bacteria; Firmicutes;
NCBI_TaxID=1423;
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Response regulator aspartate phosphatase B (E
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Interpro; IPR001440; TPR.
Pfam; PP00515; TPR; 4.
Hydrolase; Repeat; TPR repe
REPEAT 100 133
REPEAT 147 180
REPEAT 181 214
REPEAT 251 254
REPEAT 260 293
REPEAT 335 368
REPEAT 335 368
                                                                                                                                                                                                                                                                                        Y823_MYCLE
Q50049;
Q1-NOV-1997
Q1-NOV-1997
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A., Tosato V. Uchiyama S., Vandenbol M., Vannier F., Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Viari A., Wahyama S., Vandamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Voshida K., Voshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the Gram-positive bacterium Bacillu subtliis.";
                                                                                                                                                                                                                                                                                                                                                                 MYCLE
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.
                                                                                                                                                           SEQUENCE FROM N.A.
Smith D.R., Robison
                                                                                                                                                                                                                  Bacteria; Actinobacteria; Actinobac
Actinomycetales; Corynebacterineae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z81356; CAB03684.1;
EMBL; Z99122; CAB15686.1;
Subtilist; BG11965; rapB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                      MEDLINE-21128732; PubMed-11234002;
                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                               Submitted (APR-1995)
                                                                                                                                                                                                                                                                Hypothetical ML2186.
                                                                                                                                                                                                                                                 Mycobacterium leprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                          344 YFSHR
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                                                                                                                                                                                                                  Actinobacteria (class); Actinobacteridae; cterineae; Mycobacterium
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RESULT
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InterPro; IPR004652; NifR3_Y
InterPro; IPR001269; UPF0034; I.
Ffam; PF01207; UPF0034; I.
TICRFAMS; TIGR00737; nifR3_Y
PROSITE; PS01136; UPF0034; I.
Hypothetical protein; Comple
SEQUENCE 384 AA; 41100 MW
                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1993
01-JUL-1993
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             or send
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between
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the European Bioinformatics Institute.
use by non-profit institute.
                    use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                             general secretion pathway.";
MOI. Microbiol. 6:1351-1361(1992).
-!- FUNCTION: INVOLVED IN A GENERAL EXPORT OF PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  _AERHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                 "The Aeromonas hydrophila exeE gene, secretion and normal outer membrane
                                                                                                                        (Probable).
-!- SIMILARITY: BELONGS TO THE PULF/OUTF/EXEF/XPSF/XCPS FAMILY.
                                                                                                                                                                                                                                           Jiang B., Howard
                                                                                                                                                                                                                                                       MEDLINE=92349963; PubMed=1640836;
                                                                                                                                                                                                                                                                    STRAIN-Ah65;
                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                       General secretion
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Squares S., Stevens K.,
Barrell B.G.;
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EMBL; AL583924; CAC31141.1;
Leproma; ML2186; -
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n pathway protein F.
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K., Whitehead S., Woodwar
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DR PIR; S22670; S22670.

DR InterPro; IPR001902; Bact_secr_systII.

DR Pfam; PP00402; GSPII_F; 1.

DR PRINTS; PR00812; BCTERIALGSPF.

DR PROSITE; PS00804; T2SP_F; 1.

DR PROSITE; PS00804; T2SP_F; 1.

ET TRANSMEM 154 174 POTENTIAL.

FT TRANSMEM 206 226 POTENTIAL.

FT TRANSMEM 351 371 POTENTIAL.

SO SEQUENCE 388 AA; 43463 MW; D47B1628F977ED50 CRC64;

Query Match 33.3%; Score 5; DB 1; Length 388;

Best Local Similarity 100.0%; Pred. No. 77;

Matches 5; Conservative 0; Mismatches 0; Gaps 0;

Qy 10 AHLRS 14

Db 81 AHLRS 85

Search completed: November 27, 2002, 07:28:42

Job time: 6.44788 secs
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Result
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Q98a19 rhizobium 1
Q88ttu4 methanosarc
Q9bk13 paramecium
Q23610 arabidopsis
Q9cyt9 mus musculu
Q9h6c3 homo sapien
Q96f14 homo sapien
Q96f14 homo sapien
Q53668 mycobacteri
Q8tuc6 methanosarc
Q9kh39 mycobacteri
Q18509 caenorhabdi
Q50992 neisseria g
Q9vzK2 drosophila
Q24140 drosophila
Q24140 drosophila
Q9va02 drosophila
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| 33.3 | 186 5 Q | 33.3 176 | 33.3 | 33.3 169 5 Q | 33.3 168 | 33.3 152 2 (| 33.3 151 16 | 33.3 149 11 | 33.3 148 16 | 33.3 147 16 | 33.3 142 11 | 33.3 142 11 | 33.3 142 5 | 33.3 142 | 33.3 127 4 | 33.3 125 5 | 33.3 119 2 0 | 33.3 101 17 | 33.3 98 2 Q | 33.3 84 11 | 33.3 82 12 | 33.3 72 4 | 40.0 1037 5 0 | 40.0 943 16 | 40.0 943 2 0 | 40.0 942 16 | 40.0 924 16 | 40.0 |
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| 053749 mycobacteri | Q9vv69 drosophila | O54600 halobacteri | Q9nbf8 philodina r | Ф | Q9s4x5 escherichia | aeromonas | Q8yuv6 anabaena sp | _ | | Q9hzel pseudomonas | Q9d1e4 mus musculu | Q9d7m7 mus musculu | Q95we4 phlebotomus | Q20386 caenorhabdi | | Q95t72 drosophila | Q9rce0 x | Q9ya40 aeropyrum p | Q45250 brad | | OBqq17 camelpox vi | | o | | 085487 pseudomonas | w | В | Q8vuq0 pseudomonas |

ALIGNMENTS

| | 71 HAHLRS 76 | Db | |
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| | 9 HAHLRS 14 | Qy | |
| Gaps | Matches 6; Conservative 0; Mismatches 0; Indels 0; | Matc | |
| | 40.0%; Score 6; | Quer | |
| | SEQUENCE 212 AA; 23199 MW; 9C52FE82191E38A3 CKC54; | so s | |
| | ical protein; Complete proteome. | KW | |
| | | DR E | |
| | DNA Res. 7:331-338(2000). | RL [| |
| | | RT | |
| eriu | "Complete genome structure of the nitrogen-fixing symbiotic bacterium | | |
| | Yamada M., Tabata S.; | | |
| | ., Nakazaki N., Shimpo S. | | |
| | Kiyokawa C., | | |
| | Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., | | |
| s. | samizu E., Kato T., Sasamoto | | |
| | MEDLINE-21082930; PubMed-11214968; | | |
| | STRAIN=MAFF303099; | | |
| | SEQUENCE FROM N.A. | | |
| | [1] | RN | |
| | NCBI_TaxID=381; | | |
| | | | |
| | Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; | | |
| | Rhizobium loti (Mesorhizobium loti). | | |
| | MLL6193. | | |
| | Hypothetical protein mll6193. | DE E | |
| | (TrEMBLrel. 20, Last | | |
| | 01-OCT-2001 (TrEMBLrel. 18, Last sequence update) | | |
| | (TrEMBLrel. | | |
| | | | |
| | Q98A19 PRELIMINARY; PRT; 212 AA. | | |
| | | Q98A19 | |
| | | RESULT | |

RESULT 2

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RX MEDLINE-21929760; PubMed-11932238;

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

RL Linton L., McGwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McGwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

RA Linton L., McGwan P., McKernan K., Talama D.E., Grahame D.A., Guss A.M.,

RA Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

RA Hedderich R., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,

RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Metcalf W.W., Birren B.;

RA Metcalf W.Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Metcalf W.W., Birren B.;

RA Metcalf W.Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

RA Metcalf W.J., Birren B.;

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01-JUN-2002
01-JUN-2002
                                                                                                                          EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                            MEDLINE=21143069; PubMed=11230543;
Fast N.M., Kissinger J.C., Roos D.S., Keeling P.J.;
"Nuclear-Encoded, Plastid-Targeted Genes Suggest a S
Origin for Apicomplexan and Dinoflagellate Plastids.
HSSP; P56649; 1DSS.
InterPro; IPR000173; GAP_dhdrogenase.
Pfam; PF000044; gpdh; 1.
Pfam; PF02800; gpdh_C; 1.
PRINTS; PR00078; G3PDHDRGNASE.
                                                                                                                                                                                                                                                                       MO1. Biol. Evol. 18:418-426(2001).
-I- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paramecium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paramecium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9BK13;
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Archaea; Euryarchaeota; Methanococci;
Methanosarcinaceae; Methanosarcina.
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                                                                                                                                                                                                              - I - SIMILARITY: BELONGS TO THE GLYCERALDEHYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=5888;
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                                                                                                                                                   AF319452; AAK20731.1;
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                                                                                                                                                                                                                                                 3-PHOSPHO-D-GLYCEROYL PHOSPHATE
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REPLINE-98121113; PubMed-9461215;

Revan M., Bancroft I., Bent E., Love K., Goodman H., Dean C.,

RA Bergkamp R., Dirkse W., van Staveren M., Stiekema W., Drost L.,

RA Ridley P., Hudson S.A., Patel K., Murphy G., Piffaneill P., Wedler H.,

RA Ridley P., Hudson S.A., Patel K., Murphy G., Piffaneill P., Wedler H.,

RA Ridley P., Hudson S., Patel K., Murphy G., Piffaneill P., Wedler H.,

RA Ridley P., Hudson S.A., Patel K., Weitzenegger T., Pohl T. M., Erryn N.,

RA Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,

RA Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,

RA Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,

Ra Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S., Kotter P.,

Ra Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S.,

Ra Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S.,

Ra Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S.,

Ra Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Hempel S.,

Ra Auborg S., Gy I., Kreis M., Lao N., Kavanagh T., Douka A.,

Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B.,

Ra Voukelatou E., Milioni D., Hatzopoulos P., Piravandi E., Obermaier B.,

Ra Hilbert H., Duesterhoft A., Moores T., Jones J.D.G., Eneva T.,

Ra Berlian S., Marsorge W., Cooke R., Berger C.,

Ra Palme K., Benes V., Rechman S., Ansorge W., Cooke R., Berger C.,

Ra Arabidopsis thaliana.";

Raturo Solidas Sequence from chromosome 4 of

"Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of
                                                                                                                                                                                                                                                                                                                                   Query Match
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Q9CYT9;
01-JUN-2001
01-JUN-2001
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01-JAN-1998
01-JAN-1998
01-OCT-2000
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Glycolysis; NAD; Oxidoreductase.
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01-OCT-2000 (TrEMBLrel.
Hypothetical 40.0 kDa pi
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein. SEQUENCE 352 AA; 39986 MW;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
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(TrEMBLrel.
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                                                                                                      PRELIMINARY;
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; 32657 MW;
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Pred. No. 27;
0; Mismatches
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Pred. No.
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Eukaryota; Metazoa; 2810450N13Rik protein 2810450N13RIK.

Chordata;

Mus musculus

(Mouse)

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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesòle G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesòle G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesòle G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesòle G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesòle G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesòle G., Quackenbush J.,
RA Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesòle G., Quackenbush J.,
RA Schima I., Batah I., Batah G.,
RA Blake J., Bofdelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayushizaki Y., Stothenbach C., Seya T., Kawaji H., Kohtsuki S.,
RA Hayushizaki Y., Stothenbach C., Seya T., Kawaji H., Kohtsuki S.,
RA Hayushizaki Y., Stothenbach C., Seya T., Kawaji H., Kohtsuki S.,
Query Match
Best Local Similarity
                                                                                          Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK026055; BABL5337 1; -
InterPro; IPR000191; Fapy_DNA_glyco.
Pfam; PP01149; Fapy_DNA_glyco; 1.
ProDom; PD003680; Fapy_DNA_glyco; 1.
ProDom; PD003680; Fapy_DNA_glyco; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9H6C3;
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MGD; MGT.1920024; 2810450N13R1k.

InterPro; IPR000191; Fapy_DNA_glyco.

Pfam; PF01149; Fapy_DNA_glyco; 1.

ProDom; PD003680; Fapy_DNA_glyco; 1.

SEQUENCE 354 AA; 39604 MW; 863786B9E94A55CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA: FLJ22402 fis, clone HRC08117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409\!:\!685\!-\!690(2001).
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Local Similarity 100.0%;
nes 6; Conservative
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40.0%;
100.0%;
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   Score 6;
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   DB 4;
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01-MAR-2002
01-MAR-2002
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01-DEC-2001
01-JUN-2002
                                                                                                                                                                                                                                 MEDLINE=98295987; PubMed=9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; BC010876; AAH10876.1; -
InterPro; IPR000191; Fapy_DNA_glyco.
Pfam; PF01149; Fapy_DNA_glyco; 1.
ProDom; PD003680; Fapy_DNA_glyco; 1.
Hypothetical protein.
Hypothetical protein.
SEQUENCE 390 AA; 43712 MW; 2BB040D9EF68938
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 43.7 kDa protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrat.
Mammalia; Eutheria; Primates; Catarrhini; Hominid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis.

Mycobacterium tuberculosis.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Actinobacterineae; Mycobacteriaceae; 
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DeBoy R., Dodson
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n R., Gwinn M., Haft D., H
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STRAIN=C2A / ATCC 35395 / DSM 2834;

STRAIN=21929760; PubMed=11932238;

Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,

Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Guss A.M.,

Allen N., Naylor J., Stange-Thomann D.E., Grahame D.A., Guss A.M.,

Elmmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,

Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Fetry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,

Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

Metcalf W.W., Birren B.;

"The Grant Processing Proc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome. SEQUENCE 468 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The genome of Methanosarcina acetivorans and physiological diversity."; Genome Res. 12:532-542(2002).
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Archaea: Euryarchaeota; Methanococci;
Methanosarcinaceae; Methanosarcina.
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Delcher A., Utterback T., W
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Local Similarity 100.0%;
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J., Khouri H., Gill J., Mikula
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Neisseria gonorrhoeae.
Bacteria; Proteobacteria;
NCBI_TaxID=485;
                                                   01-NOV-1996 (TrEMBLrel. (01-NOV-1996 (TrEMBLrel. (01-JUN-2002 (TrEMBLrel. Suca protein (Fragment).
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SIKder D., Gupta S., Nagaraja V.;
SIKder D., Forta S., Nagaraja V.;
"A hypothetical protein.";
Submitted (MAY-2000) to the EMBL/
EMBL, AF27233; AAF76209.1; -.
                                                                                                                                                                                                                                                                                 investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z46241; CAA86317.1; -.
SEQUENCE 556 AA; 60548 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
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01-JAN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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Actinomycetales; Corynebacterineae; Mycobacteriaceae; MCBI_TaxID=1772;
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Mycobacterium smegmatis
Bacteria; Firmicutes; Ac
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Caenorhabditis.
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Last annotation update
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Pred. No
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                  Neisseriaceae;
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      RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.M.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.M.,
RA George R.A., Lewis S.E., Richards S., Champ Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Ghoris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA George R.A., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorreil J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Howland T.J., Wel M.-H., Ibeywam C.,
RA Harris N.L., Mattel B., McIntosh T.C., McIeod M.-P., McPherson D.,
RA Liu X., Mattel B., McIntosh T.C., McIeod M.-P., McPherson D.,
RA Mend Z.G., Milshina N.V., Mobarry C., Morris J., McShrefi A.,
RA Mend Z.G., Stapleton M., Stapsen H., Shih H.,
RA Shue B.C., Siden-Kinnos I., Simpson M., Skupski M.-P., Smith T.,
RA Rainer R. R., Sendar R.D.C., Stapleton M., Skipski M.-P., Smith T.,
RA Mand Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbah J.,
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Q9VZK2; Q9V144;
01-MAY-2000 (TrEMBLrel. 1:
01-MAY-2000 (TrEMBLrel. 1:
01-JUN-2002 (TrEMBLrel. 2:
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"The sucAB-lpd operon of Neisseria gonorrhoeae.";
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L36381; AAA96485.1;
Interpro; IPR001017; Dehydrogenase_E1.
Interpro; IPR004360; Gly_bleo_diox.
Interpro; IPR004360; Transketolase.
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Pfam; PF00903; Glyoxalase; 1.
Pfam; PF02779; transket_pyr; 1.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
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SCRT OR CG1130
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Best Local 9
Matches (
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InterPro; IPR00082; znf_C2H2.
Pfam; PF00096; zf-C2H2; 5.
PRINTS; PR00048; ZINCFINGER.
ProDom; PD000003; znf_C2H2; 1.
SMART; SN00355; znf_C2H2; 5.
                                                                                                                                             snail, promotes neuronal devo
Genes Dev. 9:2384-2398(1995)
-1- SUBCELLULAR LOCATION: NU
EMBL; U36477; AAA91035.1; -.
HSSP; P08048: 7ZNE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q24140
Q24140;
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InterPro; IPR000822; Znf_C2H2.
Pfam; PF000096; zff_C2H2; 5.
ProDom; PD000003; Znf_C2H2; 1.
SMART; SN00355; Znf_C2H2; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Full length Drosophila melanogaster cDNA sequence."; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AE003479; AAF47819.1; -. EMBL; AF145627; AAD38602.1; -. HSSP; P08048; 7ZNF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C., Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E., Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M., Houston K.A., Hummasti S.R., Kim E., Li P., Moshreii M., Pacleb J.M., Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T., Celniker S.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science [2]
                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
"The genome sequence of Drosophila melanogaster.";
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 6.
DNA-binding; Metal-binding; Nuclear protein; Zinc-finger.
SEQUENCE 664 AA; 72569 MW; 687F2DAABFE8968F CRC54;
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=96010286; PubMed=7557390;
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PROSITE; PS50157; ZÏNC_FĬNGER_C2H2_7; 3.
DNA-binding; Metal-binding; Zînc_finger
SEQUENCE 653 AA; 70774 MW; 15C27EE93F3FF45D
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                                                                                                                                 FlyBase; FBgn0004880;
                                                                                                                                                                                                                       Roark M., Sturtevant M.A., Emery J., "scratch, a pan-neural gene encoding
                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
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287:2185-2195(2000).
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b; Pred. No. 45;
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a zinc finger protein
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Golle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang, O., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,

RA Abril J.F., Agbyani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktarglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandarid D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottler D.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottler E.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Heusk J.,

RA Harris N.L., Harvey D., Helman T.J., Wel M.-H., Ibeyaan C.,

RA Harris N.L., Harvey D., Helman T.J., Wel M.-H., Ibeyaan C.,

RA Harris N.L., Harvey D., Helman T.J., Wel M.-H., Ibeyaan C.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D.L.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D.L.,

RA Harris N.L., Harvey D., Helman T.J., Wel M.-H., Ibeyaan C.,

RA Harris N.L., Harvey D., Helman T.J., Wel M.-H., Ibeyaan C.,

RA Harris N.L., Harvey D., Helman T.J., Wel M.-H., Ibeyaan C.,

RA Harris N.L., Harvey D., Helman T.J., Wel M.-H., Noshrefl A.,

RA Hostin D., Houston K.A., Nixon K., Nuxoris J., Noshrefl A.,

RA Harris N.L., Harvey D., Harris M., Welley D.M., Nelson D.L.,

RA Harris N., May M., Murphy B., Murphy L., Murpy D.M., Nelson D.L.,

RA Harris N., Pacle D., Noshrefl A.,

Ra Harris M., Molland R.C., Stapleton M., Skupski M.P., Smith T.,

Ra Harris M., Welson K.A., Nixon K., Nuxor K., Nuxor M., Nuxor M.,

Ra Harris M., Welson
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Best Local S
Matches 6
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01-MAY-2000
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                Pfam;
Pfam;
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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pr02779; transket nur.
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6; Conserv
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584 FSHRHA 589
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Search completed: November 27, 2002, 07:30:18 Job time: 11.4778 secs

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   US-09-893-615-1
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                                                                                                                                                                                                                                                                   SUMMARIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parameters:
                 Lipoteichoic acid
Sequence 15mer 2nd
Sequence 15mer2-12
Sequence 15mer2-13
Sequence 15mer2-10
Sequence 15mer2-17
Sequence 15mer2-17
Staphylococcus epi
Propionibacterium
                                                                                                                                                                                                        Description
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| 51 | ט כ | л . Э С | 4. | 4. | 48 | 48 | 46 | 41 | 36 | 26 | 21 | 18 | 18 | 18 | 18 | 18 | 18 | 18 | 14 | 14 | 14 | 943 | 932 | 932 | 912 | 901 | 899 | 653 | 413 | 390 | 365 | 350 | 252 | |
| 22 |) N |) i | اد | 22 | 22 | 22 | 22 | 23 | 20 | 21 | 23 | 23 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 20 | 22 | 22 | 22 | 22 | 20 | 20 | 22 | 20 | 20 | ŧ |
| AAU65435 | AMUUU / / L | AAU55771 | ARG46166 | AAM37285 | 7154 | AAM64327 | ABG07585 | ABB94072 | AAY49674 | AAB53840 | AAU88558 | ABG36782 | AAM02709 | AAM27417 | AAM14984 . | AAM54723 | ABB19398 | ABB33959 ' | AAM98008 | AAM98007 . | AAM98006 | AAU36241 | AAU37022 | AAW97701 | ABB52560 | ABB58224 | AAU33860 | ABB57870 | AAY34811 | AAY35923 | AAM25386 : | AAY35922 | AAY35921 | |
| Propionibacterium Propionibacterium | riopionibacterium | 10245001 | n abitaea | de #11 | bone m | n brain | 31p | secrete | sdp3.8 | 8 | Insulin/insulin-li | peptide | #1391 | e #1454 | ie #141 | brain ex | n #1397 | de #1465 | peptide | peptide | റ. | seudomonas ac | taphylococcus | Staphylococcus aur | Escherichia coli | rosophila mel | Staphylococcus aur | la | a pneu | ed humar | otein s | Extended human sec | Extended human sec | |

ALIGNMENTS

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New antibodies to lipoteichoic acid of gram positive bacteria to develop products for the diagnosis, prevention and treatment infections caused by gram positive bacteria
                                             WPI; 1999-095329/08.
                                                                Fischer GW,
                                                                                                                              16-JUN-1998;
                                                                                                                                                   23-DEC-1998
                                                                                                                                                                                          Staphylococcus
                                                                                                                                                                                                              Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria; immunoglobulin; phagocytosis; infection; epitope; peptide mimic; Mab 96-110.
                                                                                                                                                                                                                                                                                                   AAW94701;
                                                                                    (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED
                                                                                                         16-JUN-1997;
                                                                                                                                                                     W09857994-A2
                                                                                                                                                                                                                                                       Lipoteichoic acid epitope peptide mimic for Mab 96.110
                                                                                                                                                                                                                                                                              22-APR-1999
                                                                                                                                                                                                                                                                                                                     AAW94701 standard; peptide; 15
                                                                                                                                                                                                                                                                             (first entry)
                                                               Schuman RF,
                                                                                                         97US-0049871.
                                                                                                                                                                                          qs
                                                                                                                             98WO-US12402
                                                               Stinson JL,
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                                                               Wong
             used
of
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Claim 16;

Page 120;

150pp; English.

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RESULT 2
AAW94733
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           comprising at least part of a human immunoglobulin constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and killing of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacterial infections. The present sequence represents a specifically claimed lipoteichoic acid epitope peptide mimic that can be bound by the antibody of the invention (Mab 96-110).
         The invention relates to a monoclonal antibody (MAb) to lipoteichoic acid of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria.
                                                                                                                                 New antibodies to lipoteichoic acid of gram positive bacteria -
to develop products for the diagnosis, prevention and treatment
infections caused by gram positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention of gram posit:
                                                                                                                                                                                                                                        Fischer
                                                                                                                                                                                                                                                                                                16-JUN-1997;
                                                                                                                                                                                                                                                                                                                            16-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                         23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                      WO9857994-A2
                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15mer 2nd.12 resulting
                                                                                                                                                                                                                                                                   (JACK-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW94733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW94733 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin;
Mab 96-110; pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WRMYFSHRHAHLRSP
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                                                                                                                                                                                                                                                                  JACKSON FOUND ADVANCEMENT MILITARY MED.
                                                                                                      ر.
                                                                                                                                                                                             AAX05559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           positive bacteria,
                                                                                                    Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                             panning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       relates to a monoclonal
                                                                                                      8;
                                                                                                                                                                                                                                                                                                97US-0049871.
                                                                                                                                                                                                                                                                                                                            98WO-US12402
                                                                                                                                                                                                                                                                                                                                                                                                                                                           phagocytosis;
                                                                                                                                gram
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MAb; lipoteichoic acid; gram
ocytosis; infection; epitope;
                                                                                                                                                                                                                                      RF,
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                                                                                                    English.
                                                                                                                                positive
                                                                                                                                                                                                                                      Stinson JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          where the MAb is a chimeric immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from library panning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibody (MAb) to lipoteichoic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 20;
.8e-10;
enhance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 15;
phagocytosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       positive; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     experiments
                                                                                                                                                                                                                                                                                                                                                                                                                                                           mimic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                               of
of
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RESULT 3
AAW94714
ID AAW9
XX AAW94714
AC AAW9
XX AAW9
AC AAW9
XX Seq
XX Seq
XX WA
XX Mab
XX M
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                                                                                                                                                                                                                                                                                                                                                                                                      New antibodies to lipoteichoic acid of gram positive bacteria to develop products for the diagnosis, prevention and treatmen infections caused by gram positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-095329/08
N-PSDB; AAX05540.
                                                                                                                                                                                                                                                                                                                                                      Example 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fischer GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody; MAb; lipoteichoic acid; gram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15mer2-12/0 resulting from 15mer library panning experiment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin; phagocytosis;
wab 96-110; panning.
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15; Conserv
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Pred. No.
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2.2e-10;
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The invention relates to a monoclonal antibody (MAh) to lipoteichoic acid of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and killing of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DAA of the variable region of anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating

or preventing

infections

caused by

gram

positive bacteria.

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RESULT 4
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region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and killing of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacterial infections. Sequences AAM94705-22 represent sequences resulting from a 15mer library panning second experiment. Three series of panning experiments were conducted to identify peptide sequences to which antibody of the invention (Mab 96-110) bound strongly. The translated sequences provide lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
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                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a monoclonal antibody (MAb) to lipoteichoic acid of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin constant region and at least part of a non-human immunoglobulin variable
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DB; AAX05541.
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2.2e-10;
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RESULT 5
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                           The invention relates to a monoclonal antibody (MAb) to lipoteichoic CC acid of gram positive bacteria, where the MAb is a chimeric constant region and at least part of a human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable constant properties and constant properties and the part of a non-human immunoglobulin variable constant properties and constant properties and the placeton of the variable region of the cantibodies or peptides (encoded by a DNA of the variable region of corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for the diagnosis of gram positive bacteria infections.

CC sequences AAW94705-22 represent sequences resulting from a 15mer library conditied to identify peptide sequences of panning experiments were conducted to identify peptide sequences to which antibody of the converted conducted to identify peptide sequences to which antibody of the panning can be used for the diagnosis of gram positive bacterial infections.
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Mab 96-110; panning.
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D; Mismatches
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RESULT 6
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                                                                                                                                      The invention relates to a monoclonal antibody (MAb) to lipoteichoic acid of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin constant region and at least part of a non-human immunoglobulin variable cregion having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and ckilling of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacterial infections.

Sequences AAW94705-22 represent sequences resulting from a 15mer library conducted to identify peptide sequences of panning experiments were invention (Mab 96-110) bound strongly. The translated sequences provide lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
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Matches 15
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0; Mismatches
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                                                                    DB 20;
2.2e-10;
                                                                                  Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             positive;
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ABP38325
ID ABP3
XX
AC ABP3

ABP38325 standard;

Protein;

76

RESULT

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RESULT 7
AAW94719
ID AAW9
AAW94719
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В
                                                                                                                                                                                                                                                                                                        The invention relates to a monoclonal antibody (MAD) to lipoteichoic acid of gram positive bacteria, where the MAD is a chimeric immunoglobulin comprising at least part of a human immunoglobulin constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance plagocytosis and ckilling of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody or characterised by amino acids or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacterial infections.

Sequences AAW94705-22 represent sequences resulting from a 15mer library panning second experiment. Three series of panning experiments were conducted to identify peptide sequences to which untibody of the invention (Mab 96-110) bound strongly. The translated sequences provide lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
                                                                                                                             Matches
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Mab 96-110; panning.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infections caused by gram positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibodies to lipoteichoic acid of gram positive bacteria - to develop products for the diagnosis, prevention and treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15mer2-17/0 resulting from 15mer library panning experiment.
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   WRMYFSHRHAHLRSP
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15; Conserv
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Pred. No.
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RESULT 9
AAU48733
ID AAU4
XX AAU4
AC AAU4
XX YAVA
AC AAU4
XX YAVA
DT 27-F
XX SAPI
KW SAPI
XX SAPI
XX WO20
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Matches
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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                           SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; EIISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                        27-FEB-2002
                                                                                                                                                                                                  AAU48733
                                                                                                                                                                                                                            AAU48733 standard;
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID 3170; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid encoding a Staphylococcus epion polypeptide, useful for diagnosing and treating bacterial
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08-NOV-1997;
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                           WO200181581-A2
                                                    Propionibacterium
                                                                                                                                               Propionibacterium acnes
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6; Conser
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gene therapy.
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97US-064964P
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                                                                                                                                                                                                                            Protein;
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1 sequences
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Homo myasthenia autoimmune

gravis. disorder;

rheumatoid

autoimmune

thyroiditis

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RESULT 10
ABP06906
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02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the print specification, but was obtained in electronic format directly from WI specification, but was obtained in electronic format directly from WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Propionibacterium acnes vaccinating against and treating acne vulgaris .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skeiky YAW, Persing DH, L'maisonneuve J, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention
                                                            Human; open reading frame; ORFX; gene therapy; canror; cirrhosis; hyperproliferative disorder; psoriasis; benign tunk, ir; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAU39105-AAU68017 represent Propionibactarium acnes immunogenic polypeptides. The proteins and their associated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1;
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                                                                                                                                                                                  Human ORFX
                                                                                                                                                                                                                   24 - JUN - 2002
                                                                                                                                                                                                                                                  ABP06906
                                                                                                                                                                                                                                                                                   ABP06906 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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2000US-208841P.
2000US-216747P.
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                                                                                                                                                                                sequence
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100.0%; Pred. No.
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, Carter D
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RESULT 11
AAUG6845
ID AAUG6
XX AAG6
XX AAG6
XX 13-FE
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DE Propi
XX SAPHC
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                               treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polynucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic lupus erythematosus, hypertension, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune inflammatory eye disease. ORFX proteins are also disease and autoimmune inflammatory eye disease. ORFX proteins are also
SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human polypeptides and polynucleotides useful for diagnosing preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders -
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29-AUG-2000; 2000US-228716P.
                                                                                   13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                           N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                 useful for treating burns, incisions, ulcers, for treating osteon bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibros; reperfusion injury in various tissues and conditions resulting fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (referred to as open reading frame, ORFX, where X is 1-11491 (see Tablin the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID 13794; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shimkets RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-MAY-2001; 2001WO-US10836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-2001.
                                                      Propionibacterium acnes immunogenic protein #27741.
                                                                                                             AAU66845
                                                                                                                                        AAU66845 standard;
                                                                                                                                                                                                                                                                                                                                                                                        systemic cytokine damage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200192523-A2
                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                            49
                                                                                                                                                                                                                                     5 FSHRHA 10
                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes substantially purified human
                                                                                                                                                                                                            FSHRHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2002-106308/14.
                                                                                                                                                                                                                                                                Similarity 6; Conserv
                                                                                                                                                                                                                                                                                                                     132
                                                                                                                                                                                                            54
                                                                                                                                                                                                                                                                Conservative
                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Leach MD
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                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                              40.0%;
100.0%;
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                                                                                                                                        238
                                                                                                                                                                                                                                                                              Score 6;
Pred. No.
                                                                                                                                                                                                                                                                Mismatches
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17;
                                                                                                                                                                                                                                                                                         23;
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                                                                                                                                                                                                                                                                                         Length 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                  fibrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                          osteoporosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins
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 AAY35921
ID AAY
XX
AC AAY
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AC AAY
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DT 13-
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KW Sec
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KW haew
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RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pustulosis, hypertosis and osteomyelitis), uveits and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunoscrbant accase presence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-2000;
02-JUN-2000;
07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                            enzyme linked immunosorbent assay (ELISA).
Note: The sequence data for this patent did not form specification, but was obtained in electronic format
AAY35921;
                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides. The proteins and their associated DNA sequences are the treatment, prevention and diagnosis of medical conditions cape. P. acnes. The disorders include SAPHO syndrome (synovitis, acne.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequences AAU39105-AAU68017 represent Propionibacterium acnes polypeptides. The proteins and their associated DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; SEQ ID No 28040; 1069pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Propionibacterium acnes vaccinating against and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-616774/71.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dermatological; osteopathic; neuroprotectant.
                                           AAY35921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             treating acne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP
                                                                                                                                                                   187 AHLRSP
                                                                                                                                                                                                            10 AHLRSP
                                                                                                                                                                                                                                                           Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences
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                                              standard;
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2000US-208841P.
2000US-216747P.
                                                                                                                                                                                                                                                             Conservative
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                                              Protein;
                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptides and nucleic acids useful for diagnosing infections, especially useful
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                                                                                                                                                                                                                                                                                      .0%;
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                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                      Score 6;
Pred. No.
                                                                                                                                                                                                                                                                Mismatches
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29;
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are used in
                                                                                                                                                                                                                                                             Gaps
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Secreted protein; human; cytokine; cellular proliferation; cellular differentiation; immune system regulator; anti-in

immune system regulator;
tissue growth regulator;

tumour

inhibitor cell movement;

anti-inflammatory;

haematopoiesis

regulator;

13-SEP-1999

(first entry)

Extended

human secreted protein sequence,

SEQ ID

o .

170

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RESULT 13
AAY35922
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                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoiesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to identify individuals or the activity assess resulting from abnormal expression of the genes corresponding to the extended cDNAs. They are also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat.genetic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-AUG-1998;
17-DEC-1997;
09-FEB-1998;
                                                                                         Secreted protein; human; cytokine; cellular proliferation; cell movement; cellular differentiation; immune system regulator; anti-inflammatory; haematopotesis regulator; tissue growth regulator; tumour inhibitor; reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy; genetic disease.
                                                   Ното
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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24-JUN-1999
                          WO9931236-A2
                                                                            genetic
                                                                                        reproductive hormone regulator;
                                                                                                                                                              Extended
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                                                                                                                                                                                                                 AAY35922;
                                                                                                                                                                                                                                        AAY35922 standard; Protein; 350
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEST ) GENSET
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                                                                                                                                                                                                                                                                                                            95
                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                     8
                                                  sapiens
                                                                                                                                                                                                                                                                                                            RHAHLR 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9; Page 201-202; 516pp;
                                                                                                                                                                                                                                                                                                                                                              Similarity 6; Conserv
                                                                              disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAX97605
                                                                                                                                                           human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                    252
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                     (first entry)
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97US-0069957.
98US-0074121.
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                                                                                                                                                                                                                                                                                                                                                       40.0%; Pr
100.0%; Pr
0;
                                                                                                                                                           protein sequence,
                                                                                                                                                                                                                                                                                                                                                                           Score 6; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dumas Milne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                              DB 2
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                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                           SEQ
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                                                                                                                                                            NO.
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RESULT 14
AAM25386
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Best Local
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17-DEC-1997;
09-FEB-1998;
13-APR-1998;
                                                                                        Human; cancer; ulcer; HIV infection; human immunodéficiency virus; antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; anti-HIV; fungicide; antimutagen; cardiavascular; antianaemic; anaemia; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiahetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis; cardiac dysfunction; neuropathology; cardiac anaph; laxis; autoimmunity; genetic disease; haematopoietic disorder; platelet; disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoiesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or have chemotactic/chemokinetic, receptor/ligand, unti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in flagnostic procedures to identify individuals or independent of procedures to identify individuals or independent of the genes corresponding to the extended cDNAs. They are also useful for constructing a high resolution map of the human chromosomes. They can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 203-204; 516pp; English.
                                                                                                                                                                                                                                                                                                                          Human protein sequence SEQ ID NO:901.
                                                                                                                                                                                                                                                                                                                                                                                                                           AAM25386 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is encoded by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human secreted proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1998;
                                                           neurological
                                                                              Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 40.0%;
Similarity 100.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used
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97US-0069957.
98US-0074121.
98US-0081563.
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                                                                               Parkinson's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      therapy to control or treat genetic diseases
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      extended human secreted protein coding
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42;
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WO200153455-A2 Homo sapiens

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RESULT 15
AAY35923
ID AAY3
XX AAY
AC AAY
XX DE EXT
XX Sec
KW Cel.
KW hael
KW rep
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21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production. The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic
                                                                                 Secreted protein; human; cytokine; cellular proliferation; cell movemwiscellular differentiation; immune system regulator; anti-inflammatory; haematopolesis regulator; tissue growth regulator; tumour inhibitor; reproductive hormone regulator; chemotaxis; chemokinesis; gene therap;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
                                   Homo sapiens
                                                                     genetic
                                                                                                                                                                       Extended human secreted protein sequence, SEQ
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Alzheimer's disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH99166 to AAH99904 encode the human proteins given in AAM2522: AAM25963. The proteins can have activities based on the tissues
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                                                                                                                                                                                                                                                                            AAY35923 standard; Protein;
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; 2000US-0488725.
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17-DEC-1997;
09-FEB-1998;
13-APR-1998;
                                                                                                                                                                                                                                                                                                                                                        This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoies is regulators, tissue growth regulators, regulators of reproductive hormones or cell movement or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to identify the genes corresponding to the extended cDNAs. They are also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases.
                                                                                                                                                                                                                                                                                           Sequence
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98US-0074121.
98US-0081563.
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Search completed: November Job time: 9.32819 secs time : 27, 2002, 07:27:55

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WO9931236-A2

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US-09-134-001C-3950
US-08-372-552-1
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US-08-65-299-1
US-08-65-299-7
US-08-75-51-512-8
US-08-75-626A-50
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| | US-08-999-774A-2 | US-08-878-474-5 | US-09-430-323-54 | US-09-430-323-8 . | US-08-854-050-54 | US-08-854-050-8 | US-08-974-549A-221 | US-08-851-843A-54 | US-08-851-843A-8 | US-08-974-549A-190 | -443 | US-08-402-253-2 | US-08-628-747-2 | US-08-438-862-2 | US-08-438-864-2 | US-08-438-863-2 | -08- | 7-404-604-60 |
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ALIGNMENTS

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RESULT 2
US-08-887-534A-45
US-08-887-534A-45
; Sequence 45, Application US/08887534A
; Patent No. 6455323
; GENERAL INFORMATION:
APPLICANT: Holden, David W.
TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATURIALS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3170, Application US/09134001C
PATENT NO. 6380370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AC
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOST
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3170
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SEQ ID NO 3170
LENGTH: 76
                                    ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                US-09-567-995-41
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APPLICANT: Martelange, Val, rie
APPLICANT: De Smet, Charles
APPLICANT: De Smet, Charles
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEI
FILE REFERENCE: L0461/7054
CURRENT APPLICATION NUMBER: US/09/567,995
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/183,706
                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens
US-09-183-706-41
                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/183,706
CURRENT FILING DATE: 1998-10-30
EARLIER APPLICATION NUMBER: 09/122,989
EARLIER FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 41
                                                                                                                                                 Sequence 41, Application US/09567995 Patent No. 6303756
                                                                                                                                GENERAL INFORMATION:
                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR FILE REFERENCE: L0461/7054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 45:
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ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION UNMBER: 33,547
REFERENCE/DOCKET NUMBER: 2834
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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nes 6; Conserv
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nes 5; Conservat
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                                                             Boon-Falleur, Thierry
/ENTION: TUMOR ASSOCIATED NUCLEIC ACIDS AND USES THEREFOR
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                                                                                                                                                                                                                                                                                                        Conservative
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100.0%; Pr
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US-08-338-530A-6
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                                                                                                                  US-08-338-530A-6
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NUMBER OF SEQ ID NOS:
SEQ ID NO 41
LENGTH: 36
                                                       Best Local Similarity Matches 5; Conserv
                                                                                    Query Match
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCI
FILING DATE: 28-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 63 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELLEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: CRABB, Brendan S.
APPLICANT: STUDDERT, Michael J.
TITLE OR TUVENTION: EQUINE HERPESVIRUS GLYCOPROTEINS
43 AHLRS
                           10 AHLRS 14
                                                                                                                                TOPOLOGY: li
                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                         NAME: BENT, Stephen A REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 25-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20007-5109
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                                                                                                                                                                                                                     904136
                                                                                                                                                                          63 amino acids
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47
                                                         Conservative
                                                                                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                       UMBER: US/08/338,530A
25-JAN-1995
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100.0%; Pred. No.
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Pred. No
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0. 18;
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US-09-267-384-6 ; Sequence 6, Application US/09267384

RESULT

Patent No.

INFORMATION:

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ORGANISM: Staphylococcus epidermidis US-09-134-001C-3950
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Best Local S
Matches 5
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FILING DATE: 28-MAIL.
FILING DATE: 28-MAIL.
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REPERENCE/DOCKET NUMBER: 40268/120/CSMB
TELECOMMUNICATION INFORMATION:
"TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                              Sequence 3950, App
Patent No. 6380370
                                                                                                         CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 NUMBER OF SEQ ID NOS: 5674
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                 D ID NO 3950
LENGTH: 70
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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APPLICANT: STUDDERT, Michael J.

APPLICANT OF TAVENTION: EQUINE HERPESVIRUS GLYCOPROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 63 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
nes 5; Conservative
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linear
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100.08; P.
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100.0%; Pred. No. 30,
Live 0; Mismatches
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US-08-875-309-1

Sequence 1, Application US/08875309 Patent No. 6180600 GENERAL INFORMATION:

APPLICANT:

Jameson, Bradford A. Choksi, Swati

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RESULT 9
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Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                           TELEFAX: 215-568-3439 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Korngold, Robert
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM
                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                         102 MYFSH 106
                                                                                                                                                                                             LENGTH: 114 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
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                                                                                               Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
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                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                   3 MYFSH 7
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5. 5645837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19103
                                                                                                                                                                                                                                                                                                                               DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          One Liberty Place, 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                               33.3%; Scilarity 100.0%; F
Conservative 0;
                                                                                                                                                                                                                                                          215-568-3439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Woodcock Washburn Kurtz Mackiewicz
No. 5645837ris
                                                                                                                                                                                                                                                                         215-568-3100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/372,952
                                                                                               B; Score 5; DB 1
B; Pred. No. 50;
O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                     TJU-1440
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33;
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                                                                                                        50;
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                                                                                                                           Length 114;
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В
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                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9600310 GENERAL INFORMATION:
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Best Local 9
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SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
                                                                                                                                                                                             APPLICANT: Jameson, E
APPLICANT: Choksi, Sw
APPLICANT: Korngoli
APPLICANT: Huang, 21w
TITLE OF INVENTION: C
NUMBER OF SEQUENCES:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: DELLICA, MARK
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: DeLuca, Mark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,952
FILING DATE: 17-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-NOV-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00310
FILING DATE: 17-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                 STREET: Une __
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: Z15-568-3439
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                                                                                 COUNTRY: UZIP: 19103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                             ADDRESSEE: Woodcock Washburn Kurtz Macklewicz & Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                            INVENTION: CD8 Antagonists
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                                                                                                  USA
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                                                                                                                                                                                                                                            Korngold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                33.3%; 5cc
100.0%; Pr
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                                                                                                                                                                                                                                               Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 5; DB 4; Pred. No. 50; 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4;
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Query Match
Best Local Similarity
Thehes 5; Conserve
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US-08-815-175-3
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acid
                                                           ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                            STREET: 317.
CITY: Palo Alto
CMATE: CA
                                                                                                                                                             APPLICATION NUMBER: US/08/81
FILING DATE: Filed Herewith
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
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APPLICATION NUMBER: US 0
FILING DATE: 17-JAN-1995
                                TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hillman, Jennifer L. APPLICANT: Goli, Surya K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                            TELEPHONE:
                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                            94304
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                415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                           IBM Compatible
                                                                                                                                                                                                                                                                                          Diskette
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOVEL PROLINE-RICH ACIDIC PROTEIN
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                                                                            36,749
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                                                                PF-0225 US
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SEQUENCE CHARACTERISTICS:

ENGTH:

149 amino acids

STRANDEDNESS

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RESULT 13
US-08-762-500-1
; Sequence 1, Application US/08762500
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                                                                                                                                                                                 US-08-665-259-1
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Best Local Similarity 100.
                                                                                                                             Matches
                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           TELEPHONE: (508) 872-8400
TELEFAX: (508) 872-5415
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (508) 872-8400
                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                          10 AHLRS 14
|||||
19 AHLRS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: One Mount
CITY: Framingham
                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not
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                                                                                                                            Local Similarity es 5; Conserv
                                                                                                                                                                                                                                                                                                                                           NAME: Dugan, Deborah A. REGISTRATION NUMBER: 37,315
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/665,259 FILING DATE: 17-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                  ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             One Mountain Road
                                                                                                                                                                                                                                               179 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dackowski, William R.
Van Raay, Terence J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Connors, Timothy D.
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                                                                                                                                                                                              peptide
                                                                                                                                                                                                                       not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Timothy
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imothy C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Katherine W.
NOVEL HUMAN CHROMOSOME 16 GENES,
COMPOSITIONS, METHODS OF MAKING AND USING SAME
                                                                                                                                          33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.3%;
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                                                                                                                                           Pred.
                                                                                                                            Mismatches
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                                                                                                                                           NO.
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                                                                                                                                                       DB 3;
                                                                                                                                                       Length 179;
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SOFTWARE: Pa
SEQ ID NO 110
LENGTH: 200
                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local 9
                                                                                                                                                                                            Sequence 110, Appl Patent No. 6428967
                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 6030806
                                                 CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 132
                                                                                                      APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (508) 872-5415 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: DUGAN, DEBOTAH A.
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/665,259
FILING DATE: 17-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                   19 AHLRS 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/762,500 FILING DATE: 09-DEC-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Framingham
                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 5; Conserv
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                                  PatentIn Ver. 2.1
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United States of America
                                                                                                                                                                                                             Application US/09562737
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Pred. No.
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5. 75;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: TYPE: peptide
US-07-940-605A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT; ORGANISM: Artificial Sequence; FEATURE: OTHER INFORMATION: Description of Artificial Sequence; OTHER INFORMATION: Sequence US-09-562-737-110
Search completed: November 27, 2002, 07:32:08 Job time : 4.08494~{\rm secs}
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US-07-940-605A-12
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                                                                                                                                                       Query Match 33.3%; Score 5; DB Best Local Similarity 100.0%; Pred. No. 96 Matches 5; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/07/940,605A
FILING DATE: 04-SEP-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ARUFFO, ALEJANDRO
APPLICANT: HOLLENBAUGH, DIANE
APPLICANT: LEDBETTER, JEFFREY A.
TITLE OF INVENTION: SOLUBLE LIGANDS FOR CD40
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 SHRHA 10
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130 SHRHA 134
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NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 56:
                                                                             123 MYFSH 127
                                                                                                                    3 MYFSH 7
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Perfect score:
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15
    November 27, 2002, 07:28:06; Search time 1.38996 Seconds (without alignments) 171.849 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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  US-09-893-615-1
US-09-893-615-27
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US-09-893-615-65
US-09-893-615-65
US-09-815-242-12615
US-09-815-242-11834
US-09-815-242-11834
US-09-8164-761-34696
US-09-925-299-1380
US-09-926-299-1380
US-09-926-299-1380
US-09-926-299-1380
US-09-926-299-1380
US-09-926-299-1380
US-09-926-299-1380
US-09-926-299-1380
US-09-940-288A-10
US-09-940-192-21
US-09-815-242-5110
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29, Appl
33, Appl
35, Appl
65, Appl
65, Appl
5356, Ap
11834, A
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3, Appli
5110, Ap
6, Appli
                                                             10, Appl
21, Appl
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US-09-893-615-1
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Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wong, Hing
Stinson, Jeffrey L.
STITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID
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Fischer, Gerald W. Schuman, Richard F.

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| 356 | 0 US-09-922-261-358 | 8 10 | יַ | 26.7 | . ح | U |
|-------------------|----------------------|------|------|-----------|-----|----------|
| Sequence 17, Appl | us-10-080-100-17 | 9 | | 26.7 | .2 | 4 |
| Sequence 54, Appl | US-10-080-100-54 | 7 9 | | 26.7 | 4 | ω |
| | SU | 1 12 | 147 | 33.3 | ۍ | 2 |
| Sequence 5, Appl1 | | | 147 | 33.3 | տ | 1 |
| | 0 US-09-925-301-1394 | | 128 | 33.3 | ហ | 0 |
| Sequence 6, Appli | SD | | 1275 | | տ | 9 |
| Sequence 151, App | 0 US-09-984-198-151 | 8 10 | 103 | 33.3 | տ | 8 |
| Sequence 151, App | 0 US-09-752-639-151 | | 103 | | Ç | 7 |
| Sequence 7, Appli | 0 US-09-897-056-7 | | 1025 | | տ | σ |
| | | | 1017 | | 5 | u |
| | | 9 10 | 979 | 33.3 | 5 | 4 |
| • | 0 US-09-949-192-19 | 7 10 | 93 | 33.3 | 5 | ω |
| Sequence 54, Appl | US-09-843-676-54 | 9 | 87 | 33.3 | U. | N |
| Sequence 8, Appli | US-09-843-676-8 | 2 9 | 87 | 33.3 | υ | _ |
| Sequence 84, Appl | | 0 12 | 50 | | տ | 0 |
| Sequence 4, Appli | 0 US-09-916-109-4 | | 48 | | Ç, | 9 |
| Sequence 168, App | c | | 46 | | 5 | 80 |
| Sequence 5, Appli | 0 US-09-870-130-5 | 7 10 | 467 | 33.3 | ហ | 7 |
| Sequence 584, App | 0 US-09-925-297-584 | | 46 | 33.3 | տ | 0 |
| Sequence 2, Appli | US-08-812-393A-2 | | 44 | 33.3 | თ | 5 |
| - | 2 US-10-052-586-570 | | 42 | 33. 3 | ഗ | 4 |
| Sequence 28, Appl | | | 41 | 33 . 3 | տ | w |
| Sequence 6, Appli | 0 US-09-916-109-6 | | 387 | 33.3 | տ | 2 |
| Sequence 26, Appl | 0 US-09-740-288A-26 | | 37 | 33.3 | ر. | _ |
| Sequence 12, Appl | S | 1 10 | 37 | 33.3 | տ | 0 |

ALIGNMENTS

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COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3/
CURRENT APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
FENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DUNNER, LLP
STREET: 1300 I Street,
CITY: Washington
TYPE: amino acid
STRANDEDNESS: <U
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TOPOLOGY: Innear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID
US-09-893-615-27
              RESULT 3
US-09-903-615-29
Sequence 29, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
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US-09-893-615-27
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                                                                                                                                                                                     Matches
                                                                                                                                                                                                    Query Match
Best Local Similarity
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Best Local 9
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TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                       1 WRMYFSHRHAHLRSP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HI
DUNNER, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Conservative
                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                           LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1300 I Street, NW
                                                                                                                                                                                     Conservative
   Fischer, Gerald W.
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Pred. No.
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Pred. No.
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; TOPOLOGY: linear;
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-893-615-29
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Best Local Similarity
"~+~hes 15; Conserve
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US-09-893-615-33
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-44000
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

COMPUTER: TOM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                            NUMBER OF SEQUENCES: 89 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                       Wong, Hing
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL
CHIMERIC ANTIBODIES SPECIFIC FOR L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC
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                                                                                    STATE: DC
COUNTRY: U
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                                                                                                                     CITY: Washington
                                                                                                                                         STREET: 1300 I Street,
                                                                                                                                                                        ADDRESSEE: FINNEGAN,
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Pred. No.
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TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-893-615-33
TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-893-615-35
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US-09-893-615-35
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Best Local Similarity
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REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                    INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT 6
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Wong, Hing
Stinson, Jeffrey L.
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
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                                                                                                                                                                 TELEPAN: 202-408-4400
                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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cl Similarity 100.0%;
15; Conservative (
                                                                                       TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                                                                                      NAME: Einaudi, Carol P. REGISTRATION NUMBER: 32,220
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Pred. No. 1.9e-10;
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RESULT 6
US-09-893-615-37
Sequence 37, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
RESULT 7
US-09-893-615-65
; Sequence 65, Application US/09893615
; Patent NO. US20020082395A1
; GENERAL INFORMATION:
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Best Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/893,615

FILING DATE: 29-Jun-2001

ATTORNEY/AGENT INFORMATION:

NAME: Einaudi, Carol P.

REGISTRATION NUMBER: 32,220

REFERENCE/DOCKET NUMBER: 04995.0041-00000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-408-4400

INFORMATION FOR SEQ ID NO: 37:

OPERATION FOR SEQ ID NO: 37:
                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                     Matches
                                                                                                                   3 WRMYFSHRHAHLRSP 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Wong, Hing
Wong, Jeffrey L.
Stinson, Jeffrey L.
STITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF
CHIMERIC ANCIERIA
                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                 TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: DC
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Pred. No. 1.9e-1
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Pred. No. 1.9e-10
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APPLICANT: Fischer, Gerald W. Schuman, Richard F.

Wong, Hing Stinson, Je

Jeffrey L.

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APPLICANT: Travick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: ITENTIFICATION OF ESSENTIAL GENES IN TITLE OF INVENTION: Prokafyotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid;
TOPOLOGY: linear;
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-893-615-65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5356, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: EINAUGI, CATOI P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELEPHONE: 202-408-4000
TELEPHONE: 202-408-400
TELEPAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WRMYFSHRHAHLRSP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/893,615 FILING DATE: 29-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1300 I Street, NW
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                                                                                                                                                                                                                                                                                                                                                                                                    Wall, Daniel
Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohlsen, Kari L.
Zyskind, Judith W.
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60/253,625
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Pred. No.
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1.9e-10;
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Query Match
Best Local Similarity
6; Conserv
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SEQ ID NO 12615
LENGTH: 932
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5356
LENGTH: 899
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/257,931
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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621 FSHRHA
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                               5 FSHRHA 10
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Zyskind, Judith W.
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Camamoto, Robert T.
626
                                                                     Conservative
                                                                                                                                                                                                                              for Windows Version
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                                                                                   40.0%;
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                                                                     0,
                                                                   Score 6; DB 10;
Pred. No. 20;
0; Mismatches
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o. 19;
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RESULT 10 US-09-815-242-11834 ; Sequence 11834, Application US/09815242

PPLICANT: Haselbeck,

Robert

Ohlsen, Kari L. Zyskind, Judith W.

Daniel

INFORMATION

US20020061569A1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34696, Application US/09864761 Patent No. US20020048763A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR PILING DATE: 2000-05-23 PRIOR PILING DATE: 2000-05-23 PRIOR FILING DATE: 2000-05-23
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APPLICANT:
                                                                                     PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR TILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Aeomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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les 6; Conserv
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FILING DATE: 2000-11-27
APPLICATION NUMBER: 60/257,931
                                                                      FILING DATE: 2000-09-27
                                            APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    943
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Chen, Wensheng
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Yamamoto, Robert T.
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llarity 100.0%; Pred. No
Conservative 0; Misma:
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PCT/US01/00667
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SOFTWARE: PatentIn Ver. SEQ ID NO 1380

LENGTH: 26
TYPE: PRT
ORGANISM: Homo sapiens

FEATURE:

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RESULT 12
US-09-925-299-1380
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                         CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
                                                                                                                                       APPLICANT: Rosen et al. TITLE OF INVENTION: Nucleic Acids, Proteins and FILE REFERENCE: PA102
PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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PRIOR APPLICATION NUMBER: PCT/US01/00664
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                               11 HLRSP 15
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APPLICATION NUMBER: PCT/US01/00668
FILING DATE: 2001-01-30
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APPLICATION NUMBER: PCT/US01/00670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US01/00662 FILING DATE: 2001-01-30
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INFORMATION:
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5; Conserv
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ilarity 100.0%;
Conservative
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ED IN HELA, SIGNAL = 1.3

ED IN HEART, SIGNAL = 2.4

SED IN LUNG, SIGNAL = 1.6

SED IN SIGNAL = 1.3

SED IN FETAL LIVER, SIGNAL = 2.6

SED IN ADULT LIVER, SIGNAL = 1.7

SED IN ADULT LIVER, SIGNAL = 1.7

SED IN ADULT LIVER, SIGNAL = 1.7
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0; Mismatches
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Best Local Similarity
Thes 5; Conserve
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LOCATION: (24)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-299-1380
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US-09-923-831-41
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US-09-923-831-41
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                                                                                                                                                                                                                                                                                         Sequence 45980, Application US/09864761 Patent No. US20020048763A1
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                                   APPLICANT: Hanzel, David K.
APPLICANT: Cheb, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
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CURRENT FILLING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: 09/183,706
PRIOR FILING DATE: 2001-10-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Martelange, Val, rie
APPLICANT: De Smet, Charles
APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: TUMOR ASSOCIATED NUCLEIC
FILE REFERENCE: L0461/7054
                                                                                                                                                                                                                                       APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R.
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OTHER INFORMATION:
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nes 5; Conserv
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               APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03
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NUMBER: GB 24263.6
                                                                                                                                                                                                                      David R.
David K.
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Query Match
Best Local Similarity
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US-09-740-288A-10
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OTHER INFORMATION: MAP TO ACO17079.2

OTHER INFORMATION: EXPRESSED IN BRAIN,

OTHER INFORMATION: EXPRESSED IN PLACENT

OTHER INFORMATION: EXPRESSED IN ADULT 1

OTHER INFORMATION: EXPRESSED IN LUNG,

OTHER INFORMATION: EXPRESSED IN BONE M

OTHER INFORMATION: EXPRESSED IN BONE M
PRIOR APPLICATION NUMBER: US 60/172929
PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Annomax Sequence Listing Engine vers. 1.1 SEQ ID NO 45980
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               Sequence 10, Application US/09740288A Patent No. US20010039042A1
                                                                                                                                                         APPLICANT: Allen, Stephen
APPLICANT: Kinney, Anthony
APPLICANT: Miao, Guo-Hua
APPLICANT: Orozco, Emil
TITLE OF INVENTION: PLANT BIOTIN SYNTHASE
FILE REFERENCE: BB1429 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
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PRIOR
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APPLICATION NUMBER: US
FILING DATE: 2000-09-2
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IN LUNG, SIGNAL * 1.9
IN BONE MARROW, SIGNAL * 2
HIT: AA852449.1, EVALUE 5.00e-15
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: TYPE: PRT
: ORGANISH: Argemone mexicana
US-97-40-288A-10
US-97-40-288A-1
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Title:
Perfect score:
Sequence:
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Maximum DB
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
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    200220
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AAW12276
AAW471334
AAW4713358
AAB17987
ABB73358
AAW94729
AAW94721
AAW94705
AAW94705
                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                 Synthetic library
A glycolipid sugar
Lipoteichoic acid
Beta-2GPI Ab bindi
Exemplary pharmaco
Sequence 15mer 2nd
Sequence 15mer2-8/
Sequence 15mer2-1/
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Sequence
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                                                                                                                                                                                                                                                         Description
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| Į | | | | | |
|---------------------|----------|----|-----|-------|------|
| Drosophila) melanog | ABB71448 | 22 | 367 | 7. | |
| ibacter | AAU64601 | 22 | 117 | 47.3 | 43 |
| Peptide #3414 enco | AAM29377 | 22 | 51 | 7. | |
| Human brain expres | AAM56677 | 22 | 51 | 7. | |
| Human polypeptide, | AAM93386 | 22 | 385 | 7. | • |
| Human ORFX protein | ABP02393 | 23 | 74 | 7. | • |
| a | ABG09714 | 22 | 305 | 8 | 44 |
| - | ABB08348 | 23 | 343 | 8 | 44.5 |
| Human thoracic aor | AAW02727 | 17 | 298 | 8 | 44.5 |
| an thoracic ac | AAR48755 | 15 | 298 | 8 | |
| u | AAM51648 | 23 | 285 | 8 | 44.5 |
| acid sequen | AAY84592 | 21 | 536 | 0 | 46 |
| Human foetal prote | AAM06299 | 22 | 71 | 0 | |
| #5 which | AAW03371 | 17 | 15 | 0 | |
| which | AAW03370 | 17 | 11 | 0 | 46 |
| rg Tr | AAG54412 | 21 | 74 | ۳ | 46.5 |
| mast cell r | ABB77573 | 23 | 157 | ω. | 49 |
| AFP prot | AAG81442 | 22 | 157 | ω | 49 |
| eptide | ABG35783 | 23 | 139 | ٠ | 50 |
| #427 | AAM01745 | 22 | 139 | ٠. | 50 |
| 47 | AAM26410 | 22 | 139 | ٠. | 50 |
| #438 | AAM14004 | 22 | 139 | ٠ | 50 |
| 3 | AAM66133 | 22 | 139 | ٠. | 50 |
| brain e | AAM53750 | 22 | 139 | ٠ | 50 |
| #422 | ABB18423 | 22 | 139 | ٠. | 50 |
| ie #455 enco | ABB32949 | 22 | 139 | ٠. | 50 |
| eptide #42 | ABB27778 | 22 | 139 | ٠. | 50 |
| #9 which | AAW03375 | 17 | 15 | | 50 |
| le #7 which | AAW03373 | 17 | 11 | 4 | 50 |
| uman diagn | ABG15894 | 22 | 159 | ٥. | 51 |
| #8 which | AAW03374 | 17 | 15 | 1. | 56 |
| eptide #6 which | w | 17 | 11 | 1. | 56 |
| ynthetic librar | 227 | 17 | 15 | 5 | 69 |
| ce 15mer2-5 | 47 | 20 | 19 | 7. | 80 |
| Synthetic template | AAW12287 | 17 | 37 | 100.0 | 91 |

ALIGNMENTS

AAW12276 standard; peptide; 15 AA.

AAW12276;

15-APR-1997 (first entry)

Synthetic library peptide #1 which binds anti-T. gondii P30 antibody

Toxoplasma gondii; surface protein; antibody; screening; peptide library; diagnostic assay; immunisation; phage; fusion protein; envelop.

Synthetic.

31-JUL-1996 EP724016-A1.

29-JAN-1996; 96EP-0420030

30-JAN-1995; 95FR-0001297

(JOLI/) JOLIVET-REYNAUD C. (INMR) BIO MERIEUX.

Jolivet-Reynaud C;

WPI; 1996-343531/35

RRESULT 1
AAW12276
IID AAW1
XX AAW1
XX AAW1
XX AAW1
XX Synt
XX Synt
XX Toxc
KW Toxc
KW Toxc
KW Toxc
XX Jolia
OS Synt
XX Synt
XX IO
DE 29-J
XX JOLI
PA (IN)
PA (IN)
PA WPI:
XX New
PT Gonc
PT G New polypeptide reactive with anti-P30 antibodies against Toxoplasma gondii - useful for diagnosis or immunisation, also new nucleic acid, vectors and transformed cells

Example

<u>ب</u>

Page

7; 33pp;

French.

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RESULT 2
AAW71334
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Best Local :
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                                            AAW71332-36 represent glycolipid sugar chain replica peptides. They react specifically with an antibody against glycolipid sugar chains and inhibit adhesion and metastasis of cancer cells to a target cell
                                                                                                                                                           New peptide which reacts specifically with antibody against glyco-lipid sugar chains - useful for inhibition of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 was generated to express pentadecapeptides on the surface of a filamentous phage as a fusion protein with the PIII protein. The library was screened with immobilised anti-T. gondii P30 protein antibody lE1E7. Phages which bind this antibody were recovered and amplified by one round of infection in E. coli. The resultant phages were rescreened with the immobilised antibody and the second round screen isolated 58 bacterial colonies infected with phage. Of the 58 colonies, phage DNA first page and the second round screen isolated by the second round screen isolated.
                                                                                                            Claim 8; Page 3;
                                                                                                                                                                                                                                                                                                                                             08-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                              JP10237099-A
                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A glycolipid sugar chain peptide
                                                                                                                                                                                                             WPI; 1998-537488/46
                                                                                                                                                                                                                                           (IMMO ) IMMUNO JAPAN INC
                                                                                                                                                                                                                                                                                                             26-FEB-1997;
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15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                            sugar chain; inhibit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toxoplasma
                                                                                                                                                                                                                                                                             97JP-0042311
                                                                                                                                                                                                                                                                                                             97JP-0042311
                                                                                                          7pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                novel peptides which bind to antibodies which gondii P30 envelop protein. A peptide library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           adhesion; metastasis;
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. 1.5e-08;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 15;
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Sequence

15

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1 WHWRHRIPLQLAAGR

15

Matches Best Local

Similarity

Conservative

0;

Mismatches

Indels.

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Gaps

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RESULT 3
AAW94702
ID AAW9
XX AAW9
XX AAW9
XX Lipc
XX Monc
KW Monc
KW Mab
XX Stag
YN W09g
YN W09g
XX New
PN His
XX Lipc
XX Himmu
X
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Best Local S
Matches 15
                          Query Match
                                                                                                                                  acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacterial infections. The present sequence represents a specifically claimed lipscteichoic acid epitope peptide mimic that can be bound by the antibody of the invention (Mab 96-110).
                                                                                                                                                                                                                                                                                                                                   specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and killing of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipoteichoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a monoclonal antibody (MAb) to lipoteichoic acid of gram positive bacteria, where the MAb is a chimeric immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody; MAb; lipoteichoic acid; gram immunoglobulin; phagocytosis; infection; epitope; Mab 96-110.
                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising at least part of a human immunoglobulin constant region at least part of a non-human immunoglobulin variable region having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 16; Page 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies to lipoteichoic acid of gram positive bacteria to develop products for the diagnosis, prevention and treatment infections caused by gram positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-095329/08.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-JUN-1997;
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DB 20;
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                       Length'15;
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                                                                                                                                                                                                                                                                                            The present invention describes composition of matter (I) comprising an . CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is: CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each CC independently selected from -(L1)c-P1, -(L1)c-P1-(L2)d-P2. (L4)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L2)d-P2-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L4)f-P4-(L2)d-P2-(L4)f-P4-(L4)f-P4-(L2)d-P2-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)f-P4-(L4)
                                                                                                                                                                     Query Match
Best Local S
Matches 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-350702/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Beta-2GPI Ab binding peptide sequence SEQ ID
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                                                                                                                                                                                                                                                           Sequence
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22-OCT-1999;
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                                                                                                                          1 WHWRHRIPLQLAAGR 15
                                                                                 WHWRHRIPLQLAAGR
                                                                                                                                                                       15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide; therapeutic agent; fusion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                           15
                                                                                                                                                                       Conservative
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                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                         Score 91; DB 21;
Pred. No. 1.5e-08;
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                                                                                                                                                                                                                Length 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer
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                                                                                                                                                                     0
                                                                                                                                                                     Gaps
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1 WHWRHRIPLQLAAGR

Query Match Best Local S Matches

15; Conser

Conservative

0;

Mismatches

100.0%;

Score 91; DB 23; Pred. No. 1.5e-08;

Length 15; indels

0;

Gaps

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neuroprotective activities. (1) can be used as a therapeutic or prophylactic agent as well as for screening purposes. (1) is useful for diagnosing diseases characterised by dysfunction of their associated protein of interest, for identifying normal or abnormal proteins of interest, for identifying normal or abnormal proteins of interest in a biological sample. Additionally, (1) is useful for treating inflammatory and autoimmune diseases, tumour growth, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, infertility, and neurological degenerative diseases, tumour growth, cancer, compounds are useful for treating disorders characterised by low red blood cell levels such as anaemia. The TPO-mimetic comprising companies are useful for treating disorders characterised by megakaryocyte/platelet deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic tumour which result in thrombocytopaenia, aplastic anaemia erythematosus, and Fanconi's syndrome. ABB73403 to ABB73426 and ABL35695 to ABL35777 represent amino acid and nucleic acid sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TPO; tumour necrosis factor alpha inhibitor; TMP; TPO mimetic peptide; EPO mimetic peptide; EPO mimetic peptide; EPO mimetic peptide; EPO mimetic; antiinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiinfertility; haemostatic; dermatological; antianaemic; anorectic; antiinfertility; haemostatic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; sleep disorder; neurological degenerative disease; infertility; obesity; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a vehicle-peptide molecule (I) or its multimers. (I) can have antiinflammatory, antitumour, immunosuppressive, cytostatic, antiheumatic, antiarthritic, antidabetic, ophthalmological antianaemic, anorectic, antiinfertility, haemostatic, dermatological and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAY-2000; 2000US-0563286
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 39; Page 62; 176pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2001; 2001WO-US14310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pharmacologically active peptide SEQ ID NO:1097
  15 AA;
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RESULT 7
AAW94710
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AAW94729
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                                                                                                                                                                                                                                           The invention relates to a monoclonal antibody (MAb) to lipoteichoic CC acid of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin cCC immunoglobulin comprising at least part of a non-human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. CC The antibodies bind to whole bacteria and enhance phagocytosis and ckilling of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of CC antibodies or peptides (encoded by a DNA of the variable region of CC anti-lipoteichoic acid antibody or characterised by amino acids CC corresponding to one or more of the complementarity determining regions CC (CDRs) of the variable region of the antibody) can be used for treating CC or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacterial infections.

CC Sequences AAW94726-34 represent common peptide sequences resulting from CC all library panning experiments. Three series of panning experiments were CC conducted to identify peptide sequences to which antibody of the invention (Mab 96-110) bound strongly. The translated sequences provide CC lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antibodies to lipoteichoic acid of gram positive bacteria - used to develop products for the diagnosis, prevention and treatment of infections caused by gram positive bacteria
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N-PSDB; AAX05555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Fig 8; 150pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;
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                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin;
Mab 96-110; panr
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                                                                                                       1 WHWRHRIPLQLAAGR
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                                                                       WHWRHRIPLQLAAGR
                                                                                                                                          l Similarity
15; Conser
                                                                                                                                                                                                               19
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                                                                                                       15
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Pred. No. 2e-
0; Mismatches
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                                                                                                                                                           2e-08;
                                                                                                                                                                         DB 20;
                                                                                                                                          0;
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RESULT 8
AAW94721
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                                                                                                                                                                                                                                               Query Match
Best Local (
                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibodies to lipoteichoic acid of gram positive b to develop products for the diagnosis, prevention and infections caused by gram positive bacteria
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N-PSDB; AAX05536.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunoglobulin; phase Mab 96-110; panning
                                                                               AAW94721 standard;
                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JACK-) JACKSON FOUND ADVANCEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody; MAb; lipoteichoic acid; gram immunoglobulin; phagocytosis; infection; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15mer2-8/0 resulting from 15mer library panning experiment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Fig 6A-B; 150pp; English.
                                                                                                                                                                                                                                                                                                                                  lipoteichoic acid epitope peptide mimics to which Nab96-110 bound.
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                                                                                                                                                                                                  1 WHWRHRIPLQLAAGR
                                                                                                                                                                 WHWRHRIPLQLAAGR
                                                                                                                                                                                                                                   l Similarity
15; Conser
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                                                                                 Protein;
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                                                                                                                                                                                                                                   Score 91; DB
Pred. No. 2e-
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d treatment
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22-APR-1999

(first entry)

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ANW9470 9
ANW9470 1D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a monoclonal antibody (MAb) to lipoteichoic CC acid of gram positive bacteria, where the MAb is a chimeric constant region and at least part of a human immunoglobulin comprising at least part of a non-human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable constant region and to whole bacteria and enhance phagocytosis and continuous particles (encoded by a characterised by a lethal infection. The continuous continuou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 15; Conserv
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                              Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria; immunoglobulin; phagocytosis; infection; epitope; peptide mimic; Mab 96-110; panning.
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                              22-APR-1999
                                                                                                                                                                                                                                                                                                                                   AAW94705;
                                                                                                                                                                                                                                                                                                                                                                                                             AAW94705 standard; Protein; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15mer2-19/0 resulting from 15mer library panning experiment
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wab 96-110; panning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 WHWRHRIPLQLAAGR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WHWRHRIPLQLAAGR 15
                                                                                                                                                                             15mer2-1/0 resulting from 15mer library panning experiment.
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Pred. No.
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W09857994-A2 Staphylococcus

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RESULT 10
AAW94709
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CC Sequences AAN94705-22 represent sequences resulting from a 15mer library conducted to identify peptide sequences of panning experiments were conducted to identify peptide sequences to which antibody of the invention (Mab 96-110) bound strongly. The translated sequences provide conducted to identify peptide mimics to which Mab96-110 bound.
                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-JUN-1997;
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                                                                                                           immunoglobulin: phagocytosis;
Mab 96-110; panning.
                                                                                                                          Monoclonal antibody; MAb; lipoteichoic acid; gram immunoglobulin; phagocytosis; infection; epitope:
                                                                                                                                                                       Sequence 15mer2-7/0
                                                                                                                                                                                                       22-APR-1999
                                                                                                                                                                                                                                       AAW94709
                                                                                                                                                                                                                                                                       AAW94709 standard; Protein; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5; Fig 6A-B; 150pp; English.
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                                                                                                                                                                                                                                                                                                                                                                     1 WHWRHRIPLQLAAGR 15
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                                                                                                                                                                                                                                                                                                                                                      WHWRHRIPLQLAAGR
                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity 100
15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 91; DB 20;
Pred. No. 2e-08;
                                                                                                                                                                       from 15mer library panning experiment.
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                                                                                                                        positive; bacteria;
peptide mimic;
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RESULT 11
AAW12287
ID AAW12
XX
AC AAW12
XX
DT 15-AP
XX
TOXOP
KW TOXOP
KW diagn
XX
GS Synth
XX
PN EP724
XX
PD 31-JU
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PF 29-JP
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PR 30-JP
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INMF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a monoclonal antibody (MAB) to lipoteichoic CC acid of gram positive bacteria, where the MAB is a chimeric immunoglobulin comprising at least part of a human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocycosis and calling of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by aDNA of the variable region of anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody or the antibody) can be used for treating or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacteria infections. Sequences AAW94705-22 represent sequences resulting from a 15mer library panning second experiment. Three series of panning experiments were conducted to identify peptide sequences to which antibody of the invention (Mab 96-110) bound strongly. The translated sequences provide lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
               (JOLI/) JOLIVET-REYNAUD C. (INMR ) BIO MERIEUX.
                                                                 30-JAN-1995;
                                                                                                 29-JAN-1996;
                                                                                                                                  31-JUL-1996
                                                                                                                                                                 EP724016-A1
                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                             Toxoplasma gondii; surface protein; antibody; screening; peptide library; diagnostic assay; immunisation; phage; fusion protein; envelop.
                                                                                                                                                                                                                                                                                  Synthetic template
                                                                                                                                                                                                                                                                                                                    15-APR-1997
                                                                                                                                                                                                                                                                                                                                                     AAW12287;
                                                                                                                                                                                                                                                                                                                                                                                  AAW12287 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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15; Conser
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                                                                                                 96EP-0420030
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                                                                                                                                                                                                                                                                                  peptide
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                                                                                                                                                                                                                                                                           for overlapping peptide series
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Pred. No.
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2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 19;
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ACC XXX ACC XX
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Best Local S
Matches 15
                                                         WPI; 1999-095329/08
                            N-PSDB; AAX05534
                                                                                                                       Fischer GW,
                                                                                                                                                                                                                                                                                                              16-JUN-1998;
                                                                                                                                                                                    (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED
                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                     W09857994-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mmunoglobulin;
Mab 96-110; pan;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15mer2-5/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW94708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW94708 standard; Protein; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptide reactive with anti-P30 antibodies against Toxoplasma gondii - useful for diagnosis or immunisation, also new nucleic acid, vectors and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jolivet-Reynaud
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WHWRHRIPLQLAAGR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WHWRHRIPLQLAAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 9; 33pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                panning
                                                                                                                   Schuman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                              97US-0049871
                                                                                                                                                                                                                                                                                                              98WO-US12402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phagocytosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resulting from 15mer library panning experiment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                       RF,
                                                                                                                       Stinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 91; DB
Pred. No. 4e-
); Mismatches
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4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epitope; peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                          (JOLI/)
(INMR )
                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic
 The invention relates to
                               Example 2; Page 7; 33pp;
                                                                acid, vectors and transformed cells
                                                                            New polypeptide reactive with anti-P30 antibodies against Toxoplasma gondii - useful for diagnosis or immunisation, also new nucleic
                                                                                                                             WPI; 1996-343531/35
                                                                                                                                                             Jolivet-Reynaud C;
                                                                                                                                                                                                                                            30-JAN-1995;
                                                                                                                                                                                                                                                                          29-JAN-1996;
                                                                                                                                                                                                                                                                                                         31-JUL-1996
                                                                                                                                                                                                                                                                                                                                        EP724016-A1
                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW12277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW12277 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Fig 6A-B; 150pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 HWRHRIPLQLAAGR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 HWRHRIPLQLAAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           develop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibodies to lipoteichoic acid of gram positive bacteria - used develop products for the diagnosis, prevention and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
14; Conserv
                                                                                                                                                                                          JOLIVET-REYNAUD C.
BIO MERIEUX.
                                                                                                                                                                                                                                                                                                                                                                                                    gondii;
assay; i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                            95FR-0001297
                                                                                                                                                                                                                                                                           96EP-0420030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide #2 which binds anti-T. gondii P30 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                       immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                    surface protein; antibody; screening; peptide library;
immunisation; phage; fusion protein; envelop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.9%; St.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gram
                                 French.
novel peptides which bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          positive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 19;
 antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Peptides AAW03367-75 are peptides isolated from a peptide library, whi bind to antibody IEIE7 which recognises the P30 surface protein from Toxoplasma gondii. The peptide library was constructed by inserting a nucleic acid sequence encoding a random pentadecapeptide in the PIII envelop protein of a filamentous phage. Antibody IEIE7 was immobilise

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RESULT 14
AAW03372
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Best Local Similarity
Thes 12; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC recognise the Toxoplasma gondii P30 envelop protein. A peptide library CC was generated to express pentadecapeptides on the surface of a CC filamentous phage as a fusion protein with the PIII protein. The library CC was screened with immobilised anti-T. gondii p30 protein antibody lEIE7. CC Phages which bind this antibody were recovered and amplified by one CC round of infection in E. coli. The resultant phages were rescreened with the immobilised antibody and the second round screen isolated 58 CC bacterial colonies infected with phage. Of the 58 colonies, phage DNA CC from 30 colonies was isolated and sequenced to determine the sequence of the pentadecapeptide encoded. The peptide sequences AAM12276-86 were CC identified. Of the 30 colonies studied, this peptide sequence was CC the sequence across the phage PIII sequence (AM12287) corresponding to CC the sequence across the phage PIII sequence and putative CC pentadecapeptide was used to generate a series of overlapping CC pentadecapeptides. These peptides were used to determine the best CC peptide sequence which binds the IEIE7 antibody. Peptides AAW3367-75 CC were isolated. The new peptides can then be used, in diagnostic assays to CC detect T. gondii antibodies in a sample or to purily anti-P30 antibodies or for active immunisation against T. gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnostic
                                                                                       Claim 7;
                                                                                                                       acid,
                                                                                                                                      New polypeptide reactive with anti-P30 antibodies against Toxoplasma gondii - useful for diagnosis or immunisation, also new nucleic
                                                                                                                                                                                    N-PSDB; AAT31328.
                                                                                                                                                                                                                              Jolivet-Reynaud C;
                                                                                                                                                                                                                                                                                                           30-JAN-1995;
                                                                                                                                                                                                                                                                                                                                           29-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW03372 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                               (INMR)
                                                                                                                                                                                                                                                                            (JOLI/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 HWRHRKPLQLATGR 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 HWRHRIPLQLAAGR
                                                                                                                                                                                                   1996-343531/35
                                                                                                                       vectors and transformed cells
                                                                                                                                                                                                                                                              JOLIVET-REYNAUD
BIO MERIEUX.
                                                                                       Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               gondii; surface protein; antibody; screening; peptide library;
assay; immunisation; phage; E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            which binds anti-Toxoplasma gond11 P30 antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                           95FR-0001297
                                                                                                                                                                                                                                                                                                                                           96EP-0420030
                                                                                       33pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.8%;
85.7%;
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Pred. No. 7.
                                                                                                                            or immunisation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA
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7.2e-05;
7
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RESULT 15
AAW03374
ID AAW03374
ID AAW03374
ID AAW03374
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AC AAW03
XX AAW03
AC AAW03
XX Pepti
XX Toxop
KW Toxop
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ID 31-JU
XX PP 29-JP
PR 30-JP
XX 30-JP
XX 1/0L1
PR 30-JP
XX 1/0L1
PR 1/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Peptides AAW03367-75 are peptides isolated from a peptide library, which bind to antibody 1E1E7 which recognises the 930 surface protein from Toxoplasma gondii. The peptide library was constructed by inserting a nucleic acid sequence encoding a random pentadecapeptide in the PIII envelop protein of a filamentous phage. Antibody 1E1E7 was immobilised on the bottom of a Petri dish and the expressed peptide library was overlaid on the antibody. After washing, phages bound on the antibodies were recovered and the phage amplified by passage through E. coli. The phages were rescreened by the same method and 58 bacterial colonies were recovered. Of these, 30 were further studied and the nucleic acids encoded the peptides AAW12276-86. A series of overlapping peptides based on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on the bottom of a Petri dish and the expressed peptide library was overlaid on the antibody. After washing, phages bound on the antibodies were recovered and the phage amplified by passage through E. coli. The phages were rescreened by the same method and 58 bacterial colonies were recovered. Of these, 30 were further studied and the nucleic acid encoding the pentadecapeptide was isolated. The nucleic acids encoded the peptides AAW12276-86. A series of overlapping peptides based on the peptide template AAW12287 was constructed to identify which peptide sequences bound to the anti-p30 antibody. The peptides canning isolated peptides can two beautiful and to the anti-p30 antibody. The peptides can then be used in diagnostic assays to detect T. gondii antibodies in a sample or to purify anti-p30 antibodies or for active immunisation against T. gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide reactive with anti-P30 antibodies against Toxoplasma gondii - useful for diagnosis or immunisation, also new nucleic acid, vectors and transformed cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Page 20; 33pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-343531/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jolivet-Reynaud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (JOLI/) JOLIVET-REYNAUD C. (INMR ) BIO MERIEUX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toxoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide #8 which binds anti-Toxoplasma gondii P30 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAT31330
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assay; immunisation; phage; E.coli.
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Pred. No.
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0.0078;
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8888888
                                                   peptide template AAW12287 was constructed to identify which peptide sequences bound to the anti-P30 antibody. The peptide scanning isolated peptides AAW03367-75. The peptides can then be used in diagnostic assays to detect T. gondii antibodies in a sample or to purify anti-P30 antibodies or for active immunisation against T. gondii.
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Matches Query Match Local Similarity nes 11; Conserv Conservative 61.5%; 0; Score 56; Pred. No. Mismatches DB 17; 0.011; 17; Length 15; Indels 0, Gaps

0;

Sequence

15

AΑ;

ρ В 5 HRIPLQLAAGR 15 HRIPLQLAAGR

Search completed: November 27, Job time: 11.2819 secs 2002, 07:17:50

e j

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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41.5
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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                         283224 seqs, 96134422 residues
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PIR_73:*
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pir3:*
pir4:*
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T37981
AC2449
A48999
A75475
T08176
T50718
B70510
E64553
C64726
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AB2481
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F70636
D82679
RRWPEM
G81175
H81930
T35942
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E82162
                                                                                                                                                                      T36559
T13182
QQEC31
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hypothetical prote
tryptophan halogen
probable transcrip
G protein-coupled
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                          conserved hypothet
probable receptor-
probable transcrip
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probable epoxide h
integrase - Lactob
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ALIGNMENTS

hypothetical protein PAB1903 - Pyrococcus abyssi (strain Orsay) C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change C;Accession: C75112 R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999

#text_change 20-Jun-2000

A; Reference number: A; Accession: C75112 A; Description: Pyrococcus

A75001

abyssi

genome sequence:

insights into archaeal chromosome

RESULT C75112

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A;Kicessav...
A;Kstatus: preliminary
A;Molecule type: DNA
A;Residues: 1-649 <KAW>
A;Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49612.1; PID:g545
A;Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49612.1; PID:g545
Query Match
Best Local Similarity
Thehes 8; Conserv
                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-354 <SEE>
A;Cross-references: EMBL:AL079353; PIDN:CAB45554.1; GSPDB:GN00070; SCOEDB:SCH17.08c
A;Experimental source: strain A3(2)
                                                                                                                                                                                                                                     probable epoxide hydrolase - Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Species: Streptomyces coelicolor C;Date: 03-Dec:1999 #sequence_revision 03-Dec:1999 #text_change 21-Jan-2000 C;Accession: T36559 R;Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajand submitted to the EMBL Data Library, June 1999 A;Reference number: Z21584 R;Accession: T36559
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T36559
                                                                                      A; Gene: SCOEDB
C; Superfamily:
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C;Superfamily: hypothetical protein YPL009c
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                                Score 46.5;
Pred. No. 7.
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                 Mismatches
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1999
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RESULT 4

QOEC31
hypothetical protein C-96 rspA 3'-region -
C;Species: Escherichia coli
C;Date: 29-Sep-1999 #sequence_revision 29-9
C:Accession: A04448
C:Accession: K. --- 1082
C;Accession: H87369

G;Accession: H87369

G;Accession: H87369

G;Accession: H87369

G;Accession: H87369

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: H87369
                                                                                                                                   tryptophan halogenase, probable [imported] - Caulobacter crescentus c;Species: Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C;Accession: H87369
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H87369
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A; Residues: 1-96 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Schnier, J.; Isono, K.
Nucleic Acids Res. 10, 1857-1865, 1982
A;Title: The DNA sequence of the gene rspA
A;Reference number: A04448; MUID:82196866;
A;Accession: A04448
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C; Superfamily:
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A;Title: Genome structure of the Lactobacillus temperate phage | A;Reference number: 217631; MUID:97225795; PMID:9073065
A;Accession: T13182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             integrase - Lactobacillus phage phi-gle
C;Species: Lactobacillus phage phi-gle
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
C;Accession: T13182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:V00352; GB:J01681; GB:J01682; C;Comment: This is the hypothetical translation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-391 <KOD>
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                     WYWRRR-PKRLSAG
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 16-Jul-1999
C;Accession: A35639
C;Accession: A35639
R;Ross, P.C.; Figler, R.A.; Corjay, M.H.; Barber, C.M.; Adam, N.; Harcus, D.R.; Lynch Proc. Natl. Acad. Sci. U.S.A. 87, 3052-3056, 1990
A;Title: RTA, a candidate G protein-coupled receptor: cloning, sequencing, and tissue A;Reference number: A35639; MUID:90222168; PMID:2109324
A;Accession: A35639
A;Molecule type: mRNA
A;Residues: 1-343 <ROS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-516 <STO>
A;Cross-references: GB:AE005673; NID:g13422252; PIDN:AAK22956.1; GSPDB:GN00148
C;Genetics:
                                                                                                                          A;Cross-references: GB:M35297; NID:g206809; PIDN:AAA42087.1; PID:g206810; C;Superfamily: mas transforming protein C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Complete genome sequence of Pseudomonas aeruginosa A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: C83167
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R; Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable transcription regulator PA3830 [imported] - Pseudomonas aeruginosa (strain C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: C83167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: CC0972
C;Superfamily: Rhizobium plasmid
                                                                                                              C; Keywords:
F; 4/Binding
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                                                                                                                                                                                                                                                                                                                                                                               G protein-coupled receptor RTA -
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A; Residues: 1-270 <STO>
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8; Conservative
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.;
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer,
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frol
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Krieger, J.E.; Kuramae, E.E.; Laid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein XF1451 [imported] - Xylella fastidiosa (strain 9a5c) C:Species: Xylella fastidiosa C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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A;Cross-references: GB:Z84498; GB:AL123456;
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: ephB
C;Superfamily: tropinesterase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 be
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                                                                                                                                                                                                                                                A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;anonymous, The Xylella Nature 406, 151-157, 2000
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                                                                                                                                                                   A; Gene: XF1451
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N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: eggplant mosaic virus
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 19-Jan-2001
C;Accession: J00102
R:Osorio-Reese, M.E.; Keese, P.; Gibbs, A.
Virology 172, 547-554, 1989
A;Title: Nucleotide sequence of the genome of eggplant mosaic tymovirus.
A;Reference number: J00102
A;Reference number: J00102; MUID:90021185; PMID:2800336
A;Accession: J00102
A;Rolecule type: genomic RNA
A;Residues: 1-1839 <OSO>
A;Cross-references: EMBL:J04374
C;Superfamily: eggplant mosaic virus RNA-directed RNA polymerase
C;Reywords: ATP; nucleotide binding; nucleotidyltransferase; P-loop; RNA blosynt
C;Reywords: ATP; nucleotide-binding motif A (P-loop)
F;1027-1032/Region: nucleotide-binding motif B
F;971/Binding site: ATP (Lys) #status predicted
probable nucleoside triphosphate pyrophosphohydrolase NMAO852 [imported] C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-20 C;Accession: H81930 R;Parthill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: G81175
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-152 <TET>
A:Cross references: GB:AE002419; GB:AE002098; NID:97225863; PIDN:AAF41065.1; PID:9722A:Experimental source: serogroup B, strain MC58
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A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B A;Reference number: A81000; MUID:20175755; pMID:10710307
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genome polyprotein - eggplant mosaic virus
N;Alternate names: RNA nucleotidyltransferase
N;Alternate names: RNA polymerase (EC 2.
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6; Conser
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85.78;
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Pred. No. 93;
2; Mismatches
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Dougherty, B.
Pizza, M.
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strain MC58.
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98

; Achtman, M.; James, Jagels, K.; Leather,

K.D.; Bentley,
S.; Moule, S.;

S.D.; Churcher, C.; Klee, Mungall, K.; Quail, M.A.; #text_change 02-Feb-2001

S.R.; Mo Rajandre

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C;Accession: G87401

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Koln, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C. proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: G87401
                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
G87401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: PACE DNA
A; Molecule type: DNA
A; Residues: 1-222 <SEE>
A; Cross references: EMBL.AL035206; PIDN:CAA22764.1;
A; Cross references: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491. A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: H81930
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                      epoxide hydrolase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R:Seeger, K.J.; Harris, D.;
submitted to the EMBL Data I
A; Reference number: Z21551
A; Accession: T35942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable ABC-type transport system ATP-binding protein - Streptomyces coelic;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
C;Accession: T35942
                                                                                  C; Superfamily:
                                                                                                     C;Genetics:
A;Gene: CC1229
                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-330 <STO>
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A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-152 < PAR>
                                                                                                                                             A;Cross-references: GB:AE005673; NID:g13422557; PIDN:AAK23211.1; GSPDB:GN00148
  Query Match
Best Local S
Matches
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  Similarity
8; Conserv
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6; Conserv
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    Conservative
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85.7%;
                     47.3%;
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Library, January 1999
Score 43; DB Pred. No. 25; 1; Mismatches
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Pred. No. 11;
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  Indels
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Gaps
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RESULT 15
E82162
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C; Superfamily: hypothetical protein HI1671
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae A;Reference number: A82035; MUID:20406833; PMID:10952301 A;Accession: E82162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R. Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                paraquat-inducible protein A VC1753 [imported] - Vibrio cholerae (strain N16961 serog
C;Species: Vibrio cholerae
C;Decies: Vibrio cholerae
C;Date: 1B - Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: E82162
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Search completed: November 27, Job time: 10.112 secs
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A;Experimental source: serogroup
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A; Residues: 1-434 <HEI>
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Matches 7
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nilarity 50.0%;
Conservative
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                     2002, 07:24:13
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                                                                                                                                                                                  Score 43;
Pred. No.
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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              EX70_SCHPO
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YAKB_SCHPO
PR1_ASCHPO
PR1_SSEEP
C1B3_SSEEP
Y126_TREPA
C1B2_SHEEP
Y126_TREPA
C1B2_SHEEP
Y126_TREPA
C1B2_SHEEP
Y126_TREPA
C1B2_SHEEP
YNG_HOWAN
T2S1_STRAL
PROHO
PSAB_SYNY3
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9 schizosacch
6 homo sapien
1 helicobacte
2 schizosacch
7 mesostigma
l nephroselmi
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5 oryza sativ
l pisum sativ
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 |
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| 40 | 40 | 40 | 40 | 40 | 40 | 40 | 40 | 40 | 40 | 40 | 40 |
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| PSAB_ANAVA | PAB1_ANASP | PSAB_SYNPW | PSAB_CYAPA | PSAB_MAIZE | PSAB_CHLRE | PSAB_WHEAT | PSAB_TOBAC | PSAB_SPIOL | PSAB_PSINU | PSAB_PORPU | PSAB_PINTH |
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ALIGNMENTS

| RESULT 1 | T 1 | | | | | | | | |
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| 9 | RTA_RAT | STAI | STANDARD; | PRT; | 343 AA. | | | | |
| ភ័ក | P23749; | Rel | 20. Created) | ž | | | | | |
| ij | 01-NOV-1991 | (Rel. | 20, Last s | sequence update | ıpdate) | | | | |
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| Z è | RTA. | וידפיוי | broceru-conbred receptor kik. | tondana | | | | | |
| Š | Rattus nor | vegicus | (Rat). | | • | | | | |
| ñ | Eukaryota; Metazoa; Chordata; | Metazoa | ; Chordata | | ca; Vert | ebrata; E | uteleost | tomi; | |
| ί ۾ ڏ | Mammalia; 1 | Eutheria | ; Rodentia | | ynathi; | Sciurognathi; Muridae; Murinae; Rat | Murinae; | ; Rattus. | • |
| ž× | NCBI_TaxID=10116; | 10116; | | | | | | | |
| ₩ 2 | SEQUENCE FROM N.A. | ROM N.A. | | | | | | | |
| റ് | STRAIN-Spra | ague-Daw | ley; TISSU | E-Aorta; | | | | | |
| × | MEDLINE=90222168; PubMed=2109324; | 222168; | PubMed=2109324; | 9324; | • | | | | |
| Ã | Ross P.C., | Figler | R.A., Corj | ау м.н., | Barber | C.M., Adam | am N., | | |
| ≆≆ | "BTA a candidate C protein compled recentor: clo | ., Lynch | Candidate C protein-coupled recentor: cloping | counted t | recentor | . Cloning | sequencing | no i no | |
| ĩ; | į | distrib | ution."; | 4 | 000 | | | | |
| ř | Proc. Natl. Acad. Sci. U.S.A. 87:3052-3056(1990). | . Acad. | Sci. U.S.A | . 87:3052 | 2-3056(1 | 990). | | | |
| i ii | | ON: ORPH | FUNCTION: ORPHAN RECEPTOR. | . X | • | | | | |
| กัก | -i- TISSUE | SPECIFIC | TISSUE SPECIFICITY: SUT. VAS DEFERENS. UTERUS. AND AORTA BUT | VAS DEFI | ERENS II | TERUS A | ID AORTA | BUT ONLY | ₹ |
| റ്റ് | | DETECTAL | BLE IN LIV | ER, KIDNE | EY, LUNG | AND SAI | IVARY GI | LAND. IN | - |
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| 5 C | NOTE STATE | KITY: BE | SIMILARITY: BELONGS TO FAMILY I OF G-FROTEIN COUPLED RECEPTORS | WHITE I C | OF G-PRO | EEIN COOP | TED RECE | EPTORS. | |
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| i ii | entities re | requires | a license | agreement (See http://www.isb-sib.ch/announce | ee | ttp://www | v. isb-sik | b.ch/ann | ounce/ |
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| ₩ ? | EMBL; M352 | 97; AAA4: | 2087.1; | | | | | | |
| Ħ | EMBL; M35298; AAA42088.1; - | 98; AAA4: | 2088.1; | | | | | | |
| ž | PIR; A35639; A35639. | 9; A3563 | 9. | 3 | | | | | |
| ₩ ¥ | Pfam: PF00001: 7tm 1: | 001: 7tm | 1: 1. | | | | | | |
| ਲੋ | PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1. | 500237; | G_PROTEIN_ | RECEP_F1_ | 1; 1. | | | | |
| ž | PROSITE; P | 550262; (| G_PROTEIN_ | RECEP_F1_ | 2; 1. | | | | |
| € | G-protein | coupled : | receptor; | Transmembrane; | | Glycoprotein | in. | | |
| 3 2 | TRANSMEM | 2 ⊢ | 4 7 | 1 (POTENTIAL) | UTTALLY | 1 (POTENTIAL) | | | |
| ij | DOMAIN | 67 | 82 | CYTOPLASMIC | | (POTENTIAL). | | | |
| ij | TRANSMEM | 83 | 104 | 2 (POTENTIAL) | ٠ | | | | |
| ij | DOMAIN | 105 | 123 | × | | (POTENTIAL). | • | | |
| i | TRANSMEM | 124 | 144 | CYTODI ASMIC | | TATENOTAL | | | |
| ij | TRANSMEM | 161 | 181 | 4 (POTENTIAL) | | (POLENLINE). | | | |
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EXTRACELLULAR (POTENTIAL).
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SEQUENCE
010339;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updata)
70 kDa exocyst complex protein.
                                                                                                                                           SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEROPS; C21.001; -. InterPro; IPRO01788; RNA_dep_RNApol2. InterPro; IPR000506; Viral_helicase1. Pfam; PF00978; RNA_dep_RNApol2; 1. Pfam; PF01443; Viral_helicase1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend.anemail to license@isb-sib.ch).
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01-FEB-1991 (Rel. 17, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
RNA replicase polyprotein (EC 2.7.7.48).
Eggplant mosaic virus.
Viruses; ssRNA positive-strand viruses, no
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; RNA-directed RNA polymerase; Polyprotein; ATP-binding. NP_BIND 965 972 ATP (BY SIMILARITY). SEQUENCE 1839 AA; 204731 MW; FD8DC1F5115E7861 CRC64;
                                                                                                                    EX70_SCHPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90021185; PubMed=2800336; Osorio-Keese M.E., Keese P., Gibbs
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Pred. No. 28;
2; Mismatches
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of eggplant mosaic tymovirus.";
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RX MEDLINE-21848401; PubMed-11859360;
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RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
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RA Gollins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mangall K., Murphy L., Niblett D., Odell C.,
RA Mooney P., Moule S., Mangall K., Murphy L., Niblett D., Odell C.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Rutherford K., Rutter S., Saunders R., Squares S., Stevens K.,
RA Rylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rleger M., Schaefter M., Mueller Auer S.,
RA Gabel C., Fuths M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuths M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabel C., Fuths M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Golfeau A., Cadieu E., 
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Matches 7
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Mol. Biol. Cell 13:515-529(2002).
-i- FUNCTION: Required for exocytosis (By similarity).
-i- SUBUNIT: Sec3, sec5, sec6, sec8, sec10, sec15 and exo70 are component of exocyst complex.
-i- SIMILARITY: BELONGS TO THE EXO70 FAMILY.
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR004140; Exo70. Pfam; PF03081; Exo70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL096788; CAB46665.1; -. EMBL; AL110295; CAB53736.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no restricted the surpresentations of the surpresentation
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Balasubramanian M.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                        Transport;
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                                                                                                                                    Similarity
7; Conser
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Fungi; Ascomycota; Schizosaccharomycetes;
haromycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                     Protein transport. 615 AA; 69041 MW;
                                                                                                                                Conservative
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46.78;
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Pred.
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RESULT 4
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CRECKER
GN FLI4.
OC EUKATY
OC MCBLIN
RA GALLAN
RA GALLAN
RA GALLAN
RA PAJUSC
RA ALLAL
RT 100ps
RP ENGUEN
RA PAJUSC
RA ALLAL
RT 100ps
RC 11-SCOUEN
RA MEDLIN
RA PAJUSC
RA ALLAL
RT 100ps
RC -1- SCOUEN
RC -1- SCOUE
                     EMBL; X69878; CAA49505.1; EMBL; X68203; CAA48290.1; A EMBL; X68203; CAA482215.1; EMBL; Q43143; AAA85215.1; PIR; S36130; S36130; S36130; HSSP; P11362; 1FGK.
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01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vascular endothelial growth factor receptor 3 precursor (EC 2.7.1.112)
(VECFR-3) (Tyrosine-protein kinase receptor FLT4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 761-1190 FROM N.A.
MEDLINE-92119639; PubMed-1310071;
Aprelikova O., Pajusola K., Partanen J., Armstrong E., Alitalo R.,
Bailey S.K., McMahon J., Wasmuth J., Huebner K., Alitalo K.;
"FLT4, a novel class III receptor tyrosine kinase in chromosome 5q
qter.";
Cancer Res. 52:746-788(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YEura.
Homo sapiens (Human).
Homo sapiens (Human).
Horota; Metazoa; Chordata; Metazoa; Primates;
                                                                                                                                                                                                     use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: RECEPTOR FOR VEGF-
ACTIVITY.
-!- CATALYTIC ACTIVITY: ATP + a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-93007958; PubMed-1327515; Pajusola K., Aprelikova O., Korhonen Alitalo K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vascular endothelial growth factor receptor."; Oncogene 8:1233-1240(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Galland F., Karamysheva A., Pebusque Dubreuil P., Rosnet O., Birnbaum D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Alitalo R., /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "FLT4 receptor tyrosine kinase contains seven immunoglobulin-like loops and is expressed in multiple human tissues and cell lines."; Cancer Res. 52:5738-5743(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Placenta;
MEDLINE-93241723; PubMed-8386825;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The FLT4 gene encodes a transmembrane tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine phosphate.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: PLACENTA, LUNG, HEART, AND
SEEM TO BE EXPRESSED IN PANCREAS AND BRAIN.

SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR
PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 7 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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     HGNC:3767; FLT4
                                                                                                                                                                                an email to license@isb-sib.ch).
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ed (JAN-1996)
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SMART; SM00410; IG_like; 2.

SMART; SM00418; IGC2; 2.

SMART; SM00219; TyrKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYP; 1.

PROSITE; PS00240; RECEPTOR_TYR_KIN_III; 1.

PROSITE; PS00240; RECEPTOR_TYR_KIN_LII; 1.
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SIGNAL
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ro; IPR003600; Ig_like.
ro; IPR0010242; RTKinaseIII.
ro; IPR0010245; Tyr_pkina.
                                              Similarity 46. 7; Conservative
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                       Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                   Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                         Schizosaccharomycetales;
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SEQUENCE 43
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TIGR; HP0269; -.
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PROSITE; PS01278; UPF0004;
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ween the Swiss Institute of Bioinformatics and the EMBL outst
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oteobacteria; epsilon subdivision; Helicobacter group;
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RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA Coliver K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Kyelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Kyelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Kyelton J., Vanstreels E., Rieger M., Malsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
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RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Woodward J., Volckaert G., Holzer E., Moestl D., Hilbert H.,
RA Gabbel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Gabbel C., Zimmermann W., Wedler H., Weshhardt R., Pohl T.M.,
RA Goffeau A., Cadleu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,
RA Lucas M., Rochet M., Galilardin C., Tallada V.A., Garzon A., Thode G.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
"The genome sequence of Schlzosaccharomyces pombe.";
Nature 415:871-880(2002).
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                                                                                  PR1_ASPOF
Q05736;
Q1-JUN-1994
Q1-JUN-1994
15-JUN-2002
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Pram; pr00172; Zn_clus; 1.

SMART; SM00066; GAL4; 1.

PROSITE; ps00463; ZN2_CY6_FUNGAL_1; 1.

PROSITE; ps50048; ZN2_CY6_FUNGAL_2; 1.

Hypothetical protein; Transcription regulation; DNA-binding; Nuclear protein; Zinc; Metal-binding.

Nuclear protein; Zinc; Metal-binding.

DNA_BIND 22 50 ZN(2)-CYS(6), FUNGAL-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamiln N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Asparagus officinalis (Garden asparagus).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Wood V., Gwilliam
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                                                               Pathogenesis-related protein
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z67998; CAA91958.1;
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                                                                                                                                                                                                                                                                              189
                                                                                                                                                                                                                                                                                                                   2 HWRHRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Nuclear (Probable).
SIMILARITY: CONTAINS 1 ZN(2)-CYS(6), FUNGAL-TYPE BINUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLUSTER DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                              HWSHRIP
                                                                                                                                                                                                                                                                                                                                                              Similarity
6; Conserv
                                                                                  (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                               782 AA;
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                       STANDARD;

    Last sequence update)
    Last annotation updat

                                                                                                                              29,
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                                                                                                                                                                                                                                                                                                                                                                                                                                               89377 MW;
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                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                            Score 42; DB
Pred. No. 25;
0; Mismatches
                                                                 1 (AOPR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                               ZN(2)-CYS(6), FUNG;
; B08DAEC986BF1CF7
                                                                                                                                                                       158
                                                                                  update)
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                                                                                                                                                                                                                                                                                                                                                                                                      Length 782;
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RESULT 8
C1B3_SHEEP
ID C1B3_SHEEP
AC P80943;
DT 16-CCT-2001
DT 16-CCT-2001
DT 7-CCL1 surfe
DE (Fragment).
OS Ovis Bries
OC Ewkeryota; I
OC Mammalla; Cal
OC MCB1_TaxID=
RN [1]
RP SEQUENCE FR
RC TISSUE-Feta
RX MEDLINE-96ta
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Best Local S
Matches 6
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"Characterisation of a wound-induced transcript from the monocot asparagus that shares smilarity with a class of intracellular pathogenesis-related (PR) proteins.";
Plant Mol. Biol. 19:555-561(1992).
MEDLINE-96269982; PubMed-8662069; Ferguson E.E., Dutia R M "-"
                                                                                 Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniai
Mammalia; Eutheria; Cetartiodactyla;
Bovidae; Caprinae; Ovis.
                                                                                                                                                 16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
7-cell surface glycoprotein CDlb-3 (CDlb-3 antigen) (SCD1710)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X62103; CAA44013.1;
EMBL; X64452; CAA45784.1;
EMBL; A26571; CAA01827.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (see http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=94035138; PubMed=8220442;
Warner S.A.J., Scott R., Draper J.;
                                                                                                                                                                                          P80943;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                          Pathogenesis-related protein.
SEQUENCE 158 AA; 16921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0634; BETALLERGEN.
PROSITE; PS00451; PATHOGENESIS_BETVI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S22533; S22533.
PIR; S39754; S39754.
HSSP; O24248; 1E09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00407; Bet_v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92329716; PubMed-1627770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asparagus
                                               SEQUENCE FROM N.A
                                                                        NCBI_TaxID=9940;
                                                                                                                                      (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000916; Bet_v_I.
                                                                                                                                                                                                                                                                                     σ
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                                                                                                                                                                                                                                                                                                              WRHRIPLQLAAGR 15
                                                                                                                                                                                                                                                                                     WSHEVAVNVAAGR 18
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                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                  Score 41;
                                                                                                                                                                                                                                                                                                                                                    Pred. No.
                                                                                                  Craniata; Vertebrai
actyla; Ruminantia;
                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                           C9B9354812B00C20 CRC64;
         W.R.,
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                                                                                                                                                                                                                     232 AA.
         Hopkins J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions
                                                                                                  Vertebrata; Euteleostomi;
minantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 158
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Y126_TREPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                           Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., Khalak H., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weldman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMATN
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             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                      Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein TP0126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig;
SMART; SM00407; IG:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SUBCELLULAR LOCATION: Type I membrane protein (By sim-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY
                                                                                        spirochete.
                                                                                                                                                                                                      MEDLINE-98332770; PubMed-9665876;
                                                                                                                                                                                                                      STRAIN-Nichols;
                                                                                                                                                                                                                                                                                                 TP0126.
                                                                                                                                                                                                                                                                                                                                                              083163;
                                                                               Science
                                                                                                                   Venter J.C.
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           Y126_TREPA
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                                                               -!- SIMILARITY:
                                                                                              "Complete genome sequence of Treponema pallidum,
                                                                                                                                                                                                                                                         NCBI_TaxID=160;
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                                                                            281:375-388(1998).
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7; Conser
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223
19
123
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                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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IGc1; 1.
                                                   SOME, TO T.PALLIDUM TP0733.
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222
232
83
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50.0%;
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

N'LINKED (GLONAC. ...) (POTE
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                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LINKED (GLCNAC. . .) (P
C96DB93840B56158 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                      the syphilis
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Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C182_SHEEP
Q29422;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
17-cell surface glycoprotein CDIb-2 precursor (CDIb-2 antigen)
(SCDIB-42) (Antigen IAH-CCI4):
Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
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                                                                    InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_cl.
Pfam; PF00047; 1g; 1.
SMARP; SM00407; IGCl; 1.
Glycoprotein; Signal; Immunoglobulin
Multigene family.
                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a sheep CDID gene.";
Immunogenetics 49:225-230(1999).
-i- FUNCTION: NOT KNOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein; Transmembrane; Complete proteome TRANSMEM 74 96 POTENTIAL.
TRANSMEM 188 210 POTENTIAL.
SEQUENCE 291 AA; 31921 MW; 4963E1BD06EE67A3 CRC64;
                                                                                                                                                                                                                     EMBL; Z36891; CAA85360.1; -. HSSP; P11609; 1CD1.
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"The sheep CD1
                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                        entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Amino-terminal sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rhind S.M., Hopkins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Thymus;
MEDLINE=96269982; PubMed=8662069;
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                                                                                                                                                                                                                                                                                          tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type I membrane protein (By similarity). SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
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ns J., Dutia B.M
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Capsule polysacchar
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Photosystem
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                                                                                                                                                                                                                                                                                                                                     gene cluster: a region encoding proteins expression of capsular polysaccharide."; J. Bacteriol. 175:5978-5983(1993).
                                                               PSAB_GUITH O78507;
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                                                                                                                                                                                                                       EMBL; X74567; CAA52659.1; Polysaccharide transport;
                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=93388530; PubMed=8397187;
Pazzani C., Rosenow C., Boulnois G.
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Escherichia.
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  Guillardia
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gene cluster: a region encoding proteins involved in cell surface
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AA; 46381 MW; 73058122C28027DE CRCE4;
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RESULT 13
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complete sequence and conserved synteny groups confirm its common ancestry with red algae.";

J. Mol. Evol. 48:236-244(1999).

-i-FUNCTION: PsaA and psaB bind P700, the primary electron donor composter I (PSI), as well as the electron acceptors A0, A1, FX. PSI functions as a plastocyanin/cytochrome c6-ferredoxin
                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
TRANSMEM
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NCBI_TaxID=55529;
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COFACTOR: P700 is a chlorophyll A dimer, A0 is chlorophyll A, A1 COFACTOR: P700 is a chlorophyll A dimer, a0 is chlorophyll A, A1 is a phylloquinone and FX is a 4Fe-4S iron-sulfur center.

SUBUNIT: A psaA/B heterodimer binds the P700 chlorophyll special pair and subsequent electron acceptors. The PSI reaction center higher plants and algae is composed of one at least 11 subunits. SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast thylakoid membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE PSAA/PSAB FAMILY.
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                                                                                                        Similarity 46. 7; Conservative
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46.78;
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                                                                                                                                                                     IRON-SULFUR FX (4FE-4S) (BY SIMILARITY).
IRON-SULFUR FX (4FE-4S) (BY SIMILARITY).
P700 SPECIAL PAIR CHLOROPHYLL AXIAL
LIGAND (BY SIMILARITY).
A0 CHLOROPHYLL (BY SIMILARITY).
A0 CHLOROPHYLL (BY SIMILARITY).
A1 PHYLLOQUINONE (BY SIMILARITY).
A1 PHYLLOQUINONE (BY SIMILARITY).
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Pred. No.
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L PHYLLOQUINONE (BY SIMILARITY).
L PHYLLOQUINONE (BY SIMILARITY).
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SEQUENCE
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InterPro; IPR001230; Prenyl_site.
Pfam; PF03028; Dynein_heavy; 1.
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J. Cell Sci. 107:497-506(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN FLAGELLA. PRODUCES FORCE TOWARDS TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydomonas reinhardtii.
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                                                                                                                                    1 W-HWRHRIPL 9
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SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                 WLHWRHCVPV 2382
                                                                                                                                                                                                                                                                                                                                                                                        protein; Microtubules; Dynein; ATP-binding; Flagella;
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             sequence update) annotation update)
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COILED COIL (POTENTIAL).
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COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
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"Cloning, expression, and church of the color of
                                                                                                                                                                                                                                                                                                                                                                                                                             PDB; 1BKZ; 04-NOV-98.
PDB; 2GAL; 04-NOV-98.
PDB; 3GAL; 04-NOV-98.
PDB; 4GAL; 04-NOV-98.
PDB; 5GAL; 04-NOV-98.
PDB; 5GAL; 04-NOV-98.
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Acharya K.R.;
Acharya K.R.;
Structural basis for the recognition of carbo
galectin-7.";
Biochemistry 37:13930-13940(1998).
Biochemistry 37:13930-13940(1998) IN CELL-CELL
-I- FUNCTION: COULD BE INVOLVED IN CELL-CELL
-I- FUNCTION: ORDERSSARY FOR NORMAL GROWTH
                                                                                                                                                                                                                                                                              Pfam; PF00337; Gal-bind_lectin; SMART; SM00276; GLECT; 1. PROSITE; PS00309; GALAPTIN; 1.
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                                                                                                                                                                                                                   BINDING
                                                                                                                                                                                                                                       Galaptin; Lectin; 3D-structure. INIT_MET 0 0
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EMBL; U06643;
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MEDLINE-98434364; PubMed-9760227;
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"Galectin-7, a human 14-kDa S-lectin, specifically keratinocytes and sensitive to retinoic acid.";
Dev. Biol. 168:259-271(1995).
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MEDLINE-95246905; PubMed-7729568;
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MEDLINE-95197604;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SIMILARITY: BELONGS
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SUBURIT: MONOMER.
SUBCELLULAR LOCATION: MAY BE SECRETED BY A NON-CLASSICAL SECRETORY
HERHRLPL
                                            HWRHRIPL
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                                                                                          Conservative
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AAA86820.1; -.
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sen H.H., Flint T.,
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75.0%;
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                                                                                                                                                                                     MW;
                                                                                        Score 40; DB Pred. No. 9.3; 2; Mismatches
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9.3;
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Q53608;
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16-OCT-2001 (Rel. 4
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(R.SalI).
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                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GTOGAC AND CLEAVES AFTER G-1.
-!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give specific double-stranded fragments with terminal 5'-phosphates.
                                                                                                                                                                                                                                                                                                                                                                                     system.";
Gene 151:167-172(1994).
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MEDLINE=95129852; PubMed=7828868;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Rodicio M.R.,
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SalI (EC 3.1.21.4)
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O03969 bacteriopha
O8ujm3 agrobacteri
O29897 archaeoglob
O2236 arabidopsis
O9kyn3 streptomyce
O9a9k8 caulobacter
O8zw38 pyrobaculum
O8u137 pyrococcus
O9hxh2 pseudomonas
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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | | 37 | 36 | 35 | | ω u | 32 | | 30 | | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 |
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| 42 | 42 | 42 | 42 | 42 | 42.5 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 43 | 44 | 44 | 44.5 | 44.5 | 44.5 | 44.5 |
| 46.2 | 46.2 | 46.2 | 46.2 | 46.2 | 46.7 | 47.3 | 47.3 | 47.3 | 47.3 | 47.3 | 47.3 | 47.3 | 47.3 | 47.3 | 47.3 | 47.3 | 47.3 | 47.3 | 47.3 | 47.3 | 47.3 | 47.3 | 48.4 | œ | 48.9 | 48.9 | 48.9 | 48.9 |
| 296 | 292 | 289 | 266 | 207 | 639 | 930 | 716 | 566 | 561 | 527 | 491 | 486 | 444 | 434 | 367 | 334 | 330 | 322 | 222 | 186 | 152 | 152 | 636 | 522 | 483 | 467 | 356 | 343 |
| Ν. | 16 | 10 | N | 16 | 16 | N | 16 | 4 | 1 | σ | 4 | 4 | ω | 16 | v | | 16 | σ | 16 | σ | 16 | 16 | 16 | 13 | 11 | 11 | 16 | 11 |
| Q9RMP1 | Q9K3Q1 | Q42702 | Q9RFV1 | Q9RW71 | Q9K4H5 | Q9AQS0 | Q8YLZ5 | Q9BZB8 | P70166 | Q9VGT1 | Q98ZB7 | Q9Н8V5 | Q9C197 | Q9KR89 | Q9VPE8 | Q52445 | Q9A8W9 | Q8SZE2 | Q9ZBF8 | Q9BGP1 | Q9JVG2 | Q9K0G3 | Q9PDC8 | Q9YGX4 | Q8VDX5 | Q99PQ2 | P95276 | Q8VCJ6 |
| Q9rmpl mycobacter1 | Q9k3q1 streptomyce | Q42702 chlamydomon | Q9rfv1 mycobacter1 | Q9rw71 deinococcus | Q9k4h5 streptomyce | Q9aqsO bacillus sp | Q8ylz5 anabaena sp | Q9bzb8 homo sapien | O | Q9vgtl drosophila | Q9bzb7 homo sapien | Q9h8v5 homo sapien | Q9c197 amanita mus | Q9kr89 vibrio chol | Q9vpe8 drosophila | Q52445 pseudomonas | Q9a8w9 caulobacter | Q8sze2 drosophila | Q9zbf8 streptomyce | Q9bgp1 macaca fasc | Q9jvg2 neisseria m | | | | Q8vdx5 mus musculu | | P95276 mycobacteri | Q8vcj6 mus musculu |

ALIGNMENTS

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RESULT
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                                                                                                                                                                                             Query Match
Best Local
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MCCombie W.R., de la Bastide M., Spiegel L., Kirchoif K., Preston R.,
KLIIT K., Nascimento L., Bell M., Balija V., Baker J., Vil M.D.,
Zutavern T., Santos L., Miller B., Cunnius D.M., Shah R., King L.,
Bahret A., Yang C., Dike S., O'Shaughnessy A., Palmer L., Dedhia N.;
"Genomic sequence for Oryza sativa, Nipponbare strain, clone
OSNNBb0081F12, from chromosome 10, complete sequence.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AC090488; AAM01014.1;
EMBL; AC090488; AAM01014.1;
-SEQUENCE 62 AA; 7306 MW; 4B141DB22AB8DD41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8S754 PRELIMINARY; PRT; 62 AA. Q8S754; Q8S754; Q1-JUN-2002 (TrEMBLrel. 21, Created) Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update) Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update) Hypothetical 7.3 kDa protein. QSJNBB0081F12.14.
                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).

Gukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                              1 WHWRHRIPLQLAAGR 15
                                                              WEWRHPRPLPCAADK 59
                                                                                                                               Similarity
8; Conserva
                                                                                                                               Conservative
                                                                                                                                            52.7%;
53.3%;
                                                                                                                                            Score 48; I
Pred. No. 2.
                                                                                                                               Mismatches
                                                                                                                                            DB 10; Length 62; 2.5;
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RESULT
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Best Local s
Matches 9
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Ehrhartoideae; On
NCBI_TaxID=4530;
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01-MAR-2001
01-JUN-2002
                    A physical map of the Leishmania major Friedlin genome Res. 8:135-145(1998).

EMBL; AL133436; CAB62823.1; -

InterPro; IPR001055; cNNP_binding.

InterPro; IPR001064; Crystallin.

SMART; SM00100; CNNP; 1.

PROSITE; PS00888; CNMP_BINDING_1; UNKNOWN_1.

PROSITE; PS00825; CNMP_BINDING_3; 2.

PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                 Ivens A.C., Lewis S.M., Bagherzad Smith D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Han B., Feng Q., Mu J., Zhou B., Chen Z.H., Li Y., Zhu J.J., Tang Y.S., Zhao Q., Liu Y.L., Huang Y.C., Yu Z., Fan D.L., Chen Weng Q.J., Zhang L., Lu Y.Q., Yu S.L., Zhu J., Liu X.H., Hu X., Lei H.Y., Zhang Y.J., Wang R., Li C., Lu Y., Chen X.C., Zhang Y.Hu H., Jia P.X., Li T., Qian Y.M., Ying K., Hong G.F.;
"Oryza sativa indica (Guangluai4) genomic DNA, chromosome 4, BAC clone: H0711G06 (+H0113C06).";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL44215; CAC09515.1; -.
InterPro; IPR003880; Ppantne_attach.
Pfam; PF03092; BT1; 1.
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-FRIEDLIN;
Zimmermann W., Wambutt R.,
Rajandream M.A., Barrell B.
Submitted (DEC-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
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Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-FRIEDLIN;
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H0711G06.21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE 402 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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9; Conser
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Best Local S
Matches 8
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01-MAY-2000
01-MAR-2002
   STRAIN-A3(2);
STRAIN-A3(2);
MEDLINE-97000351; PubMed-8843436;
Pedenbach M., Kieser H.M., Denapa
                                                                                                                                                                                                                                                                                                             Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Streptomycineae; Streptomycetaceae; St
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 Redenbach M
Kinashi H.,
                                                                                                            James K.D., Parkhill
Submitted (JUN-1999)
                                                                                                                                                   STRAIN-A3(2);
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                                                                                                                                                                                                                                                                                                       Actinomycetales; Streptomycineae; NCBI_TaxID=1902;
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Archaea; Euryarchaeota;
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                                                                                                                                                                                                                                                                      SEQUENCE FROM
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                                                                                                                                                                         SEQUENCE FROM
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Nature 417:141-147(2002).
EMBL; AL079353; CAB45554.1; -.
                                                                                                                                                                                                    Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases EMBL; X98106; CAA660758.1; -. EMBL; X90510; CAA62092.1; -. EMBL; X90510; CAA62092.1; -. InterPro; IPR002104; Phage_integrase. Pfam; PF00589; Phage_integrase; 1. SEQUENCE 391 AA; 45517 MW; 076325FB09107A21 CRC64;
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"Genome structure of the Lactobacillus
"Genome structure and the putative
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MEDLINE-97225795; PubMed-9073065;
KOdaira K.I., Oki M., Kakikawa M., Watanabe N., Hirakawa
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NCBI_TaxID=176299;
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Plasmid AT.
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ATTG OR ATU5453 OR AGR_PAT_
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802 AA; 86916 N
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Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., M Houmiel K., Gordon J., Vaudin M., Tartchouk O., Epp A., Liu Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Mar Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub Cielo C., Slater S.;
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Science 294.2323-2328(2001).
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genome of the natural genetic engineer Agrobacterium tumefaciens
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                                                             Score 46.5;
Pred. No. 42
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STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
de la Bastide M.R., Parnell L.D., Kaplan N., Gnoj L., Hameed
Schutz K., Hasegawa A., Gottesman T., Shohdy N., Granat S., J
Johnson A.F., Lodhi M., Dedhia N., Martienssen R., McCombie w
A. thaliana BAC 732N15 from chromosome V.";
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EMBL; AC002534; AAB70030.1; -.
EMBL; AC002534; AAB70030.1; -.
SEQUENCE 505 AA; 58451 MW; 627A823DD89032D0 CRC64;
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MEDLINE-98049343; PubMed-9389475;

Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

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Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykos S.M.,

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Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
Q9KYN3;
Q9KYN3;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O22236, PRELIMINARY; PRT; 505 AA.
022236; O1-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat)
Hypothetical 58.5 kDa protein.
T32N15.6.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Nature 390:364-370(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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211 AA; 23303 MW; 927825BC1EFC1B46 CRC64;
  (TrEMBLrel. 15,
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C STRAIN-ATCC 19089 / CB15;

C STRAIN-ATCC 19089 / CB15;

X MEDLINE-21173698; PubMed-11259647;

X Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.

A Nierman W.C., Feldblyum T.V., Laub M.T., Ohta N., Maddock J.R.,

A POTOCKA I., Nelson W.C., Newton A., Stephens C., Phadke N.D., El

A DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry

A Kolonay J.F., Smit J., Craven M.B., Vamathevan J., Ermolaeva M., Whi

A Viterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., Whi

Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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STRAIN-A3(2) / M145;

STRAIN-A3(2) / M145;

Bentley S.D. / Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Bentley S.D. / Chater K.D. Harris D.E., Quail M.A., Kleser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Marren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                               Q9A9K8;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2002 (TrEMBLrel. 20,
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Nature 417:141-147(2002).
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                                                                                       TIGR;
                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                       Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
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NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                            NCBI_TaxID=155892;
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                                                                                       CC0972;
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11; Conserv
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CE 126 AA; 13263 MW;
 Similarity
9; Conserv
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516 AA;
 Conservative
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                49.5%;
75.0%;
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64.7%;
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                Score 45;
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Pred.
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Best Local
                                                                                                                                                                                         STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422; Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.; "The complete sequence of the Pyrococcus furiosus submitted (FEB-2002) to the EMBL/GenBank/DDBJ data EMBL; AE010242; AALBISIG.1; -. Hypothetical protech: Complete proteome. SEQUENCE 649 AA: 75072 MW; B66A4194DFD81F1A CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein PAE1989.
PAE1989.
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein PF1392.
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SEQUENCE 59
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PROSITE; PS00061; ADH_SHORT; UNKNOWN, 1.
Hypothetical protein; Complete proteome SEQUENCE 595 AA; 67145 MW; D91343AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00037; fer4; 2.
Pfam; PF01507; PAPS_reduct; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Genome sequence of the aerophilum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pyrococcus furiosus
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InterPro; IPR002198;
InterPro; IPR002500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pyrobaculum aerophilum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VCBI_TaxID=2261;
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   2 HWRHRIPLQLAAG
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8; Conserv
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                                                                   Conservative
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67145 MW; D91343AB940C4896 CRC64;
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61.5%;
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Pred. No. 55;
0; Mismatches
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                                                               Score 45; DB Pred. No. 60; 2; Mismatches
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B66A4194DFD81F1A CRC64;
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                                                                                                                            Length 649;
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Q9C1M7;
Q1-JUN-2001
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                                                                                                                            SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1:

MEDLINE-2043737; PubMed-10984043;

MEDLINE-2043737; PubMed-10984043;

MEDLINE-2043737; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Wastbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

Nature 406:959-964 (2000).
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ATP-binding.
SEQUENCE 4083 AA;
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                                                               EMBL; AE004800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetales; Eremotheciaceae; NCBI_TaxID=33169;
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NCBI_TaxID=287;
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
                              InterPro;
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77: AAK20175.1; -.
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Gapop 10.0 , Gapext 0.5
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| US-08-592-646A-28 Sequence 28, Application US/08592646A Sequence 28, Application US/08592646A Patent No. 5851355 GENERAL INFORMATION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA ITILE OF INVENTION: GONDII AND APPLICATIONS ITILE OF INVENTION: GONDII AND APPLICATIONS ITILE OF INVENTION: GONDII AND APPLICATIONS INUMBER OF SEQUENCES: 63 CORRESPONDENCE ADDRESS: ADDRESSEE: OLIFF & BERRIDGE, PLC STREET: P.O. Box 19928 CITY: Alexandria STATE: VA COUNTRY: USA COUNTRY: USA COUNTRY: USA ITILE OF INVENTION: PC-DOS/MS-DOS SOFTMARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION NUMBER: US/08/592,646A FILING DATE: 26-JAN-1996 CLASSIFICATION NUMBER: US/08/592,646A FILING DATE: 26-JAN-1996 CLASSIFICATION NUMBER: WB 36923 TELECHONE: JOS 386-2787 INFORMATION FOR SEQ ID NO: 28: SEQUENCE CHARACTERISTICS: LENGTH: 15 amino acids TYPE: amino acids STRANDEDNESS: not relevant TOPOLOGY: linear MOLECULE TYPE: peptide US-08-592-646A-28 | 28 59 64.8 15 4 US-09-165-422-21 Seque 29 56 61.5 11 2 US-08-592-646A-7 Seque 30 56 61.5 11 4 US-09-165-422-7 Seque 31 56 61.5 15 2 US-08-592-646A-9 Seque 32 56 61.5 15 2 US-08-592-646A-9 Seque 33 52 57.1 15 2 US-08-592-646A-20 Seque 34 52 57.1 15 2 US-08-592-646A-43 Seque 35 51 56.0 15 2 US-08-592-646A-44 Seque 36 51 56.0 15 2 US-08-592-646A-44 Seque 37 51 56.0 15 2 US-08-592-646A-49 Seque 40 50 54.9 11 4 US-09-165-422-4 Seque 40 50 54.9 11 4 US-09-165-422-8 Seque 41 50 54.9 15 2 US-08-592-646A-10 Seque 42 50 54.9 15 2 US-08-592-646A-41 Seque 43 50 54.9 15 2 US-08-592-646A-45 Seque 44 50 54.9 15 4 US-09-165-422-10 Seque 45 50 54.9 15 4 US-09-165-422-41 Seque 46 50 54.9 15 4 US-09-165-422-41 Seque 47 50 54.9 15 4 US-09-165-422-41 Seque 48 50 54.9 15 4 US-09-165-422-41 Seque 49 50 54.9 15 4 US-09-165-422-41 Seque 40 50 54.9 15 4 US-09-165-422-41 Seque 41 50 54.9 15 4 US-09-165-422-41 Seque 42 50 54.9 15 4 US-09-165-422-41 Seque 43 50 54.9 15 4 US-09-165-422-41 Seque |
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RESULT 3
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SOUTH CO. 1. STUDIES OF TOXOPLASMA

GENERAL INFORMATION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA

GONDII AND APPLICATIONS

GONDII AND APPLICATIONS
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GENERAL INFORMATION:
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Matches 15; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 703 836-6400
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TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
TITLE OF INVENTION: GONDII AND APPLICATIONS
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ZIP: 22320
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TOPOLOGY: 11
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REFERENCE/DOCKET NUMBER: WPB 36923
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REGISTRATION NUMBER: 30,0
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                            ZIP: 22320
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                   CURRENT APPLICATION DATA:
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
                                                                                                                                                      CITY: Alexandria
STATE: VA
                                                                                                                                       COUNTRY: USA
APPLICATION NUMBER: US/09/165,422
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P.O. Box 19928
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Pred. No. 1.8e-08;
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                                   Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent NO. 637289/
Patent NO. 637289/
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
APPLICANT: JOLIVET-REYNAUD, COLETTE
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
GONDII AND APPLICATIONS
                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: BETYIDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 15; Conserv
                 Query Match
Best Local
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 28:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 02-Oct-1998
CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22320
COMPUTER READABLE FORM:
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                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
 l Similarity
15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                          TOPOLOGY: linear
ULE TYPE: peptide
NCE DESCRIPTION: (
                                                                                                                                                                  TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Alexandria
STATE: VA
                                                                                                                                                  STRANDEDNESS: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
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100.0%; ilarity 100.0%; Conservative (
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                                                                                            SEQ ID NO:
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Score 91; DB 4;
Pred. No. 1.8e-08;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                       WPB 36923
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                                    DB 4; Length 15;
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US-09-165-422-59
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                                                                                                                                                            Sequence 59, Application US/09165422
Patent No. 6372897
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
APPLICANT: JOLIVET-REYNAUD, COLYPEPTIDES OF TOXOPLASMA
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
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NAME: BEITIGGE, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: P.O. Box
CITY: Alexandria
STATE: VA
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                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                           1 WHWRHRIPLQLAAGR 15
COMPUTER READABLE FORM:
                                                                                                                      NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acids
                                                                                    ADDRESSEE: OLIFF & BERRIDGE, PLC STREET: P.O. Box 19928
                                                   CITY: Alexandria STATE: VA
                               COUNTRY: USA
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P.O. Box 19928
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VENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
VENTION: GONDII AND APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                           GONDII AND APPLICATIONS
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Pred. No.
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TELEFAX: 703 836-2787 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

TOPOLOGY:

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STRANDEDNESS:

TOPOLOGY:

OLECULE

not relevant

NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787

WPB 36923

ATTORNEY/AGENT INFORMATION:

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RESULT 7
US-08-592-646A-27
; Sequence 27, Application US/08592646A
; Patent No. 5851535
; Patent No. 5851535
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEPAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN PLANEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
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nes 15; Conserv
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CITY: Alexandria
                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                           ADDRESSEE:
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NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 59:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                 22320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/165,422 FILING DATE: 02-Oct-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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COMPUTER: IBM PC compati
                                                                                                                                                                                                                    VA
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                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                      GONDII AND APPLICATIONS
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P.O. Box 19928

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TOPOLOGY: linear

HOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-165-422-27
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US-09-165-422-27
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                                                   Sequence 26, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colett
TITLE OF INVENTION: MIMOTOPIC POLY
TITLE OF INVENTION: GONDII AND APP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 27, Application US/09165422
Patent No. 6372897
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
APPLICANT: JOLIVET-REYNAUD, COLETTE
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
                                                                                                                                                                                                                                                                                                            Matches
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TELEPAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                          Local Similarity 100 les 14; Conservative
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NAME: Berridge, William P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-Oct-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: OLIFF & BERRIDGE, PLC STREET: P.O. Box 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                  JOLIVET-REYNAUD, COlette
VENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
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100.0%; Pr
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100.0%; Pred. No. 1.1e-0
ative 0; Mismatches
                                     GONDII AND APPLICATIONS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GONDII AND APPLICATIONS
                                                                                                                                                                                                                                                                                                                            Score 86; Pred. No.
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1.1e-07
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RESULT 10
US-08-592-646A-29
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GENERAL INFORMATION:
APPLICANT: JOLIVET-REYN
TITLE OF INVENTION: MIM
TITLE OF INVENTION: GON
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
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TELEFAX: 703 836-2787 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/592,646A
FILING DATE: 26-0AN-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                     ATTORNEY/AGENT INFORMATION:
NAME: BETTIDGG, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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NAME: BETILDGE, WILLIAM P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
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TELEPHONE: 703 836-6400
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CTTY: Alexandria
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CITY: Alexandria
STATE: VA
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TYPE: amino acid
STRANDEDNESS: not relev
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                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 22320
                                                         TELEPHONE:
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VENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
VENTION: GONDII AND APPLICATIONS
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O. Box 19928
                                                           703 836-6400
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100.0%;
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RESULT 12
US-09-165-422-29
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                  Sequence 29, Application US/09165422 Patent No. 6372897 GENERAL INFORMATION:
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Patent No. 6372897
GENERAL INFORMATION:
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Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                               Matches
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INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: not rei
TOPOLOGY: linear
MOLECULE TYPE: peptide
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les 13; Conser
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-OCT-198
CLASSIFICATION: CUMKNOWNDATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: OLIFF & BERRIDGE, PLC
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TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES (
GONDII AND APPLICATIONS
APPLICANT: JOLIVET-REYNAUD, Colette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                               WHWRHRIPLQLAA 15
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                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Berridge, William P. REGISTRATION NUMBER: 30,024
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100.0%;
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100.0%;
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Pred. No
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SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-165-422-29
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US-08-592-646A-25
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Best Local Similarity
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TELEPHONE: 703 836-6400
TELEPAX: 703 836-2787
INFORMATION FOR SEO ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                   APPLICATION NUMBER: FILING DATE: 26-JAN
                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                           COUNTRY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-Oct-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: OLIFF &
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5, 5851535
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STATE: VA
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P.O. Box 19928
                                                                                                                                                                                                                               USA
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VENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
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                                                                                                                                                                          Floppy disk
                                                     26-JAN-1996
N: 435
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                                                                                     US/08/592,646A
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Pred. No.
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                                                                                                                        Version #1.30 ·
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1e-06;
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REFERENCE/DOCKET NUMBER: WPB 36923

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                                                                 Query Match
Best Local S
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Best Local Similarity 100.0%;
Matches 12; Conservative (
                                                     Matches
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TYPE: amino acid
STRANDEDNESS: not releva
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 25:
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LENGTH: 15 amino acids
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                                                    Local Similarity hes 12; Conserv
              1 WHWRHRIPLQLA 12
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                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: 05/09/165,422
FILING DATE: 02-Oct-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HEM PC compatible
COMPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                        MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO: 25:
                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: peptid
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: WPB 36923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Alexandria
STATE: VA
                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  not relevant
                                                                 83.5%;
                                                                 Score 76; DB 4; I pred. No. 4.3e-06;
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Pred. No.
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US-08-592-646A-24
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GENERAL INFORMATION:
                                                                                        Best
                                                                       Matches
                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver:
SOFTWARE: Patentin Release #1.0, Ver:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-CAN-1996
FILING CATE: 26-CAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELEPHONE: 703 836-6400
                                                                                                                                                                                                                                                                     TELEPHONE: 703 836-640 TELEFAX: 703 836-2787 INFORMATION FOR SEQ ID NO:
                                                                                                                                                            TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDENESS: not relev
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
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                                                                   Local Similarity 100 nes 11; Conservative
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P.O. Box 19928
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/ENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
/ENTION: GONDII AND APPLICATIONS
                                                                                                                                                                                linear
                                                                                                                                                          peptide
                                                                                                                                                                                                not relevant
                                                                                      79.18;
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                                                                                                                                                                                                                                                                       24:
                                                                       0;
                                                                                        Score 72;
Pred. No.
                                                                       Mismatches
                                                                                        1.9e-05
                                                                                                         DB 2;
                                                                                                     Length 15;
                                                                       Indels
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Search completed: November 27, 2002, 07:25:10 Job time : $2.72201 \ \text{secs}$

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Result
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Perfect score:
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Maximum DB
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Query
Match
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Exemplary pharmaco
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Lipoteichoic acid
Beta-2GPI Ab bindi
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| 21 | 20 | 22 | 22 | 22 | 21 | 23 | 22 | 23 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 22 | 23 | 22 | 22 | 20 | 22 | 23 | 23 | 17 | 17 | 17 | 17 | 22 | 23 | 17 | 17 | 20 | 17 |
| 1660 | | 76 | AAU27652 | ABG11767 | AAY87094 | ABG33893 | α | AAU83145 | 7 | AAG91895 | ABB65319 | AAU49292 | AAB87149 | AAB87148 | AAB87147 | AAB87146 | AAB87068 | ABP04200 | AAU50446 | AAB87070 | AAY27622 | AAU46742 | ABP33821 | ABP33970 | AAW03375 | AAW03371 | | Ξ | S | ABB83482 | AAW03374 | w | 4 | AAW12287 |
| ĸ | Human secreted pro | Staphylococcus aur | 2 | human di | | | | Novel secreted pro | Corynebacterium gl | C glutamicum prote | Drosophila melanog | onibacteri | | | Human secreted pro | Human secreted pro | | Human ORFX protein | Propionibacterium | mature T | Human secreted pro | 0 | hydrolas | RF29 | #9 whi | # | ide #4 | Peptide #7 which b | ila | n cytoskeleto | 1de #8 | #6 which | equence 15mer2-5 | Synthetic template |

ALIGNMENTS

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RESULT 1
AAW12276
ID AAW1
XX AW1227
AC AAW1
XX Synt
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KW TOXC
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PN 29-2
XX 31-2
XX NEW
PT GON
XX JOI
PA (INI
XX JOI)
PA (INI
XX NEW
PT GON
PT GON
New polypeptide reactive with anti-P30 antibodies against Toxoplasma gondii - useful for diagnosis or immunisation, also new nucleic acid, vectors and transformed cells
                                                                                                                                                                                                                                                                     Synthetic.
                                                        WPI; 1996-343531/35.
                                                                                 Jolivet-Reynaud C;
                                                                                                             (JOLI/) JOLIVET-REYNAUD C. (INMR ) BIO MERIEUX.
                                                                                                                                                         30-JAN-1995;
                                                                                                                                                                                   29-JAN-1996;
                                                                                                                                                                                                                31-JUL-1996
                                                                                                                                                                                                                                          EP724016-A1
                                                                                                                                                       95FR-0001297
                                                                                                                                                                                   96EP-0420030
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Toxoplasma gondii; surface protein; antibody; screening; peptide library; diagnostic assay; immunisation; phage; fusion protein; envelop.

Synthetic library peptide #1 which binds anti-T. gondii P30 antibody.

15-APR-1997 AAW12276;

(first entry)

AAW12276 standard; peptide; 15

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RESULT 2
AAW71334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel peptides which bind to antibodies which CC recognise the Toxoplasma gondii P30 envelop protein. A peptide library CC was generated to express pentadecapeptides on the surface of a CC filamentous phage as a fusion protein with the PIII protein. The library CC was screened with immobilised anti-T. gondii P30 protein antibody lEIE7. CC Phages which bind this antibody were recovered and amplified by one CC round of infection in E. coli. The resultant phages were rescreened with the immobilised antibody and the second round screen isolated S8 CC bacterial colonies infected with phage. Of the 58 colonies, phage DNA CC from 30 colonies infected with phage. Of the 58 colonies, phage DNA CC from 30 colonies moded. The peptide sequence of CC the pentadecapeptide encoded. The peptide sequences AAMI2276-86 were CC clentified. Of the 30 colonies studied, this peptide sequence was compensated a template peptide sequence (AAMI2287) corresponding CC pentadecapeptide was used to generate a series of overlapping CC pentadecapeptides. These peptides were used to determine the best peptide sequence which binds the IEIE7 antibody. Peptides AAMI3367-75 CC were isolated. The new peptides can then be used in diagnostic assays to detect T. gondii antibodies in a sample or to purify anti-P30 antibodies or for active immunisation against T. gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local :
                            AAW71332-36 represent glycolipid sugar chain replica peptides. They react specifically with an antibody against glycolipid sugar chains and inhibit adhesion and metastasis of cancer cells to a target cell. The peptides can be used to prevent cancer metastasis.
                                                                                                                                                            New peptide
glyco-lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycolipid sugar chain; inhibit; adhesion; metastasis; cancer cell
                                                                                                            Claim 8;
                                                                                                                                             metastasis
                                                                                                                                                                                                                                                                                                                                         08-SEP-1998.
                                                                                                                                                                                                                                                                                                                                                                       JP10237099-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A glycolipid sugar chain peptide
                                                                                                                                                                                                          WPI; 1998-537488/46.
                                                                                                                                                                                                                                                                         26-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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                                                                                                                                                                                                                                          (IMMO ) IMMUNO JAPAN
                                                                                                                                                                                                                                                                                                         26-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 AA;
                                                                                                                                                        which reacts specifically with antibody against sugar chains - useful for inhibition of cancer
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                                                                                                            Japanese.
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. 1.4e-08;
ches 0;
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Sequence

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RESULT 3
AAW94702
                                      The invention relates to a monoclonal antibody (MAb) to lipoteichoic acid cof gram positive bacteria, where the MAb is a chimeric immunoglobulin cc comprising at least part of a human immunoglobulin constant region and cc at least part of a non-human immunoglobulin variable region having capecificity to lipoteichoic acid of gram positive bacteria. The cc antibodies bind to whole bacteria and enhance protection from lethal infection. The antibodies corpeptides (encoded by a DNA of the variable region of anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or cc acid antibody or characterised by amino acids corresponding to one or cc of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating or preventing infections cc caused by gram positive bacteria. They can also be used for the diagnosis of specifically claimed lipoteichoic acid epitope peptide mimic that can be cc bound by the antibody of the invention (Mab 96-110).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibodies to lipoteichoic acid of gram positive bacteria - to develop products for the diagnosis, prevention and treatment infections caused by gram positive bacteria
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 16; Page 120; 150pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-095329/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fischer GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus
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mab 96-110.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lipoteichoic acid epitope peptide mimic for Mab 96-110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monoclonal antibody; MAb; lipoteichoic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
15; Conserv
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    Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phagocytosis; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                          English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 15;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; DB 19;
. 1.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cid; gram positive; bacteria;
epitope; peptide mimic;
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of
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C The present invention.

C The present invention.

C FC domain, pharmacologically active peptides, and linkers. where (1) C FC domain; X1 and X2 = are each 3C (X1)a.F1-(X2)b, where: F1 = an FC domain; X1 and X2 = are each 3C (X1)a.F1-(X2)b. P2-(X2)b. P3-(X2)b. P3-(
RESULT 5
ABB73358
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AAB17987
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Best Local :
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                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel composition of matter comprising an Fc domain and pharmacologically active peptides, useful for treating autoimmune diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMGE-) AMGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-OCT-1998;
22-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor vascular endothelial growth factor; matrix metalloproteinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MMP;
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immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist;
MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1;
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
                                                                                                                                                                                   Local
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                                                                                  WHWRHRIPLQLAAGR
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                                                                                                                                                                  l Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 598; 608pp;
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                                                                                                                                                                  Conservative
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99US-0428082.
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                                                                                                                                                                                 Score 15; DB 21;
Pred. No. 1.4e-08;
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Query Match Best Local Matches 1

Local Similarity 100 nes 15; Conservative 1 WHWRHRIPLQLAAGR 15

100.0%;

Score 15; DB 23; Pred. No. 1.4e-08;

Length

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Mismatches

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Gaps

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The present invention describes a vehicle-peptide molecule (I) or its comultimers. (I) can have antiinflammaticy, antitumour, immunosuppressive, cytostatic, antitrheumatic, antiarthritic, antidiabetic, ophthalmological, antianaemic, anorectic, antiinferthilty, haemostaric, dermatcological and consurprotective activities. (I) can be used as a therapeutic or compondition of contrological and consurprotective activities. (I) can be used as a therapeutic or compondition of interest, for identifying normal purposes. (I) is useful for contein of interest, for identifying normal or abnormal proteins of interest, for identifying normal or abnormal proteins of interest, as a part of diagnostic kit to detect the presence of their conteins of interest in a biological sample. Additionally, (I) is useful conteins of interest in a biological sample. Additionally, (I) is useful conteins of inflammatory and autoimmune diseases, tumour growth, cancer, infertility, and neurological degenerative diseases, tumour growth, cancer, confinetic compounds are useful for treating disorders characterised by compounds and continuents. The TPO-mimetic comprising compounds are useful for treating disorders characterised by compounds and continuents. The treating d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO; erythropoietin; TPO; tumour necrosis factor alpha inhibitor; TPF-alpha inhibitor; interleukin l antagonist; IL-1 antagonist; TMP; TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist; MMP inhibitor; antinflammatory; antitumour; immunosuppressive; cytostatic; antirheumatic; antiarthritic; antiabetic; ophthalmological; antianaemic; anorectic; antiinfertility; haemostatic; dermatological; neuroprotective; inflammatory disease; autoimmune disease; tumour growth; cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity; sleep disorder; neurological degenerative disease; anaemia; thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 39; Page 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel vehicle-peptide molecule or its multimers useful for treating inflammatory and autoimmune diseases, cancer, rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders and infertility -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176pp; English.
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RESULT 6
AAW94729
ID AAWS
RESULT 7
AAW94710
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                                                                                                                                                                                                                           The invention relates to a monoclonal antibody (MAb) to lipoteichoic acid of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and chiling of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for the diagnosis of gram positive bacteria infections.

CC Sequences AAW94726-34 represent common peptide sequences resulting from all library panning experiments. Three series of panning experiments were conducted to identify peptide sequences to which antibody of the invention (Mab 96-110) bound strongly. The translated sequences provide lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
                                                                                                                                                Query Match
Best Local
                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibodies to lipoteichoic acid of gram positive bacteria - used to develop products for the diagnosis, prevention and treatment of infections caused by gram positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria; immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
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15; Conserv
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                                                                                                                                 Score 15; DB Pred. No. 1.7 O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from library panning experiments
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                                                                                                                                 DB 20;
1.7e-08;
nes 0;
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                                                                                                                                   Gaps
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RESULT 8
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                                                                                                                                                                                                                              Query Match
Best Local S
                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies to lipoteichoic acid of gram positive bacteria to develop products for the diagnosis, prevention and treatment infections caused by gram positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunoglobulin; phagocytosis;
mab 96-110; panning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW94710;
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                                              AAW94721;
                                                                         AAW94721
                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15mer2-8/0 resulting from 15mer library panning experiment.
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                                                                                                                                                                                   1 WHWRHRIPLQLAAGR
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DB; AAX05536.
                                                                                                                                                                                                                  Similarity
15; Conserv
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                                                                           standard;
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                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                               AA;
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                                                                           Protein;
                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stinson JL,
                                                                            19
                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                  Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oteichoic acid; gram infection; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                            A
                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                  DB 20;
1.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wong
                                                                                                                                                                                                                                              Length 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide mimic;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                     0
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22-APR-1999

(first entry)

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ARBSULT 9
AAW9470
ID AAW9
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AC AAW9
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DT 22-A
XX
DE Sequ
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AMA
Mab
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Best Local S
Matches 15
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                  Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria; immunoglobulin; phagocytosis; infection; epitope; peptide mimic; Mab 96-110; panning.
                                                                                     Sequence
                                                                                                                                                                                         AAW94705 standard; Protein; 19
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacterial infections. Sequences AAW94705-22 represent sequences resulting from a 15mer library panning second experiment. Three series of panning experiments were conducted to identify peptide sequences to which antibody of the invention (Mab 96-110) bound strongly. The translated sequences provide lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antibodies to lipoteichoic acid of gram positive bacteria - used to develop products for the diagnosis, prevention and treatment of infections caused by gram positive bacteria
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                                                                                                                        22-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin; phac
Mab 96-110; panning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15mer2-19/0 resulting from 15mer library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;
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                                                                                                                                                                                                                                                                                                   WHWRHRIPLOLAAGR 15
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15; Conserv
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                panning
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                                                                                                                      (first entry)
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                                                                                 resulting
                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                   Score 15;
Pred. No.
                                                                                 from 15mer library
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                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   DB 20;
1.7e-08;
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                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                 panning
                                                                                                                                                                                                                                                                                                                                                                                   Length 19;
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                                                                                   experiment.
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                                                                                                                                                                                                                                                                                             RESULT 10
AAW94709
ID AAW94
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Staphylococcus WO9857994-A2. 23-DEC-1998. Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria; immunoglobulin; phagocytosis; infection; epitope; peptide mimic; Mab 96-110; panning.

Sequence 15mer2-7/0 resulting from 15mer library panning experiment.

AAW94709; 22-APR-1999

(first

entry)

AAW94709 standard;

Protein;

19

A

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The invention relates to a monoclonal antibody (MAb) to lipoteichoic acid of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and killing of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacteria infections.

Sequences AAW94705-22 represent sequences resulting from a 15mer library panning second experiment. Three series of panning experiments were conducted to identify peptide sequences of panning experiments were invention (Mab 96-110) bound strongly. The translated sequences provide lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
                                                                                                            Query Match
Best Local S
Matches 15
                                                                                                                                                                                                                         Sequence
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                                                                                                                                       Local Similarity
  w
                                                 1 WHWRHRIPLQLAAGR 15
WHWRHRIPLQLAAGR
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                                                                                                               Conservative
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                                                                                                            Score 15; DE
Pred. No. 1.7
); Mismatches
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                                                                                                                                       DB 20;
1.7e-08;
                                                                                                               0
                                                                                                                                                                 Length 19;
                                                                                                               0,
                                                                                                            Gaps
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of
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RESULT 11
AAW12287
ID AAW12
XX AAW12
XX Synth
XX Toxol
KW Toxol
KW Toxol
KW Glagi
XX Syntl
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a monoclonal antibody (MAb) to lipoteichoic CC acid of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin corporation and at least part of a non-human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and killing of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of cantibodies or peptides (encoded by a DNA of the variable region of corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacterial infections.

CC sequences AAM94705-22 represent sequences resulting from a 15mer library panning second experiment. Three series of panning experiments were conducted to identify peptide sequences to which antibody of the invention (Mab 96-110) bound strongly. The translated sequences provide lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                     Toxoplasma diagnostic
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to develop products for the diagnosis, prevention and treatment
infections caused by gram positive bacteria
                          (JOLI/) JOLIVET-REYNAUD C. (INMR ) BIO MERIEUX.
                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic template peptide for overlapping peptide series
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUN-1997;
                                                                                                                    30-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                     gondii; surface protein; antibody;
assay; immunisation; phage; fusion
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Pred. No.
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hes 0;
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B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                      screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide library;
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RESULT 12
AAW94708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel peptides which bind to antibodies which crecognise the Toxoplasma gondii P30 envelop protein. A peptide library CC was generated to express pentadecapeptides on the surface of a CC filamentous phage as a fusion protein with the PIII protein The library CC was screened with immobilised anti-T. gondii P30 protein antibody lEIE7. CC phages which bind this antibody were recovered and supplified by one CC round of infection in E. coli. The resultant phages were rescreened with the immobilised antibody and the second round screen isolated 58 cancerial colonies antibody and the second round screen isolated 58 cancerial colonies was isolated and sequenced to determine the sequence of the pentadecapeptide encoded. The peptide sequences AAW12276-86 were CC identified. Of the 30 colonies studied, this peptide sequence was cencoded once. A template peptide sequence (AAW12287) corresponding to the sequence across the phage PIII sequence and putative pentadecapeptide was used to generate a series of overlapping corresponded corresponded. These peptides were used to determine the best pentadecapeptides. These peptides were used to determine the best corresponded once and putative the best corresponded once and putative the best corresponded once are the phage PIII sequence and putative the best corresponded to the phage pentades were used to determine the best corresponded once and putative the best corresponded once and putative the pentades are pentades and putative the best corresponded once and putative the best corresponded to the pentades and putative the penta
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Best Local
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                                      WPI; 1999-095329/08
                                                                             Fischer GW,
                                                                                                                                                                                                                                                                                                                           Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                      Mab
                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody; MAb; lipoteichoic acid; gram immunoglobulin; phagocytosis; infection; epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15mer2-5/0 resulting from 15mer library panning experiment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW94708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW94708 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or for active immunisation against T. gondii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jolivet-Reynaud
                                                                                                                                                            16-JUN-1997;
                                                                                                                                                                                                     16-JUN-1998;
                                                                                                                                                                                                                                              23-DEC-1998
                                                                                                                    (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED
                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin;
Mab 96-110; pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 WHWRHRIPLQLAAGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WHWRHRIPLQLAAGR
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15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                  panning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                             Schuman
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A
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                                                                                                                                                          97US-0049871
                                                                                                                                                                                                     98WO-US12402
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                                                                                                                                                                                                                                                                                                                                                                                       phagocytosis;
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                                                                             RF,
                                                                               Stinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 37;
                                                                                                                                                                                                                                                                                                                                                                                          positive;
                                                                                                                                                                                                                                                                                                                                                                                            mimic;
                                                                                                                                                                                                                                                                                                                                                                                                                 bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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N-PSDB; AAX05534

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a monoclonal antibody (MAb) to lipoteichoic CC acid of gram positive bacteria, where the MAb is a chimeric comparising at least part of a human immunoglobulin comprising at least part of a human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable cregion having specificity to lipoteichoic acid of gram positive bacteria. CC The antibodies bind to whole bacteria and enhance phagocytosis and complete that infection. The cartibodies or peptides (encoded by a DNA of the variable region of cc anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions cc (CDRs) of the variable region of the antibody) can be used for treating cc or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacteria infections.

CC Sequences AAW94705-22 represent sequences resulting from a 15mer library cc conducted to identify peptide sequences to which antibody of the convention (Mab 96-110) bound strongly. The translated sequences provide cc invention caid epitope peptide mimics to which antibody -110 bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                 diagnostic
              Claim
                                          acid, vectors and
                                                                                                     N-PSDB;
                                                                                                                                                 Jolivet-Reynaud C;
                                                                                                                                                                                                                               30-JAN-1995;
                                                                                                                                                                                                                                                           29-JAN-1996;
                                                                                                                                                                                                                                                                                          31-JUL-1996
                                                                                                                                                                                                                                                                                                                        EP724016-A1
                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                Toxoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide #6 which binds anti-Toxoplasma gondii P30 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW03372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW03372 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        w antibodies to lipoteichoic acid of gram positive bacteria - us
develop products for the diagnosis, prevention and treatment of
fections caused by gram positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 HWRHRIPLQLAAGR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                       polypeptide reactive with anti-P30 antibodies against Toxoplasma
ii - useful for diagnosis or immunisation, also new nucleic
                                                                                                     1996-343531/35
DB; AAT31328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HWRHRIPLQLAAGR
              7;
                                                                                                                                                                               JOLIVET-REYNAUD C.
BIO MERIEUX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
              Page
                                                                                                                                                                                                                                                                                                                                                                               gond11; surface protein; antibody; screening; peptide library;
assay; immunisation; phage; E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig 6A-B; 150pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
              19;
                                                                                                                                                                                                                             95FR-0001297
                                                                                                                                                                                                                                                           96EP-0420030
                                            transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No.
                                            cells
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1.7e-07;
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RESULT 14
AAW03374
ID AAW0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC Peptides AAW03367-75 are peptides isolated from a peptide library, which to antibody LELE? which recognises the P30 surface protein from CC Toxoplasma gondii. The peptide library was constructed by inserting a CC nucleic acid sequence encoding a random pentadecapeptide in the PIII CC envelop protein of a filamentous phage. Antibody LELE? was immobilised CC on the bottom of a Petri dish and the expressed peptide library was CC overlaid on the antibody. After washing, phages bound on the antibodies CC were recovered and the phage amplified by passage through E. coli. The CC phages were rescreened by the same method and 58 bacterial colonies were recovered. Of these, 30 were further studied and the nucleic acid cencoding the pentadecapeptide was isolated. The nucleic acids encoded CC the peptides AAW12287 was constructed to identify which peptide consequences bound to the anti-P30 antibody. The peptides canning isolated ceptides AAW03367-75. The peptides constructed to identify which peptide cassays to detect T. gondii antibodies in a sample or to purify anti-P30 antibodies in a sample or to purify anti-P30 cantibodies in a sample or to purify anti-P30 antibodies in a sample or to purify anti-P30 antibodies in a sample or to purify anti-P30 cantibodies in a sample or to purify anti-P30 antibodies in a sample or to purify anti-P30 cantibodies in a sample or to purify anti-P30 antibodies in a sample or to purify anti-P30 antibodies in a sample or to purify anti-P30 antibodies canning the page to the page to
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toxoplasma diagnostic
                                                                                                                                                                                                     New polypeptide reactive with anti-P30 antibodies against Toxoplasma gondii - useful for diagnosis or immunisation, also new nucleic acid, vectors and transformed cells
                                                                                                                                                                Claim 7;
                                                                                                                                                                                                                                                                                         WPI; 1996-343531/35.
N-PSDB; AAT31330.
                                                                                                                                                                                                                                                                                                                                                      Jolivet-Reynaud
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW03374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                             (JOLI/) JOLIVET-REYNAUD (INMR) BIO MERIEUX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP724016-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide #8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 HRIPLQLAAGR 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
11; Conser
                                                                                                                                                                Page 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gondii;
assay; i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which binds anti-Toxoplasma gondii P30 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              95FR-0001297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; surface protein; antibody;
immunisation; phage; E.coli.
                                                                                                                                                              33pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.3%;
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Pred. No.
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0.0001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening; peptide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 11;
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Peptides AAW03367-75 are peptides isolated from a peptide library, which bind to antibody IELE7 which recognises the P30 surface protein from Toxoplasma gondii. The peptide library was constructed by inserting a nucleic acid sequence encoding a random pentadecapeptide in the PIII envelop protein of a filamentous phage. Antibody IELE7 was immobilised on the bottom of a Petri dish and the expressed peptide library was overlaid on the antibody. After washing, phages bound on the antibodies

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RESULT 15
ABB83482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   were recovered and the phage amplified by passage through E. coli. The phages were rescreened by the same method and 58 bacterial colonies were recovered. Of these, 30 were further studied and the nucleic acid encoding the pentadecapeptide was isolated. The nucleic acids encoded the peptides AAW12276-86. A series of overlapping peptides based on the peptide template AAW12287 was constructed to identify which peptide sequences bound to the anti-P30 antibody. The peptide scanning isolated peptides AAW3367-75. The peptides can then be used in diagnostic assays to detect T. gondii antibodies in a sample or to purify anti-P30 antibodies or for active immunisation against T. gondii.
The present sequence is the protein sequence for a human cytoskeleton-associated protein (CSAP). The CSAP and its coding sequence are useful in the diagnosis, treatment and prevention of a cell proliferative disorder such as actinic keratosis, atherosclerosis, psoriasis, primary thrombocythaemia, leukaemia; a viral infection such as
                                                                                                                                                                                                                                                                                                                                                                                                                                        Warren
Gandhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JAN-2001; 2001US-260085P.
13-FEB-2001; 2001US-268554P.
14-FEB-2001; 2001US-269111P.
23-FEB-2001; 2001US-271211P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cytoskeleton-associated protein; CSAP; CSAP-11; cell proliferative disorder; viral infection; neurological disorder; transgenic animal, antiatherosclerotic; antipsoriatic; antiinflammatory; virucide; anticonvulsant; vasotropic; cerebroprotective; nootropic;
                                                                                                                                                     Claim 1; Page 134-135; 167pp; English
                                                                                                                                                                                                                                                         treating
                                                                                                                                                                                                                                                                                                                                                                                                              Gietzen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-JAN-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroprotective; cytostatic.
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A, Duggan BM, Xu Y, Walia
R, Khan FA, Thangavelu K,
KJ, Lal PG, Sanjanwala MM,
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ALIGNMENTS

C.Species: Bacillus halodurans
C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: B83740
R;Takaml, H; Nakasone, K; Takaki, Y.; Macno, G.; Sasaki, R.; Masui, N.; Fuji, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83740
A A;Cross-references: GB:AP0015(A;Experimental source: strain C;Genetics: hypothetical protein BH0722 [imported] - Bacillus halodurans (strain C-125)

A;Gene: Query Match Best Local вн0722 GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BAB04441.1; GSPDB:Gce: strain C-125 40.0%; Pr 100.0%; Pr 0; DB . 19;

밁 Ş 9 LQLAAG 14 |||||| 18 LQLAAG 23 18

Matches

Similarity 6; Conser

Conservative

Score 6; DB 2; Pred. No. 19; 0; Mismatches

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Length 82;

RESULT H91187 N

A; Reference number: A99629; M A; Accession: H91187 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-11 <HAY> Query Match
Best Local Similarity
6; Conserv A; Experimental source: C; Genetics: A; Gene: ECs4472 hypothetical protein ECs4472 [imported] - Escherichia coli (strain 0157:H7, substrain C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Date: 18-Jul-1801 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001 C;Accession: H91187 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, Qsaswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796 A;Cross-references: GB:BA000007; PIDN:BAB37895.1; PID:g13363947; A;Experimental source: strain O157:H7, substrain RIMD 0509952 40.0%; Score 6; Pred. No. DB . . . 25; Ŋ Length 111; GSPDB:GN00154 substrain റ ڡ

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C;Accession: S60210
R;Hidaka, T.; Goda, M.; Kuzuyama, T.; Takei, N.; Hidaka, M.; Seto, H Mol. Gen. Genet. 249, 274-280, 1995
A;Title: Cloning and nucleotide sequence of fosfomycin biosynthetic A;Reference number: S60207; MUID:96091152; PMID:7500951
A;Accession: S60210
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S57954
                                                                                                                                                   fomA protein - Streptomyces wedmorensis
C;Species: Streptomyces wedmorensis
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997, #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeference number: A69250; MUID:98049343; PMID:9389475
A;Accession: F69381
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R;Mouncey, N.J.: Mitchenall, L.A.; Pau, R.N.
submitted to the EMBL Data Library, June 1995
A;Description: Mutational analysis of genes of
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C;Species: Azotobacter vinelandii
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 08-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Do.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               flagellin (flaB1-1) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
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A:Status: nucleic acid sequence not A:Molecule type: DNA
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A; Residues: 1-142 <MOU>
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A; Accession: S57954
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A; Dolecule type: DNA
A; Residues: 1-309 < KUR>
A; Cross-references: GB: AE008917; PIDN: AAL52733.1;
A; Cross-references: Strain 16M
                                                                                                                                                                                                                                                                                                                                                      hypothetical exported protein BMEI1552 [imported] - Brucella melitensis (strain C;Species: Brucella melitensis C;Species: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Start codon: GTG C;Superfamily: Methanobacterium thermoautotrophicum
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A;Cross-references: EMBL:D38561; NID:g1060999; PID:g1061005
A;Note: the nucleotide sequence was submitted to the EMBL D3
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                                                                                                                                                                                                                         A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit A;Reference number: AD3252; PMID:11756688 A;Accession: AB3446
                                                                                                                                                                                                                                                                               R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, Qil, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwan ki, S.; Church, G.M.; Dantels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J., J. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 05-Dec-1997 #sequence_revision
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A;Experimental source: strain Delta H
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A; Residues: 1-254 <MTH>
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|96 LQLAAG
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6 RIPLQL

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R: Davles, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fras
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.;
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: D87068
                                                                                                                                                                                                                                  A;Cross-references: GB:AL591985; PIDN:CAC49524.1; PID:g15141011; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymb
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barlo
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisl
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.;
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing enda A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: D95982
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hypothetical protein Mil274 [imported] - Mycobacterium leprae C:Species: Mycobacterium leprae C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change C:Accession: D87068
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R.; Davies,
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A; Genome: plasmid
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A; Residues: 1-334 <KUR>
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nes 6; Conserv
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A.; Hamlin, N.;
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RESULT 10

references: DDBJ:AB000619; NID:g2749770; PIDN:BAA24108.1;

PID:d1025015;

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C:Accession: D75486

R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.: Peterson,
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.: Utterback,
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: D75486
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D75486
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                                             R;Chen, L.; Sato, M.; Inoko, H.; Kimura, M. Blochem. Blophys. Res. Commun. 240, 261-268, 1997
A;Title: Molecular cloning and analysis of novel cDNAs specifically A;Reference number: JC5788; MUID:98049818; PMID:9388464
A;Accession: JC5788
                                                                                                                                                                                    tsec-1 protein (A and B) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 24-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 05-Nov-1999
C;Accession: JC5788; JC5789
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A; Residues: 1-342 <BAD>
A; Cross-references: EMB
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JC5788
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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C; Superfamily: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-344 \max.
A; Cross-references: GB: AE001927;
A; Cross-references: strain R1
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A; Molecule type: mRNA
A; Residues: 1-347 <CHE>
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A; Residues: 1-344 <WHI>
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T.; Zalewski,
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alpha-1-antiproteinase S-1 precursor - rabbit (C:Species: Oryctolagus cuniculus (domestic rabbit) (C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000 C:Accession: JX0267 R;Saito, A.; Sinohara, H. J. Biochem. 113, 456-461, 1993 A:Reference number: JX0267; MUID:93293795; PMID:8514734 A:Accession: JX0267; MUID:93293795; PMID:8514734 A:Accession: JX0267; MUID:93293795; PMID:8514734
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                                                                                                                             F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-413/Product: alpha-1-antiproteinase S-1 #status experimental <MAT>
F;65,102,266/Binding site: carbohydrate (Asn) (covalent) #status predic
                                                                                                                                                                                                           A;Cross-references: GB:D16104; NID:g286191; PIDN:BAA03678.1; PID:g303762
A;Experimental source: liver
A;Note: part of this sequence, including the amino end of the mature protein, was confix C;Superfamily: antithrombin III
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A; Residues: 1-413 <SAI>
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Mol. Gen. Genet. 215, 381-387, 1989
A;Title: Structure of the dnaA region of Pseudomonas putida: conservation among three ba
A;Reference number: JY0002; MUID:89218947; PMID:2540413
A;Accession: JY0002
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C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Jun-1999
C;Accession: JV0002
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C;Comment: This protein plays a role in mammalian spermatogenesis.
F;38-80,201-332/Domain: coiled-coil #status predicted <CDC>
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A; Accession: type: mRNA
A; Residues: 1-347 <CH2>
                                                                                                                                                                                           C; Keywords: glycoprotein
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A; Residues: 1-367 <FUJ>
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                                                                   Query Match
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b; Pred. No. 74;
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Search completed: November 27, Job time: 6.25869 secs

2002, 07:31:20

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-413 <RAY>
A;Cross-references: GB:L12139; NID:g405551; PIDN:AAA57133.1;
C;Superfamily: antithrombin III
                                                                                                                                                                                                                                                                R;Ray, B.K.; Gao, X.; Ray, A.

J. Biol. Chem. 269, 22080-22086, 1994

A;Title: Expression and structural analysis of a novel highly inducible gene encoding A;Reference number: A54968; MUID:94350954; PMID:8071331
                                                                                                                                                                                                                                                                                                                             alpha-1-antitrypsin precursor - rabbit (Species: Oryctolagus cuniculus (domestic rabbit) (C; Species: Oryctolagus cuniculus (domestic rabbit) (C; Date: 11-Nov-1994 *sequence_revision 11-Nov-1994 *text_change 16-Jul-1999 (C; Accession: A54968 R; Ray, B.K.; Gao, X: Ray, A.
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| SOURCE ORGANISM REFERENCE AUTHORS TITLE | ACCESSION VERSION KEYWORDS | RESULT 1 MMIG013 LOCUS DEFINITION | | 5 4 | ω . | 200 | o o | 8 2 2 | 5 | ມ ເມ ກ 4- ຕ ນ 2 ເ | 2 2 | 2 | o w o | 8 2 | 2 N 2 O | 2 4 | · ω . ω | 21 | 201 | 9 B | 70 | ມຕ | 4 υ | . ω . ω | ωu | ا د ا | w w | ωt | υw | | ωw | Result No. So |
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Structural characterization of antiidiotypic antibodies. Evidence that Ab2s are derived from the germline differently than Ab1s J. Exp. Med. 169 (2), 519-533 (1989)
     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (09-JAN-1989) K. Meek, University of Texas Southwestern Medical School, 5323 Harry Hines Blud. Microbiology, Dallas Texas
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/translation="QIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPK
PWISATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCHQWSSNPPTFGGGTK
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Putterman, C., Deop
Direct Submission
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20143847
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Mammalia; Eutheria;
1 (bases 1 to 318)
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               AF178619
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318 bp mRNA 18-3 immunoglobulin light chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Putterman, C., Deocharan, B. and Diamond, B. Molecular analysis of the autoantibody re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="immunoglobulin light chain variable region"
/protein_id="AAD54373.1"
/protein_id="5853224"
/translation="GIYLFQSPAILSASPGEKVTMTCRASSSVSYMLWYQQKPGSSPK
PMIYATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="BALB/c"
/db_xref="taxon:10090"
/cell_line="39-9"
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/note="from peptide-immunized mouse"
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Rodentia;
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Pred. No. 1.8e-89;
D; Mismatches 9;
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Sciurognathi;
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thi; Muridae;
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murinae; Mus
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                                                                                          CCATGCTGGAAATAAGA 318
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307; Conserv
 AR096128
Sequence
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Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia: Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (17-AUG-1999) Rheumatology/Medicine, Albert Einstein College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, U. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
1 (bases 1 to 318)
Putterman,C., Deccharan,B. and Diamond,B.
Molecular analysis of the autoantibody response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Putterman, C., Deocharan, B. and Diamond, B.
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  6 from
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/protein_id="AAD54372.1"
/db_xref="Gi:$85322"
/translation="KIVISQSPAILSASPGQKVTMTCRASSSVSYMLWYQQKPGSSPK
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/strain="BALB/c"
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/cell_line="8-3"
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321 bp
patent US 6005091.
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Pred. No. 2.8e-89;
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 307; Conser
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Sequence 6
AR210527
                                                                                                Blackburn, M. Neal., Church, W. Robert., Feuerstein, G. Zeev., Gross, M. Stuart., Nichols, A. John., Padlan, E. Aqustin., Patel, A. Haribhai. and Sylvester, D. Robert. Anti-factor IX/IXa antibodies
Patent: US 6391299-A 6 21-MAY-2002;
Location/Qualifiers
                                                                                                                                                               1 (bases 1 to 321)
Blackburn, M. Neal.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 321)
Blackburn, M.Neal., Church, W.Robert., Feuerste Gross, M.Stuart., Nichols, A.John., Padlan, E.Ag. Patel, A. Haribhai. and Sylvester, D. Robert. Nucleic acids encoding immunoglobulin domains Patent: US 6005091-A 6 21-DEC-1999; Location/Qualifiers
                                                                                                                                                                                                        Unknown
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                                                          /organism="unknown"
92 c 79 g
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92 c 79 g
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          94.5%;
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pred. No. 4.5e
0; Mismatches
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Pred. No. 4.5e-89;
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             4.5e-89;
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AR000010
AR000010.1
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Anderson, D.R., Hanna, N., Leonard, J.E., Newman, R.A., F
Rastetter, W.H.
Therapeutic application of chimeric and radiolabeled
human B lymphocyte restricted differentiation antigen
of B cell lymphoma
Patent: US 5736137-A 6 07-APR-1998;
                                                                                                                                                                                                                                                                             Unknown
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Similarity 96.5%;
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Pred. No. 4.5e-89;
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         Unclassified.

(bases 1 to 384)
Anderson,D.R., Hanna,N., Newman,R.A., Chimeric and radiolabelled antibodies antigen and use thereof for treatment Patent: US 6399061-A 6 04-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.

1 (bases 1 to 384)

1 (bases 1, Newman, R.A., Re Anderson, D.R., Hanna, N., Leonard, J.E., Newman, R.A., Re Rastetter, W. H.

Therapeutic application of chimeric and radiolabeled a human B lymphocyte restricted differentiation antigen of B cell lymphoma

Patent: US 5843439-A 6 01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 96.
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                                                        ATGACTTGCAGGGCCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA 120
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Sequence 6 from Patent EP1005870
AX032417
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                                                                                                                                                                                                                                          Therapeutic application of chimeric antibodies to human b lymphocyte restricted differentiation antigen for treatment of {\bf b}
                                                                                                                                                                                                                                                                        1 (bases 1 to 384)
Rastetter, W.H., Hanna, N., Leonard, J.E.,
                                                                                                                                                                                                                                                                                                       unidentified
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                                                                                                                                                                                                                                                                                                                                   AX032417.1 GI:10279390
                                                                                                                                                                                                                           Patent:
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                                                                                                                                                                                                                 lymphoma
nt: EP 1005870-A 6 07-JUN-2000;
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Location/Qualifiers
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105 c 93 g
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105 c 93 g
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BD004717 556666
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C A61K39/395, A61K31/375, A61K31/573, A61K31/664, A61K31/704,
A61K45/00, A61P35/00,
PC C07K16/28, C07K16/46, G01N33/53//C12N5/10, C12N15/09, C12P21
PC C12P21/08,
PC (C12P21/08,
PC (C12P21/02, C12R1:91), (C12P21/08, C12R1:91), C12N5/00, C12N1
PC (C12P21/02, C12R1:91), (C12P21/08, C12R1:91), C12N5/00, C12N1
PC (C12P21/02, C12R1:91), (C12P21/08, C12R1:91), C12N5/00, C12N1
PT SOURCE 1, 384
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PN JP 2001010974-A/5
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PR 13-NOV-1992 US 07/978891,03-NOV-1993 US
DURRELL R ANDERSON,WILLIAM H RASTETTER,NABIL HANNA,
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JP 2001010974-A/5.
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/db_xref="taxon:9606"
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1 (bases 1 to 9
Anderson, D.R., H
Rastetter, W.H.
Sequence 3
AR060920
AR060920.1
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Unclassified.
Unclassified.
1 (bases 1 to 9209)
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2 Anderson, D.R., Hanna, N., Newman, R.A., Reff, M.E. and Rastetter, Indicator, Indic
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Sequence 3 from patent US 6399061.
AR211052
AR211052.1 GI:21514277
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1 (bases 1 to 9209)
Anderson,D.R., Hanna,N., Leonard,J.E., Newman,R.A., Reff,M.E. an Rastetter,W.H.
Therapeutic application of chimeric and radiolabeled antibodies
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                                                                                                                      TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCAGCAGAGTGGAGGCTGAA
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                                         CAAATTGTTCTCCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGGAGAAGGTCACA 1104
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ACCATGCTGGAAATAAGA 318
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Therapeutic application of chimeric antibodies lymphocyte restricted differentiation antigen f
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IDEC PH
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Rastetter, W.H., Hanna, N., Leonard, J.E., Newman, R.A.,
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                   307;
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PC 461K39/395, 461K31/375, 461K31/573, 461K31/664, 461K31/704, 461K45/00, 461F35/00, 461F35/00, 61F35/00, 61F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OS Homo sapiens (human)
PN JP 2001010974-A/2
PD 16-JAN-2001
PF 21-APR-2000 JP 2000126317
PR 13-NOV-1992 US 07/978891,03-NOV-1993
DURRELL R ANDERSON,WILLIAM H RASTETTER,NABIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BD004714 9209 bp DNA linear PAT 31. Chimeric antibody against human B lymphocyte limited differentiation antibody for remedy of B cell lymphoma and therapeutic use of radiolabeled antibody.

BD004714 BD004714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anderson, D.R., Rastetter, W.H., Hanna, N., and Reff, M.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 9209)
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Perfect score:
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2: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
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/SIDS2/gcgdata/geneseg/genesegn-embl/NA2001a.DAT:*
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| Result No. | Score | Query Match | Query Match Length DB | | ID | Description |
|---------------|-------|----------------|--------------------------|----|----------|--------------------|
| ۳ | 300.4 | 94.5 | 321 | 18 | AAT77377 | Mouse anti-human F |
| ν | 300.4 | 94.5 | 321 | 24 | ABK23937 | Murine BC2 light c |
| ω | 298.8 | 94.0 | 384 | 15 | AAQ65630 | Murine variable re |
| 4 | 298.4 | 93.8 | 19001 | 19 | AAV61793 | Traget plasmid Mol |
| G | 297.2 | 93.5 | 449 | 21 | AAA43472 | Mouse secreted exp |
| ტ | 297.2 | 93.5 | 708 | 21 | AAA63530 | DNA encoding a dim |
| 7 | 297.2 | 93.5 | 9208 | 15 | AAQ65629 | Vector contg. TCAE |
| 6 0 | 295.6 | 93.0 | 318 | 18 | AAT79900 | Anti-Factor IX MAD |
| 9 | 295.6 | 93.0 | 318 | 24 | ABK24005 | Mouse-human light |
| | | | | | | |

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 3 5 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 | 19 | 18 | 17 | 16 | 15 | 14 | <u>μ</u> | 12 | 11 | 10 |
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| 278 | 278 | 280.2 | 280.2 | 281.2 | 281.2 | 281.4 | 281.4 | 281.8 | 283.4 | œ | • | • | 287.6 | ٠. | • | • | | 289.4 | 290.8 | 290.8 | 292.4 | 293 | 293 | 95. | 95. | 95. | 95. | 95. | 95. | | 95. | 95. | 95. | | |
| 87.4 | 87.4 | 88.1 | | | | | | • | • | 89.3 | | | • | | 90.6 | • | • | • | • | • | 91.9 | • | • | • | • | • | • | • | • | 93.0 | • | • | • | 93.0 | 93.0 |
| 420 | 321 | 711 | 711 | 759 | 758 | 711 | 711 | 321 | 1590 | 765 | 318 | 3217 | 705 | 435 | 435 | 1280 | 1239 | 765 | 732 | 732 | 387 | 1925 | 387 | 426 | 426 | 426 | 426 | 426 | 426 | 404 | 404 | 0 | 0 | 335 | ω |
| 12 | 10 | 21 | 17 | 22 | 21 | 18 | 15 | 14 | 20 | 22 | 24 | 20 | 20 | 14 | 12 | 22 | 22 | 22 | 20 | 17 | 13 | 21 | 13 | 19 | 19 | 19 | 18 | 18 | 18 | 22 | 20 | 10 | œ | 24 | 18 |
| AAQ11970 | AAN91661 | AAZ98748 | AAT17728 | AAC60426 | AAA60937 | AAT65006 | AAQ55180 | AAQ39412 | AAX24806 | AAC86591 | AAS97128 | AAV72076 | AAV72047 | AAQ36613 | AAQ15115 | AAC86564 . | AAC86563 | AAC86590 | AAV72081 | AAT42508 | AAQ20983 | AAA15019 | AAQ27350 | AAV18594 | AAV18558 | AAV03927 | AAT51043 | AAT70869 | AAT36317 | AAH22071 | AAV82358 | AAN91147 | AAN70972 | ABK24004 | AAT79899 |
| Sequence encoding | | Nucleotide sequenc | bB2 so | L6 sFv DNA. Unide | Chimeric L6 anti-t | Single-chain anti- | Sequence encoding | Mab32 light chain | A5B7 F(ab')2 codin | _ | Anti-NKG2D hybrido | IRES-based A587 ch | Plasmid pNG3/A5B7V | Anti-IL2R-alpha an | IL-2 chimeric anti | Anti-CD20 single c | a | DNA encoding a fus | 4 | Murine ASB57 Light | Encodes Variable r | DNA encoding a CD- | Encodes A5B7 antib | Mouse 2H7 antibody | 2H7 | H7 antibo | Coding sequence fo | light cha | | 2H7 light chain va | se antibody | 2H7 Vh sequence. | | Ligh | Anti-Factor IX MAD |

ALIGNMENTS

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26-DEC-1997
                           AAT77377;
                                                   AAT77377 standard; cDNA; 321
(first entry)
                                                   ВР
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Mouse anti-human Factor IX antibody BC2 light chain cDNA

Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody; humanised antibody; antibody engineering; light chain; CDR; complementarity determining region; myocardial infarction; angina; atrial fibrillation; stroke; kidney damage; pulmonary embolism; deep vein thrombosis; coronary angioplasty; shunt; prosthesis; pulmonary embolism; deep vein thrombosis; coronary angioplasty; disseminated intravascular coagulation; artificial organ; sepsis; SS.

RESULT 1
AAT77377
ID AAT77377
XX AAT77377
XX AAT77
XX AAT7
XX AAT7
XX Phrc
DT 26-I
DT 24-OCT-1996; 17-JAN-1996; 17-JAN-1997; (SMIK) SMITHKLINE BEECHAM CORP. (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE. 24-JUL-1997. WO9726010-A1 Mus musculus 96US-0029119 96US-0010108 97WO-US00759

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RESULT 2
ABK23937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC AAW24520) of mouse anti-human Factor IX monoclonal antibody BC2.
CC Claimed humanised antibodies (see AAW24510-18) contain CDRs (see
CC AAW24504-99) of BC2 heavy and light chains inserted into framework
CC regions of selected human antibody sequences. They have self-
CC limiting neutralising activity, and are useful as anticoagulant
CC agents in treatment of thrombosis associated with myocardial
CC infarction, unstable angina, atrial fibrillation, stroke, renal
CC damage, pulmonary embolism, deep vein trombosis, percutaneous
CC transluminal coronary angioplasty, disseminated intravascular
CC coagulation, sepsis, or artificial organs, shunts or prostheses
CC (claimed). Also claimed are chimeric antibodies (see AAT79900), and
CC Fab and F(ab') 2 fragments. The claimed antibodies do not cause
CC uncontrolled bleeding (contrast heparin and warfarin) since they
CX
C provide only partial inhibition of coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
Human; mouse; BC2; animal post-thromboembolic induced ischaemia;
thrombolytic agent; anti-factor IX antibody; plasminogen activat
thromboembolic stroke; cerebroprotective; anticoagulant; Thrombo
vasotropic; cardiant; PCR primer; anti-respiratory syncytial vir
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Nichols AJ, Padlan
                                                           Murine
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                                                                                                                                                                                    ACCAAGCTGGAAATCAAA
                                                         BC2 light
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                                                                                                                             standard; cDNA;
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                                                        chain variable
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A, Patel AH, Sylvester
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Pred. No. 3.3e-77;
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                                                        region
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          activator; ss
Thrombolytic;
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RESULT 3
AAQ65630
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AC AAQ6
XX

AAQ65630 standard;

DNA;

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ВP

AAQ65630

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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                               rne invention relates to a method for treating an animal post-thromboembolic induced ischaemia or reducing a required dose of a thrombolytic agent in treatment of an animal post-thromboembolic induced ischaemia, comprising administering an anti-factor IX antibody or its fragment, optionally in combination with a plasminogen activator or thrombolytic agent. The method is useful for treating post-thromboembolic-induced ischaemia, for preventing thromboembolic stroke in an animal, and for reducing a required dose of a thrombolytic agent. Sequences ABK23932-ABK24009 represent DNA molecules encoding antibodies and PCR primers used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example
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                                                                                                                                                                                                                                                                                                                                                                              Sequence
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ACCAAGCTGGAAATCAAA
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318
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Pred. No. 3.3e
0; Mismatches
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RESULT 4
AAV61793
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Best Local S
Matches 306
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            AAV61793;
                               AAV61793 standard;
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03-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 306; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                sequence is the murine variable region light chain ine anti-CD20 monoclonal antibody 2BS. also AAQ65629-35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    musculus
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                                                                                            ACCATGCTGGAAATAAGA
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rapid depletion of peripheral B cells, also new
les and hybridomas
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    Rhesus macaque p
    Photinus sp.
    Salmonella typh:

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Cytomegalovirus.
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on; vector; neomycin phosphotransferase;
arker; immunoglobulin; CD20; C2B8; human;
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from the sequence given in the
specification. It is included to
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| the sequence gi- iffication. It i- tain the nucleot ification for th | "This base represents a nucleotide from the sequence given in the specification. It is included to maintain the nucleotide numbering specification for this sequence" or this base represents a nucleotide | these bases represent nucleotides from the sequence given in the specification. They are included maintain the nucleotide numbering specification for this sequence" | specification for this sequence" 13382 These bases represent nucleotides from the sequence given in the specification. They are included maintain the nucleotide numbering specification for this sequence". | "these bases represent nucleotides from the sequence given in the specification. They are included maintain the nucleotide numbering specification for this sequence" 12422 n n these bases represent nucleotides from the sequence given in the specification. They are included maintain the nucleotide numbering | specification for this sequence" 1 "this base represents a nucleotide from the sequence given in the specification. It is included to maintain the nucleotide numbering specification for this sequence". 12062 | Truese bases represent nucleotites from the sequence given in the specification. They are included maintain the nucleotide numbering specification for this sequence" 8522 * K * These bases represent nucleotides from the sequence given in the specification. They are included maintain the nucleotide numbering | specification of this lift in this lift in the specification of the spec |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the nucleotide sequence of novel target plasmid Molly. The plasmid includes the murine dihydrofolate reductase (DHFR) components that it is considered that the Escherichia coli beta-galactosidase gene, baculovirus coling, a cassette comprising the promoter and enhancer elements from cytomegalovirus and SV40 virus, the E. coli beta-glucuronidase (GUS) gene, firefly luciferase gene, Salmonella typhimurium histidinol dehydrogenase gene (HiSD) and transposon This neomycin phosphotransferase (neo) gene sequences, in a pBR-derived backbone, and also an anti-B cell antigen CD20 chimeric antibody C2B8 gene. The invention provides a novel method for integrating a desired exogneous DNA at a target site within the genome of a mammalian cell via homologous recombination. This involves transfecting the contains a unique sequence that is foreign to the mammalian cell genome and which provides a substrate for homologous recombination, the transfection with a 'target plasmid', such as Wolly or Mandy (see AN61794), containing a sequence which provides for homologous recombination with the unique sequences contained in the mammalian cells, typically an immunoglobulin or other secreted mammalian glycoprotein. The homologous recombination system utilises the new cene as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nmunoguoputi of order system utilises the neo gene as a compologous recombination system utilises the neo gene as a series of the neo gene is split into 3 of 
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4-MAR-1997;
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Chemokinetic; proliferative; immunomodulatory, haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; Cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antibacterial; antifungal; antiviral; antidiabetic; cantiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective; Conotropic; antiparkinsonian; antipsoriatic; cerebroprotective; anticonvulsant; and antidepressant. The sESTs can be used for gene contemps and in vaccines. The sESTs are useful as probes for the contemps and in vaccines of tull-length cDNAs and genomic DNA concludes which correspond to the sESTs. Proteins encoded by the sESTs care useful in assays for determining biological activity and raising cantibodies. They may be useful for treatment of autoimmune disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (sthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, costeoporosis, osteoarthritis, central nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W Human; mouse; chicken; rat; secreted expressed sequence tag; sEST;

W expressed sequence tag; EST; probe; chemotactic; proliferative;

W immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic;

W thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal;

W antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian;

W antiulcer; osteopathic; neuroprotective; nootropic; antiparkinsonian;

W archiverective; anticonvulsant; antidepressant; gene therapy;

KW derebroprotective; anticonvulsant; antidepressant; gene therapy;

KW vaccine; autoimmune disorder; multiple sclerosis; allergic condition;

KW insulin dependent diabetes; asthma; mycloid cell deficiency; ulcer;

KW insulin dependent diabetes; asthma; mycloid cell deficiency; ulcer;

KW vaccine; autoimmune disorder; Alzheimer's disease; stroke;

KW central nervous system disorder; Alzheimer's disease; stroke;

KW central nervous system disorder; Alzheimer's disease; stroke;

KW parkinson's disease; Huntington's disease; coagulation disorder;

KW haemophilia; thrombosis; inflammatory disorder; Crohn's disease;

KW tumour; infection; depression; psoriasis; ss.
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                                                                                                                                                                                                                                                                                                                          AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (sESTs), isolated from human, mouse, chicken and rat tissue sources. The sESTs can have a range of activities depending on the tissues they were isolated from. The activities include:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Merberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jacobs K,
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Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 214; 803pp; English.
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Bowman MR;
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Best Local Sim
Matches 305;
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Chimeric
                                                                                                                                                                                                                             complement system; regamma receptor; cytotoxic effector cell; host immune cell; programmed cell death; allergic disorder; cancer; autoimmune disease; allergic asthma; atopic dermatitis; Crohn's diseas allergic bronchopulmonary aspergillosis; allergic rhinitis; cancer; Graves's disease; food allergy; allergic contact dermatitis; cancer; B-cell lymphoma; rheumatoid arthritis; ulcerative colitis; psoriasis; pigeon breeder's disease; hepatitis; leprosy; Lyme disease; pigeon breeder's disease; hepatitis; leprosy; Lyme disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA45926 to AAA45931 represent linker variants which are given
                                                                                                                                          CDS
                           misc_feature
                                                                           misc_feature
                                                                                                    sig_peptide
                                                                                                                                                                                                                     diabetes
                                                                                                                                                                                                                                                                                                                      Anti-CD20 antibody; dimeric immunoglobulin; immunoglobulin;
                                                                                                                                                                                                                                                                                                                                               DNA encoding a dimeric anti-CD20 light chain polypeptide
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"encodes human kappa light chain constant region"
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                                                                                                               "dimeric anti-CD20 light chain polypeptide"
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                                                  murine
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                                                   anti-human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC invention. The specification describes a method for producing an communoglobulin (Ig) G/IgG dimer. The method comprises genetically CC engineering a monoclonal antibody to introduce a cysteine molecule CC which inhibits formation of intramolecular disulphide bridges between CC sister heavy chains on the same antibody molecule. The dimer is a CC homodimer or heterodimer that is capable of activating components of the CC complement system, and has the ability to activate and kill cells via the CC complement cascade. The dimer is also capable of binding to Fogamma CC creeptors on cytotoxic effector cells and on host immune cells, and is CC capable of initiating programmed cell death. The IgG/IgG dimers may be CC used to treat allergic disorders, cancers and autoimmune diseases such as allergic bronchopulmonary aspergillosis, allergic CC rhinitis, atopic dermatitis, Crohn's disease, Graves's disease, food CC allergies, allergic contact dermatitis, CLL cancers and/or B-cell CC unphomas. They may also be used to treat a range of other diseases and CC disorders such as rheumatoid arthritis, ulcerative colitis, psoriasis, CC pigeon breeder's disease, hepatitis, leprosy. Lyme disease, diabetes mellitus, candidiasis and aplastic anaemia. They are also useful for CC inducting hyper-cross-inking of membrane antigens and for the
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetically engineering immunoglobulin (Ig) treatment of cancers, allergic disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 708
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                                                                                                                                                                                                                                                                                                                    CAAATTGTTCTCCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTCACA 126
                             ACCATGCTGGAAATAAGA 318
                                                                            TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA
                                                                                                                                                                                                         TCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC
                                                                                                                                                                                                                                                        ATGACTTGCAGGGCCAGCTCAAGTGTAAGTTACATCCACTGGTTCCAGCAGAAGCCAGGA
                                                                                                                                                                                                                                                                        ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA 120
                                                                                                                                                                                          TCCTCCCCCAAACGCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCCTGTTCGC
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The dimeric immunoglobulin is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP; 180
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Pred. No. 3.5e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence shows a vector contg. TCAE8, a gene encoding a chimeric anti-CD20 antibody for treatment of B cell lymphomas. TCAE8 contains 4 transcriptional cassettes, human Ig light and heavy chain constant regions, dihydrofolate reductase, neomycin phosphotransferase and murine variable regions. The vector can be used to produce
                                                                                                                                                     1164
                                                                                                                                                                                                                                                        1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibodies which cause depletion of peripheral blood B cells, including those associated with lymphoma. They mediate complement-dependent lysis and lyse target cells by antibody-dependent cellula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B cell lymphoma chimeric antibody; CD20; peripheral blood cell lysis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ65629 standard;
                                                    1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating B cell lymphoma with chimeric antibody - accusing rapid depletion of peripheral B cells, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-NOV-1992;
03-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9411026-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vector
                                                                                                                                                                                                                                                                                                                                                      1044 CAAATTGTTCTCCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTCACA 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9208 BP; 2237 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               See also AAQ65629-35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IDEC-) IDEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAY-1994
                                                                                                                                                                                                      121
                                                                                                   181
                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                 1 CAAATTGTTCTCTCCCAGTCTCCCAGCAATCCTGTATCTGCATCTCCAGGGGAAAAGGTCACA 60
                                                                                                                                                                                                                                                                                ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGCTACCAGCAGAGAGCCAGGA 120
  TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCAGCAGAGGGGGGGAA
                                                                                                                                                     TCCTCCCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCCTGTTCGC
                                                                                                                                                                               TCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC
                                                                                                                                                                                                                                                           ATGACTTGCAGGGCCAGCTGAAGTGTAAGTTACATCCACTGGTTCCAGCAGAAGCCAGGA
                                                    TTCAGTGGCAGTGGGTCTGGGACTTCTTACTCTCTCACCATCAGCAGAAGTGGAGGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 95.9
05; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and hybridomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 3; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAE
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93US-0149099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 DNA
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95.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2399 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 297.2; DB
Pred. No. 7e-76;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JΕ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2388 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Newman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             against CD20
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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RESULT 8
AAT79900
ID AAT79900
ID AAT79900
ID AAT79
AX AAT7
AX AAT7
AX AAT7
AX Thrc
KW Thrc
KW Chin
OS 
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                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1284
                                                                                                                                                                                                                                                                                                                                                                                                                 This cDNA sequence encodes a mouse-human chimeric antibody light chain (AAW24532) in which the variable region is derived from mouse anti-human factor IX monoclonal antibody BC2 cDNA (see AAT79899) and human sequences from the immunoglobulin RF-TS3'CL framework. It was obtained by PCR amplification (see AAT79897-98) of BC2 cDNA and insertion of the PCR product into P9HZHC 1-3 cDNA of SC2 cDNA and insertion of the PCR product into Typication (see AAT77374). Claimed anti-Factor IX chimeric antibodies are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombosis; therapy; Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT79900 standard;
                                                                                                                                                                                                                                                                                                                                                 Sequence 318 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAW24532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9726010-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chimeric antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT79900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 7; Page 128; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inhibiting thrombosis with self-limiting antibody (factor - avoids uncontrolled bleeding by providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blackburn MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP. (UYVE-) UNIV VERMONT & STATE AGRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
  121
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                                                                                                 61
                                                                                                                                                                         1 CAAATTGTTCTCTCCCAGGCTCTCCCAGCAATCCTGTTCTGCATCTCCAGGGGAAAAGGTCACA
                                                                          ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1997-385117/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCTCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC
                                                                                                                                                CAGATAGTACTCCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAAAGGTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCAAGCTGGAAATCAAA 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCATGCTGGAAATAAGA 318
                                                ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA
                                                                                                                                                                                                                                                    304;
                                                                                                                                                                                                                                                                                                                                                                                                  in the treatment of thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ĘĄ,
                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IX MAD chimeric light chain cDNA.
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Church WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96US-0029119
96US-0010108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y, ractor ix; anticoagulant; monoclonal antibody;
antibody engineering; light chain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EA,
                                                                                                                                                                                                                                                                                                                                                 A; 91 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                      93.0%;
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                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                      Score 295.6; DB 1
Pred. No. 8.1e-76;
                                                                                                                                                                                                                                                                                                                                              78 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
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                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                             DB 18; · Length 318;
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RESULT 9
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ID ABKX
XX ABKZ2
XX ABKZ
XX ABKZ
XX ADKZ
XX Huma
DE MOUS
KW Chirc
KW Chirc
KW Chirc
KW Chirc
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OS Chim
OS Chi
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                                                                    The invention relates to a method for treating an animal post-thromboembolic induced ischaemia or reducing a reguired dose of a thrombolytic agent in treatment of an animal post-thromboembolic induced ischaemia, comprising administering an anti-factor IX antibody or its fragment, optionally in combination with a plasminogen activator or thrombolytic agent. The method is useful for treating thromboembolic-induced ischaemia, for preventing thromboembolic stroke in an animal, and for reducing a required dose of a thrombolytic agent. Sequences ABK3393-ABK24009 represent DNA molecules encoding agent. Sequences ABK3393-ABK24009 represent DNA molecules encoding
                                                                                                                                                                                                                                                                                                                                                                                                               Treating post-thromboembolic induced i administering anti-factor IX antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       thrombolytic agent; anti-factor IX antibody; plasminogen activator; ss thrombolytic stroke; cerebroprotective; anti-coagulant; Thrombolytic; vasotropic; cardiant; PCR primer; anti-respiratory syncytial virus; heavy chain variable region; light chain variable region.
  Sequence
                                                       antibodies
                                                                                                                                                                                                                                                                                                                                          Example 7; Page 154-155; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barone FC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-2000; 2000US-0571434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-OCT-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-APR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK24005 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM CORP
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DB; AAU81002.
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  318
                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blackburn MN,
  B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000WO-US27438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapiens
  79
                                                    primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA;
  A; 91 C;
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                                                       used
  78 G;
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                                                    represent DNA
the method of
  70 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                             ischaemia in an animal y in combination with a
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                                                                                                                                                                                                                                                                                                                                                                                                                             plasminogen
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Matches Query Match

304;

Conservative

<u>.</u>

Mismatches

Indels Length

Gaps

0

318; 0

Local Similarity

93.0%;

Score 295.6; DB 24; Pred. No. 8.1e-76;

61

В 5

 \vdash -

CAAATTGTTCTCCCCAGTCTCCCAGCAATCCTGTCTGCATCTCCAGGGGAAAAGGTCACA

ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA CAGATAGTACTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTCACA

120 60

60

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RESULT 10
AAT79899
ID AAT79899
ID AAT79899
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This cDNA sequence was obtained by PCR amplification (see AAT79897 and AAT79898) of the light chain variable region (see also AAT77377) of mouse anti-human factor IX monoclonal antibody BC2 cDNA. The amplification resulted in the addition of ScaI, NarI ends to the VL region. The PCR product was ligated into ScaI, NarI-digested F9HZHC 1-3 (see AAT77374) and digested with ScaI, NarI to produce a mouse-human chimeric light chain F9CHLC (see AAT79900, AAR74532). Claimed anti-Factor IX chimeric antibodies are useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric Mus musculus. Chimeric synthetic.
                                                                                                                                                                                                                                                                                                       Inhibiting thrombosis with self-limiting factor - avoids uncontrolled bleeding by
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blackburn MN,
Nichols AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-OCT-1996;
17-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9726010-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thrombosis; therapy;
                                                                                                                                                                                                                              Example 7; Page 126; 150pp;
                                                                                                                                                                                                                                                                                   inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTCCCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCTCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Church WI
Padlan EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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96US-0010108.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   n WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ractor IX; anticoagulant; monoclonal antibody;
ntibody engineering; light chain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335
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tel AH, Sylvester
                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGRIC COLLEGE.
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ter DR;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; mouse; BC2; animal post-thromboembolic induced ischaemia; thrombolytic agent; anti-factor IX antibody; plasminogen activator; ss thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic; vasotropic; cardiant; PCR primer; anti-respiratory syncytial virus; heavy chain variable region; light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine
                                                                                                                                                                                                                                                                                                                             15-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                       05-OCT-2000; 2000WO-US27438
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200187339-A1
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                                                                                                                                                                P-PSDB;
                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                   22-NOV-2001
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                                                                                                                                                                                     2002-082944/11.
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                                                                                                                                                                                                                                    Blackburn
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                                                                                                                                                                                                                                    Feuerstein
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Pred. No. 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.2e-76;
hes 14;
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Treating post-thromboembolic administering anti-factor IX

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ischaemia in in

naemia in an animal by combination with a plasminogen

Example activator administering

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152-153;

163pp;

English

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Best Local S
Matches 304
                                                                                                                                       Chimeric
Chimeric
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                                                                                                                                                                                                  03-OCT-2002
09-APR-1991
                                                                                                                                                                 Chimeric
                                                                                                                                                                                                                                            AAN70972 standard;
                                                                                                                                                                                2H7 VL sequence in which the VK gene contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 335 BP; 80
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                                                                                                                                                                                                                                                                                                                                TCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC
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                                                                                                                                                                                                                                                                                      ACCAAGCTGGAAATCAAA 318
                                                                                                                                                                                                                                                                                                                                                                  TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA
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                                                                                                                                                                                                                                                                                                       ACCATGCTGGAAATAAGA 318
                                                                                                                                                                                                                                                                                                                                                         TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA
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/label=FR2
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/label=FR1
                                                                                    /label=leader
67..138
                                         /*tag= c
/label=CDR1
                                                                                                     /*tag=
                                                                                                                      Location/Qualifiers
                                 66..210
                                                           39..165
                                                                                                                                                                Anti-cancer
                                                                                                                                                                                                                                            CDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; 97 C; 85 G;
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95.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 295.6; DB :
Pred. No. 8.2e-76;
0; Mismatches 14
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                                                                                                                                                                antibody; ss
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prodn. of immunoglobulin chains and molecules - is by recombinant DNA procedures, with chimeric antibodies etc. related to cancer
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DB; AAP70628.
              ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA
 CAAATTGTTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTCACA
                                                                                                                                                                                   ATGACTTGCAGGGCCAGCTCAAGTGTAAGTTACATGCACTGGTACCAGCAGAAGCCAGGA
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                                                                                                                                                                                                                                                                                                             Conservative
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349.403
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/label=CDR3
355..403
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232..327
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95.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence, derived from M13 subclones of gene fragments, carries the variable region of chimeric immunoglobulin sequence. The antibodies useful in passive immunisation avoiding negative reactions. They are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polynucleotide(s) encoding Immunoglobulin molecules used for efficient prodn. of chimeric human or non-human class switched antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               also useful in assaying and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; ; 7pp; English
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                                                                                              TCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC 180
                                                                                                                                                                                           ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA 120
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DB; AAP94778.
                          TTCAGTGGCAGTGGGGCCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA
                                                                                                                                                                   ATGACTTGCAGGGCCAGCTCAAGTGTAAGTTACATGCACTGGTACCAGCAGAAGCCAGGA
                                                                      TCCTCCCCAAACCCTGGATTTATGCCCCATCCAACCTGGCTTCTGGAGTCCCTGCTCGC
Similarity
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320..352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in vitro imaging
                                                                                                                                                                                                                                                                                                                                                       Score 295.6; DB 1
Pred. No. 8.7e-76;
0; Mismatches 14
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                                                                                                                                                                                                                                                                                                                                                         14;
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Matches

Conservative

Mismatches

14;

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RESULT 14
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Query Match
Best Local Similarity
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01-NOV-1985;
24-JUL-1987;
11-JAN-1988;
08-DEC-1992;
22-FEB-1993;
09-DEC-1994;
06-JUN-1995;
                                            The present sequence encodes the mouse antibody 2H7 light chain variable region. Antibody 2H7 is specific for human B-cell antigen. The antibody sequence was used to construct a chimeric human-mouse antibody, in the course of the invention. The chimeric antibody is expressed in a secretion vector comprising a pelB pectate lyase secretion signal peptide. The pelB pectate lyase secretion seguence is useful for producing a protein such as a chimeric antibody in a bacterial host.
                                                                                                                                                        реів
                                                                                                                                                                                                       Wall
                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
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                                                                                                                          Example 4; Fig 22; 98pp; English.
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                                                                                                                                                                                                                                                                                                                                           06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pelB pectate lyase; secretion signal;
light chain; B-cell antigen; antibody
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DB; AAW89541.
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                             BP;
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85US-079398.
85US-0077528.
87US-0077528.
98US-0142039.
92US-098755.
93US-098755.
93US-0357234.
95US-0472696.
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93.0%;
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                             C; 93 G;
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Score 295.6; DB 2
Pred. No. 8.7e-76;
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                             98 T;
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         DB 20;
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RESULT 15
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29-MAR-1990;
08-DEC-1992;
25-MAY-1995;
01-NOV-1985;
27-OCT-1986;
24-JUL-1987;
The present invention describes a method for preparing an immunoglobulin that is capable of binding antigen involves modular assembly of antibodies through gene cloning and expression of light and heavy chains. The cloned immunoglobulin gene can be produced by expression in
                                                                                                                                           Preparing immunoglobulins or genetically engineered antibodies large scale production of antibodies involves modular assembly antibodies through cloning and expression of light and heavy ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic
                                                                                                         Example
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DB; AAB98093.
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90US-0501092
92US-0987555
95US-0450731
85US-0793980
86WO-US02269
87US-0077528
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                                                                                                                                                                                                                                                                                                               AY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC genetically engineered organisms. The method comprises: (a) expressing, CC in a bacterial cell, of a first nucleic acid that encodes a bacterial cc signal sequence operably linked to either the heavy chain or heavy chain CC fragment, and a second nucleic acid that encodes a bacterial signal CC sequence operably linked to either the light chain or light chain CC fragment, and obtaining the immunoglobulin from the periplasmic space or CC culture medium; or (b) operably linking a nucleic acid encoding a continue medium; or the light chain variable region or both of the covariable region or the light chain variable region or both of the covariable regions, and obtaining the immunoglobulin from the periplasmic space or culture medium. The bacterial signal sequences bring about the CC variable regions, and obtaining the immunoglobulin from the periplasmic space or culture medium. The bacterial signal sequences bring about the CC space or culture medium. The bacterial signal sequences bring about the CC transport of the heavy chain or heavy chain fragment, or the variable regions through the cytoplasmic cor light chain fragment; or the variable regions through the cytoplasmic cor by a heavy chain variable region and a light chain variable region. The method is useful for producing genetically engineered antibodies of cor desired variable region specificity and constant region properties. The method is also useful large scale production of human antibodies. CC AAH21985 to AAH22082 and AAB98085 to AAB98097 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 304
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ACCAAGCTGGAGCTGAAA
                                 ACCATGCTGGAAATAAGA
                                                                   TCCTCCCCCAAACCCTGGATTTATGCCCCCATCCAACCTGGCTTCTGGAGTCCCTGCTCGC
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nilarity 95.6%;
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Pred. No. 8.7e-76;
D; Mismatches 14
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time completed: November me : 187.766 secs 27, 2002, 03:53:51 밁

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Perfect score:
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    Contact: Robert Strausberg, Ph.D.

Email: gapbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologics, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.linl.gov
Plate: LLAM1107 row: o column: 04

High quality sequence stop: 639.

Location/Qualifiers

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BF7823458 MR1-HT113
BG9321317 PC0-C7047
BG9321327 QV1-C7041
BF894856 QV1-M7016
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REFERENCE
AUTHORS
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                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 959)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ939046 959 bp n
AGENCOURT_8946838 NCI_CGAP_CO24 Mus
IMAGE:6395050 5', mRNA sequence.
BQ939046 GI:22354524
                                                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                     High quality sequence stop: 517.
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/lab_host="PH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/db_xref="taxon:10090"
/organism="Mus musculus"
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602891339F1 NCI_CGAP_Lu29
mRNA sequence.
BI104783
BI104783.1 GI:14555676
                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11101 row: 1 column: 07
High quality sequence stop: 532.
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Tissue Procurement: Gilbert Smith, Ph.D.
                                                                                                                                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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                                                                                       ocation/Qualifiers
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                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 798)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                              found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11004 row: g column: 01 High quality sequence stop: 797.
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148 c 113 g 132 t
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Stem cell origin."
/lab_host="DH10B"
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4989720"
                                                                                                Location/Qualifiers
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91.5%;
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Pred. No. 9.3e-72;
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                                                                                                         http://image.llnl.gov
Plate: LLAW11177 row: e column: 17
High quality sequence stop: 738.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 755)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections, 1 (100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602915167F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5065720
                                                                                                                                                                                                                        Email: ggapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
BI150509
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5065720"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NCI_CGAP_CO24"
/lab_host="DH10B (TI phage-resistant)"
/note="0rgan: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo d'
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 222 c 179 g 172 t
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BQ946795.1
EST.
                                                                                                                                                                                                                                                                    1 (bases 1 to 918)
NIH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ946795 918 bp rAGENCOURT_8949642 NCI_CGAP_CO24 Mus IMAGE:6474845 5', mRNA sequence.
                                                                                                                                                                                    cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                        http://image.llnl.gov
Plate: LLAM14012 row:
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                 e: LLAM14012 row: k column: quality sequence stop: 714. Location/Qualifiers
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/organism="Mus musculus"
/strain="PVB/N"
/db_xref="tack:0:10090"
/clone="IMAGE:674845"
/clone_lib="NCI_CGAP_co24"
/lab_host="DH10B (T1 phage-r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stem cell origin."
/lab_host="DH10B"
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   (T1 phage-resistant)"
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Sciurognathi; Muridae;
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; Murinae; Mus
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                                                                                                                                                                                                  Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                            BG090240
                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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1 (bases 1 to 312)
                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG090240 312 bp mRNA linear EST 26-JAN-20 ut58el0.yl Soares_mouse_NMGB_bcell mus musculus CDNA clone IMAGE:3332082 5' similar to TR.09U410 09U410 MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN VARIABLE
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    Location/Qualifiers
1. .312
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/clone_lib="Soares_mouse_NMGB_bcell"
/lab_host="DH10B (phage-resistant)"
/note="Organ: germinal B-cell; Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: NC
Site_2: Eco RI; 1st strand cDNA was primed with a
oligo(dT) primer [5'
                                                                                          /clone="IMAGE:3332082"
                                                                                                          /db_xref="taxon:10090"
                                                                                                                          /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                    GI:12572803
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91.2%;
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Rodentia;
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Pred. No. 3.7e-71
0; Mismatches 2
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Murinae; Mus
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                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                   Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 413)
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National Cancer Institute, Cancer Genome Anat
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Location/Qualifiers
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8 c 79 g 70 t
                  /organism-"Mus musculus"
/db_xcef="taxon:10090"
/clone="the-"Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
/tissue_type="mammary gland"
/lab_host-"DH10B"
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92.6%;
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pT7T3D-Pac (Pharmacia) with a
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vs14f01.rl Barstead mouse irradiated colon MPLRB7 Mus musculus cDiclone IMAGE:1138201 5' similar to gb:X67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence.
                                                                                                                                                             WashIngton University School of MedicineP
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                  Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                           Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 396)
                                                                                                                         Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                           Contact: Marra M/Mouse EST Project
                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                 Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA691311.1
                     Seq primer: -28ml3 rev2 ET from Amersham
                                                                                                        Email: mouseest@watson.wustl.edu
                                            MGI:619473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polylinker; 1st strand cDNA was propared from mammary gland tissue from a lactating female, and was then primed with a Not I - Oilgo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "a a 113 c 94 g 100 t
Location/Qualifiers
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91.1%;
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Pred. No. 9.9e-71;
0; Mismatches 28
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                                                                                                                                                                  Louis, MO 63108
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Best Local Sim
Matches 281;
                                                                                                                                             AUTHORS
TITLE
                                                                                                                                JOURNAL
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                                                                                                                                                                                                                                                                                         mRNA sequence.
BF165585
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601777486F1 NCI_CGAP_Lu29 Mus
                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 871)
                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith,
                                                                                                                                Unpublished (1999)
                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                             EST
                                                                                                                                                                                                                                                                              BF165585.1 GI:11045937
                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                              house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/cione="IMAGE:1138201"
/clone_lib="Barstead mouse i
/dev_stage="8 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vector. Library constructed by Bob Barstead 107\ c 91\ g 94\ t
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92.4%;
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Rodentia;
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Pred. No. 1.5e-69;
0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                        871 bp
                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                       op mRNA linear EST 30-OCT-2000 musculus cDNA clone IMAGE:4019109 5',
                                                                                Ph.D
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                                                                                                                                    AUTHORS
TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGCTGCCACTTATTTCTGCCAGCAGTATCATAGTTACCCACGGACGTTCGGTGGAGGC
                                                                                                                                                                                                                                                         mRNA sequence.
BG964349
BG964349.1 GI
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution informat

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://image.llnl.gov
Plate: LLAM9270 row: 1
                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                      National Institutes of Health, Mammalian
                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 865)
                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                 BG964349
602831966F1 NCI_CGAP_Co24 Mus
                                                                                                                                                     NIH-MGC http://mgc.nci.nih.gov/
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a 240 c 201 g 204 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="spontaneous
Stem cell origin."
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:4019109"
/clone_lib="NCI_CGAP_Lu29"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCAAGCTGGCAA 402
                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can
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National Institutes of Health, Mammalian
Unpublished (1999)
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602099949F1 NCI_CGAP_Co24
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Mammalia; Eutheria;
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http://image.llnl.gov
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/clone_lib="NCI_CGAP_CO24"
/clone_lib="NCI_CGAP_CO24"
/lab_host="DH108 (Tl phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo d
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/db_xref-"taxon:10090"
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Rodentia;
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Pred. No. 3.5e-69;
D; Mismatches 29;
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Sciurognathi; Muridae;
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285; Conserv
Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10986 row: o column: 19

High quality sequence stop: 726.
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1 (bases 1 to 728)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1
Site_2: Sall; Cloned unidirectionally. Primer:
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/clone="IMAGE:4219669"
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Best Local Similarity
Matches 284; Conserv
                                                                                                                                                                                                             TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCAAGCTGGAAATCAAA 371
                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information cal
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 639)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                    BF583310.1
                                                                                                                                                                                                                                                                                                                                                                            BF583310 639 bp mRNP 602101781F1 NCI_CGAP_CO24 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence
                        http://image.llnl.gov
Plate: LLAM9815 row: b column:
High quality sequence stop: 636.
                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                      house mouse
                                                                      found through the I.M.A.G.E.
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Site_2: SalI; Cloned unidirectionally. primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 198 c 168 g 160 t
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Pred. No. 2.5e-68;
0; Mismatches 34;
                                                                         Consortium/LLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAGCTGGAGCTGAAA 393
                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1. (bases 1 to 743)
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BI106381
                                                               High quality sequence stop:
Location/Qualifiers
                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL
http://image.llnl.gov
Plate: LLAM11105 row: g column: 07
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo d7
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 174 c 149 g 147 t
/organism="Mus
/strain="CZECH
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/strain="FVB/N"
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Pred. No. 3.1e-68;
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    . musculus"
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Search completed: November 27, 2002, 05:29:45 Job time: 1336.29 secs
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                                                                    304 ATGCTGGAAATAAGA 318
| ||||||||| | | |
325 AAGCTGGAAATCAAA 339
                                                                                                                                                                                                                 GCTGCCACTTATTTCTGCCAGCAGTATCATAGTTACCCACGGACGTTCGGTGGAGGCACC
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/site_2: NotI; Cloned unddirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
97 a 214 c 168 g 164 t
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1: /cgn2_6/ptodata/1,

2: /ggn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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US-08-783-853A-6
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| 84.4 | 84.4 | 84.4 | 84.9 | 84.9 | 85.3 | 85.5 | 85.9 | 85.9 | 85.9 | 85.9 | 85.9 | 85.9 | 86.0 | 88.1 | 88.1 | 88.1 | 88.4 |
| 390 | 390 | 390 | 708 | 669 | 331 | 292 | 393 | 393 | 393 | 393 | 393 | 384 | 292 | 711 | 711 | 711 | 759 |
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| US-08-487-113D-79 | US-08-483-389-79 | US-08-482-882-79 | US-08-190-199A-60 | US-08-190-199A-66 | US-08-836-561-32 | US-09-280-028-3 | US-09-393-385B-2 | US-08-673-799C-2 | US-08-483-528B-2 | US-08-438-562-39 | US-08-116-778E-39 | US-08-656-586-1 | US-08-308-494A-12 | PCT-US95-10740-4 | US-08-668-706B-4 | US-08-468-252-4 | US-08-902-486-8 |
| • | • | Sequence 79, Appl | • | ` | • | | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 39, Appl | Sequence 39, Appl | Sequence 1, Appli | Sequence 12, Appl | Sequence 4, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 8, Appli |

ALIGNMENTS

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INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08783853A Patent No. 6005091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Gross, Mitchell
APPLICANT: Fewerstein, Glora
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
APPLICANT: SYLVESTER, DANIEL
TITLE OF INVENTION: OF THROMBOSIS
                                                                                                                                                              FILING DATE: 24-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P504
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/783,853A FILING DATE: 16-JAN-1997 CLASSIFICATION:
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Church, William
Gross, Mitchell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/09344050 Patent No. 6391299 GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT:
APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS: ADDRESSE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhal
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT
TITLE OF INVENTION: OF THROMBOSIS
                                                                                                                               SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                         PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                 STREET: 709 Swedeland CITY: King of Prussia STATE: PA
                                                                                      APPLICATION NUMBER: FILING DATE: 24-JU CLASSIFICATION:
                                                                                                                                                           COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
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                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                    COUNTRY:
                                            FILING DATE:
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Gross, Mitchell
Feuerstein, Giora
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                                                                                                  UMBER: US/09/344,050
24-JUN-1999
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Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
                                                                                                                                                       APPLICANT: LEONARD, John E.
APPLICANT: NEWMAN, Roland A.
APPLICANT: REFF, Mitchell E.
APPLICANT: REFF, Mitchell E.
APPLICANT: RASTETTER, William H.
TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
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HYPOTHETICAL: I
ANTI-SENSE: NO
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                NUMBER OF SEQUENCES:
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                                                      STATE: Virginia COUNTRY: United States
                                                                                   STREET: P.O. Box CITY: Alexandria
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TOPOLOGY: lin
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   COMPUTER:
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OPERATING SYSTEM:

PC-DOS/MS-DOS

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US-08-149-099C-6
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                                                             Sequence 6, Application Patent No. 5843439
GENERAL INFORMATION:
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Best Local Similarity
Matches 307; Conserv
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           APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 12-NOY-1992
ATTORNEY/AGENT INFORMATION:
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                                                                            , Application US/08478967A 5843439
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HANNA, Nabil
LEONARD, John E.
NEWMAN, Roland A.
REFF, Mitchell E.
RASTETTER, William H.
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96.5%;
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Pred. No. 9.7e-86;
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US-08-478-967A-6
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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NAME/KEY:
LOCATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION UMBER: 35,030
REFERENCE/DOOVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
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APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/978,891
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MEDIUM TYPE: Floppy disk
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 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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TYPE: nucleic acid
STRANDEDNESS: single
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TCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC
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                                                              ATGACTTGCAGGGCCAGCTCAAGTGTAAGTTACATCCACTGGTTCCAGCAGAAGCCAGGA
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96.5%; Pred. No. 9.7e-86;
tive 0; Mismatches 11
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US-08-475-815B-6
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                                                                                                                         Matches
                                                                                                                                                        Query Match
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                                                                                                                                         Best
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INFORMATION FOR SEQ ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LEONARD, JOHN E.

APPLICANT: NEWMAN, ROLAND A.

APPLICANT: REFF, MITCHELL E.

APPLICANT: RASTETTER, WILLIAM H.

TITLE OF INVENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3000
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APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
US
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                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/149,099 FILING DATE: 03-NOV-1993
                    61 ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA 120
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1100 New York Avenue, N.W., Ninth FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                              202-822-0944
                                                                                                                       Conservative
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                                                                                                                                                                                                       CDS
1..384
                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                         DNA (genomic)
                                                                                                                                     94.5%;
                                                                                                                    Score 300.4; DB 4; Pred. No. 9.7e-86; 0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                            23522-0157
                                                                                                                                                     Length 384;
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US-08-149-099C-3
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US-08-149-099C-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5736137 GENERAL INFORMATION:
                                                                                                                                                            TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: RASTETTER
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                         REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                  HYPOTHETICAL:
ANTI-SENSE:
                                                   MOLECULE TYPE:
                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                        TOPOLOGY:
                                                                                     STRANDEDNESS:
                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 03-NOV-1993 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                          LENGTH:
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P.O. Box 1404
                                                                                                                           9209 base pairs
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NEWMAN, ROLand A.
REFF, Mitchell E.
REFF, Mitchell E.
REFF, MITCHELL E.
RESTETTER, WIlliam H.
VENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
VENTION: THERAPEUTIC APPLICATION OF CHIMERIC AND
VENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
VENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
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Query Match

94.5%;

Score 300.4;

DB 1;

Length 9209;

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RESULT 7
US-08-478-967A-3
APPLICATION NUMBER: US/08/478,967A
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
APPLICATION NUMBER: US 07/978,891
FILING DATE: 12-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-014
TELECOMMUNICATION INFORMATION:
TELEPINNE: (703) 836-6620
TELEFAX: (703) 836-6021
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Applic
Patent No. 5843439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: REFF, Mitchell E.
APPLICANT: RASTETTER, William H.
APPLICANT: RASTETTER, William H.
TITLE OF INVENTION: THERAPPUTIC APPLICATION OF CHIMERIC AND
TITLE OF INVENTION: RADIOLABELED ANTIBODIES TO HUMAN B LYMPHOCYTE RESTRICTED
TITLE OF INVENTION: DIFFERENTIATION ANTIGEN FOR THE TREATMENT OF B CELL
TITLE OF INVENTION: LYMPHOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1045
                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1285
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CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CAAATTGTTCTCTCCCAGTCTCCCAGCAATCCTGTGCATCTCCAGGGGAAAAGGTCACA 60
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                                                                                                                                                                                                                                                                                                                                                           P.O. Box 1404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HANNA, Nabil
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                                                                                                                                                                                                                                                                            Floppy disk
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                                                       012712-014
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0; Mismatches 11
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US-08-475-815B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, V.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815B
FILING DATE: 07-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DN
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1345
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LENGTH: 9209 base pair
 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1285
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                                                                                                                                                   COUNTRY: U:
ZIP: 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
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                                      UMBER: US/08/475,815B
07-JUN-1995
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  US 08/149,099
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Pred. No. 3.2e-85;
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                                                                                 Version
                                                                                  #1.30
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SEQUENCE CHARACTERISTICS:
LENGTH: 9209 base pairs
TYPE: nucleic scid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                      Sequence 2, Application Patent No. 5830698 GENERAL INFORMATION:
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              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                      APPLICANT: REFF, Mitchell E.
APPLICANT: BARNETT, Richard Spence
APPLICANT: MCLACHLAN, Karen Retta
TITLE OF INVENTION: NOVEL METHOD F
TITLE OF INVENTION: SPECIFIC SITES
TITLE OF INVENTION: RECOMBINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                              1345
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3000
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NAME: Teskin, Robin L.
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APPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1045 CAAATTGTTCTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAAGATCACA 1104
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nes 307; Conserv
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REGISTRATION NUMBER: 35,030
                                                                                                                                   STREET: P.O. Box CITY: Alexandria
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                                                                                                COUNTRY:
                                                                                                                                                                     ADDRESSEE:
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                                                                                E: Virginia
TRY: United States
22313-1404
                                                                                                                                                     P.O. Box 1404
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                                                                                                                                                                                                                                                                                       REFF, Mitchell E. BARNETT, Richard Spence
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                     BURNS, DOANE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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                                                                                                                                                                                                                      NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE
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Pred. No. 3.2e-85;
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                                                                                                                                                                                                                                                                                                        Sequence 2, Application Patent No. 5998144
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Best Local Similarity
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                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 18986 base pairs
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                     APPLICANT: MCLACHLAN, Karen Retta
TITLE OF INVENTION: MOVEL METHOD FOR INTEGRATING GENES AT
TITLE OF INVENTION: SPECIFIC SITES IN MAMMALIAN CELLS VIA HOMOLOGOUS
TITLE OF INVENTION: RECOMBINATION AND VECTORS FOR ACCOMPLISHING THE S
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                             APPLICANT:
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TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Virginia
                                                                                         COUNTRY:
                                                                                                                                         STREET:
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TOPOLOGY: linear
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REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
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                                                                              22313-1404
                                                                                                                                         P.O. Box 1404
                                                                                           United States
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                                                                                                                                                                                                                                                             REFF, Mitchell E. BARNETT, Richard Spence
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      Version
      #1.30
                                                                                                                                                                                                      FOR ACCOMPLISHING THE SAME
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US

us/09/023,715

FILING DATE

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                                                                                                                                                                                                                                                                            Sequence 2, Application US/09343485A
Patent No. 6413777
GEMERAL INFORMATION:
APPLICANT: REFF, MITCHELL R.
APPLICANT: BARNETT, RICHARD S.
APPLICANT: MCLACHLAN, KAREN R.
APPLICANT: MCLACHLAN, KAREN R.
APPLICANT: MCLACHLAN, KAREN R.
APPLICANT: MCLACHLAN, KAREN R.
APPLICANT: MCLACHLAN, FAREN R.
APPLICANT: MCCACHLAN, FAREN R.
APPLICANT R.
APPLICANT
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Best Local
   SEQ ID
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SOFTWARE: PatentIn
SEQ ID NO 2
                                                       CURRENT APPLICATION NUMBER: US/09/343,485A CURRENT FILING DATE: 1999-06-30 PRIOR APPLICATION NUMBER: 09/023,715 PRIOR FILING DATE: 1998-02-13 PRIOR APPLICATION NUMBER: 08/819,866 PRIOR APPLICATION NUMBER: 08/819,866 PRIOR FILING DATE: 1997-03-14 NUMBER OF SEQ ID NOS: 3
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STRANDEDNESS: sind
TOPOLOGY:

NOLECUIF
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TELEPHONE: (703) 836-6520
TELEFAX: (703) 836-2021
FORMATION FOR SEQ ID NO: 2:
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REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CAAATTGTTCTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAAAAGGTCACA 60
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Pred. No. 4.2e-85;
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Best Local Similarity
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                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                    ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS: BURNS, DO
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                                                                                                                                                                                                                                                        699 Prince
                                                                                                                                                                                                          USA
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WENTION: Therapeutic Application of Chimeric and

WENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted

WENTION: Differentiation Antigen for the Treatment of B-Cell
                                                                                                                                                                                                                                                                                                                                                                                             Leonard, John E.
Newman, Roland A.
Reff, Mitchell E.
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Pred. No. 4.2e-85;
D; Mismatches 11
                                                                                                             Version
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US-08-476-275-2
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Patent No. 5776456
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Best Local Similarity
                                                                                                                                                                                                   GENERAL INFORMATION:
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                     APPLICANT: Leonard, John E.
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
APPLICANT: Restetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Differentiation Antibodies to Human B Lymphocyte |
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B
TITLE OF INVENTION: Lymphoma
NUMBER OF SEQUENCES: 11
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REFERENCE/OCCKET NUMBER: 012712-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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           CORRESPONDENCE ADDRESS:
                                                                                                                                                                     APPLICANT:
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LOCATION:
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67..384
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DOANE,
SWECKER & MATHIS
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RESULT 14
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Best Local Sim
Matches 305;
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APPLICATION NUMBER: US 08/149,099

FILLING DATE: 03-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/978,891

FILLING DATE: 13-NOV-1992

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 2:
                                                           1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                  1285
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                                                                                                                                                                                                                                                                                          1105
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                          1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
CHROMOSOME/SEGMENT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                               1045 CAAATTGTTCTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTCACA 1104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                           61 ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCCAGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Teskin, Robin L. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/476,275 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                              1 CAAATTGTTCTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAAAAGGTCACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 9209 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                       TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCAGCAGAGTGGAGGCTGAA 240
                                                                                                                                                                                                                              TCCTCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC 180
                                                                                                                                                                                                                                                                                       ACCAAGCTGGAAATCAAA 1362
                                                                        ACCATGCTGGAAATAAGA 318
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; Pred. No. 3.3e:
0; Mismatches
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Sequence 104, Application US/08783853A Patent No. 6005091

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                                                                                                                                                                                                                                            Matches 304;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,
FILING DATE: 16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhal
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT
TITLE OF INVENTION: OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:
ORIGINAL SOURCE:
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FILING DATE: 24-OCT-1996
ATTORNEY/AGENT INFORMATION:
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 181
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia
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                                                                                                                                                                                                                                                                                                                              LOCATION: 1...318
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Coding Sequence
                                                                                                                                                                                        1 CAAATTGTTCTCTCCCAGTCTCCCAGCAATCCTGTATCTCCAGGGGAAAAGGTCACA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 318 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
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TTCAGTGGCAGTGGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA 240
                                                   TCCTCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC 180
                                                                                                                                     ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA 120
                                                                                                                                                                       CAGATAGTACTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTCACA 60
                               TCCTCCCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC 180
                                                                                                     ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA 120
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16-JAN-1997
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US-09-344-050-104
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 318 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/76
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                           FEATURE:
                                                                                                    ANTI-SENSE: NO
                                                                                                                 TOPOLUGE:
MOLECULE TYPE: CD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: OF THROMBOSIS NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sylvester, Daniel TITLE OF INVENTION: ANTICOAGULANT
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OPERATING SYSTEM:
                           NAME/KEY: Coding Sequence LOCATION: 1...318
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               OTHER INFORMATION:
                                                                                                                                                              STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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Church, William
Gross, Mitchell
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                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGENTS USEFUL IN TREATMENT
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Query Match

93.0%;

Score 295.6;

DB 4;

Length 318;

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| rch c | 301 | 301 | 241 | 241 | 181 | 181 | 121 | 121 | 0 | 6 | | | Best Loc Matches |
| Search completed: November 27, 2002, 03:55:49 | D1 ACCAAGCTGGAAATCAAA 318 | ~ | 41 GATGCTGCCACTTATTACTGCCAGCAGTGGAGTATTAACCCCACGGACGTTCGGTGGAGGC 300 | _ | B1 TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCAGCAGAGTGGAGGCTGAA 240 | | 21 TCCTCCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC 180 | | 61 ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA 120 | 61 ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA 120 | 1 CAGATAGTACTCTCCCAGTCTCCCAGCAATCCTGCATCTCCCAGGGGAAAAGGTCACA 60 | 1 CAAATTGTTCTCTCCCAGTCTCCCAGCAATCCTGTCTGCATCTCCAGGGGAAAAGGTCACA 60 | Best Local Similarity 95.6%; Pred. No. 2.9e-84; Matches 304; Conservative 0; Mismatches 14; Indels 0; Gaps 0; |
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Job time: 72.1419 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                    score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                Score
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Match
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Gapop 10.0 ,
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//SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000_DAT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT:*
                                                                                                                                                                                              Length
 106
106
107
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                AAW24532
AAU81002
AAW24520
AAW24531
AAW24531
AAW24531
AAW81001
AAR55214
AAB30694
AAB30695
                                                                                                                                                                                                                                                    SUMMARIES
             Anti-Factor IX MAb
Mouse-human light
Mouse anti-human F
Murine BC2 light c
Anti-Factor IX MAb
Murine BC2 light c
Murine BC2 light c
Murine GC3 light c
Murine GC4 light c
Murine GC4 light c
Murine GC4 light c
Murine GC5 light c
Murine GC6 anti-C
Sequence encoded
                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                                                     printed
 RESULT 1
AAW24532
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| 475 | 475 | 475 | 475 | 475 | 478 | 482 | 484 | 484 | 486 | 486 | 489 | 489 | 489 | 491 | 501 | 503 | 504 | 504 | 507 | 507 | 507 | 507 | 507 | 507 | 514 | 516 | 516 | 516 | 516 | 516 | 516 | 516 | 516 | 516 |
|--------------------|----------|--------------------|-------|-------------|--------------------|-------------------|--------------|----------|----------|-----|--------|-----|----------|---------|-------------------|---------------|-----------------|------------|----------|------|--------------------|------|-----------|-------------|---------|----------|--------|---------------|---------|----------------|---------|-------------|-------|--------------|
| 85.4 | 85.4 | 85.4 | 85.4 | 5 | 86.0 | 6 | 7 | .7 | .7 | 7. | 7. | .7 | 7. | 8 | | 0 | .0 | | 1 | 1. | | 1. | 1 | | | Ν | ٥. | | 2 | | | ε, | 92.8 | |
| 97 | 97 | 97 | 97 | 97 | 107 | 237 | 252 | 252 | 246 | 107 | 237 | 237 | 236 | 108 | 105 | 106 | 145 | 145 | 235 | 235 | 235 | 235 | 129 | 129 | 633 | 128 | 128 | 128 | 128 | 128 | 128 | 128 | 128 | 128 |
| 21 | 20 | 17 | 17 | 11 | 13 | 21 | 22 | 21 | 15 | 14 | 18 | 17 | 15 | 16 | 18 | 23 | 14 | 12 | 21 | 20 | 20 | 17 | 13 | 13 | 21 | 22 | 20 | 19 | 19 | 19 | 18 | 18 | 18 | 10 |
| AAY51369. | 342 | AAR99874 | m | 731 | 72 | 059 | 8 | AAB12562 | 5 | 426 | 16 | 2 | 4 | 38 | 2 | 8 | 7 | 32 | AAB08025 | 7 | 7 | 617 | 3 | 07E | 96 | AAB98093 | 5 | 5 | 0 | 52 | 24 | 34 | 058 | AAP94781 |
| Mouse monoclonal a | antibody | Monoclonal antibod | l ant | domain of a | Sequence encoded b | Amino acid sequen | L6 sFv prote | L6 anti- | TNF diab | ne | ain an | ш | of the s | EGFR ar | Kappa light chain | i-NKG2D hybri | ti-IL2R-alpha a | imeric ant | c ant | pEE1 | Plasmid pNG3/A5B7V | 5B57 | 7 antibod | rocessed va | no acio | 1 | e anti | e 2H7 antibod | antibod | se 2H7 antibod | ht chai | light chain | ntibo | 7 VL gene. S |

ALIGNMENTS

Anti-Factor IX MAb chimeric light chain.

27-DEC-1997 AAW24532;

(first entry)

AAW24532 standard; Protein; 106 AA

Blackburn MN, Church WR, Feuerstein GZ, Nichols AJ, Padlan EA, Patel AH, Sylveste Chimeric Mus musculus. Chimeric Homo sapiens. Chimeric synthetic. WPI; 1997-385117/35 24-OCT-1996; 17-JAN-1996; 17-JAN-1997; Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody; chimeric antibody; antibody engineering; light chain. (SMIK) SMITHKLINE BEECHAM CORP. (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE. 24-JUL-1997 WO9726010-A1 96US-0029119 96US-0010108 97WO-US00759 sylvester DR; : :

AAT79900

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RESULT 2
AAU81002
ID AAU8
XX AAU8
AC AAU8
DT 09-A
DE MOUS
XW Humm
KW Throc
KW Throc
KW Hoav
OS Chim
OS Chim
XX WO2C
XX WO2C
XX WO2C
PN WO2C
XX WO1-P
DR 15-A
XX WPI;
DR WPI;
D
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Best Local S
Matches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric - Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This polypeptide comprises a mouse-human chimeric antibody light chain in which the variable region is derived from mouse anti-human factor IX monoclonal antibody BC2 (see AAM24531) and human sequences from the immunoglobulin RF-TS3 (Cl framework. It can be expressed in transfected mammalian cells utilising a CDNA construct (see AAT79900) obtained by PCR amplification (see AAT79887-98) of BC2 CDNA and insertion of the PCR product into F9HZHC 1-3 CDNA (see AAT77374). Claimed anti-Factor IX chimeric antibodies are useful in the treatment of thrombosis.
                                                                                       Treating post-thromboembolic administering anti-factor IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; mouse; BC2; animal post-thromboembolic induced ischaemia; thrombolytic agent; anti-factor IX antibody; plasminogen activator; thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic; vasotropic; cardiant; anti-respiratory syncytial virus; heavy chain variable region; light chain variable region.
                                                                      activator
                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                            15-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                            05-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 7;
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                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                            22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200187339-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU81002 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse-human light chain polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibition
                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                              2002-082944/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSINPRTFGGGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101;
                                                                                                                                                                                                                                             S,
                                                                                                                                                                       ABK24005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ng thrombosis with self-limiting avoids uncontrolled bleeding by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
                                                                                                                                                                                                                                             Blackburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                            2000WO-US27438
                                                                                                                                                                                                                                                                                                                                            2000US-0571434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150pp;
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Z
                                                                                                                                                                                                                                             Feuerstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 526; DB Pred. No. 1.8e 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                            induced ischaemia in antibody in combinati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽
                                                                                                                                                                                                                                        GZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 18;
l.8e-30;
                                                                                               combination
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                                                                                                                                                                                                                                           Toomey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                               animal with a
                                                                                                                   γď
                                                                                            plasminogen
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Example 7;

Page 155-156;

163pp; English

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RESULT 3
AAW24520
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for treating an animal post-thromboembolic induced ischaemia or reducing a required dose of a thrombolytic agent in treatment of an animal post-thromboembolic induced ischaemia, comprising administering an anti-factor IX antibody or its fragment, optionally in combination with a plasminogen activator or thrombolytic agent. The method is useful for treating post-thromboembolic-induced ischaemia, for preventing thromboembolic stroke in an animal, and for reducing a required dose of a thrombolytic agent. Sequences AAU80972-AAU81004 represent antibodies and vector polypeptides used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                   humanised antibody; antibody engineering; light chain; CDR complementarity determining region; myocardial infarction; angina; atrial fibrillation; stroke; kidney damage; pulmonary embolism; deep vein thrombosis; coronary angiopl disseminated intravascular coagulation; artificial organ;
WPI; 1997-385117/35
                    Blackburn MN,
Nichols AJ,
                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                        (SMIK )
                                                                                            24-OCT-1996;
17-JAN-1996;
                                                                                                                                                      24-JUL-1997.
                                                                                                                                                                                                                                                                                                                                                            shunt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW24520
                                                                                                                               17-JAN-1997;
                                                                                                                                                                              WO9726010-A1
                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse anti-human Factor IX antibody BC2 light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-DEC-1997
                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                            prosthesis.
                                                        SMITHKLINE BEECHAM CORP
UNIV VERMONT & STATE AGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                therapy; Factor IX; anticoagulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                      , Church WR,
Padlan EA, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                          96US-0029119
96US-0010108
                                                                                                                               97WO-US00759
                                                                                                                                                                                                                 /label=
                                                                                                                                                                                                                                         /note-
                                                                                                                                                                                                                                                                          /note= "(Claim 23)"
                                                                                                                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                                                                             Socation/Qualifiers
                                                                                                                                                                                                                                                    /label- CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94.6%;
                                                                                                                                                                                                                                      "(Claim
                                                                                                                                                                                                     "(Claim
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                                                                                                                                                                                                                                                                                         CDR1
                       Patel
                      Feuerstein GZ, Gı
tel AH, Sylvester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107
                                                         AGRIC COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 526; DB 23;
Pred. No. 1.8e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                       Gross
er DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                 monoclonal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                       organ; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                   angioplasty;
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N-PSDB; AAT77377

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regions of selected human antibody sequences. They have self-
limiting neutralising activity, and are useful as anticoagulant
agents in treatment of thrombosis associated with myocardial
infarction, unstable angina, atrial fibrillation, stroke, renal
damage, pulmonary embolism, deep vein thrombosis, percutaneous
transluminal coronary angioplasty, disseminated intravascular
coagulation, sepsis, or artificial organs, shunts or prostheses
(claimed). Also claimed are chimeric antibodies (see AAW24532),
Fab and F(ab')2 fragments. The claimed antibodies do not cause
uncontrolled bleeding (contrast heparin and warfarin) since they
provide only partial inhibition of coagulation.
                                                                                                                                                                                                                                                                                                     Human; mouse; BC2; animal post-thromboembolic induced ischaemia;
thrombollytic agent; anti-factor IX antibody; plasminogen activator;
thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic;
vasotropic; cardiant; anti-respiratory syncytial virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU80976 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibodies (see AAW24510-18) contain CDRs (see AAW24504-09) of heavy and light chain variable regions inserted into framework
Treating post-thromboembolic induced ischaemia in
                                                                                                                                                                  05-OCT-2000; 2000WO-US27438
                                                                                                                                                                                                22-NOV-2001
                                                                                                                                                                                                                              WO200187339-A1
                                                                                                                                                                                                                                                                                                                                                                                  Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU80976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial
                                            WPI; 2002-082944/11.
                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                   15-MAY-2000; 2000US-0571434
                                                                                                                                                                                                                                                                                       heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence comprises the light chain variable region of mouse human Factor IX monoclonal antibody BC2. Claimed humanised
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWIYATSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSGSGSGTSYSLTISRVEAEDAATYYCQQWSINPRTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                BC2 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 66-67; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.6%;
                                                                                                                                                                                                                                                                                         region;
                                                                          Feuerstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      526;
No. 1.
                                                                          GZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 18;
..8e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 107;
 an animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
bу
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and
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RESULT 5
AAW24531
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Best Local S
Matches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      post-thromboembolic induced ischaemia or reducing a required dose of a thrombolytic agent in treatment of an animal post-thromboembolic induced ischaemia, comprising administering an anti-factor IX antibody or its fragment, optionally in combination with a plasminogen activator or thrombolytic agent. The method is useful for treating post-thromboembolic-induced ischaemia, for preventing thromboembolic stroke in an animal, and for reducing a required dose of a thrombolytic agent. Sequences AAU80972-AAU81004 represent antibodies and vector polypeptides used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 administering anti-factor IX antibody in combination with a plasminogen
                                                                                                          WPI; 1997-385117/35
N-PSDB; AAT79899.
                                                                                                                                                                                                                       24-OCT-1996;
17-JAN-1996;
                                                                                                                                                                                                                                                                                                                                   Chimeric Mus musculus.
Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                      Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody; chimeric antibody; antibody engineering; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW24531 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Page 97; 163pp; English.
                                                                      Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial
                                                                                                                                                          Blackburn MN,
                                                                                                                                                                                                                                                             17-JAN-1997;
                                                                                                                                                                                                                                                                                    24-JUL-1997
                                                                                                                                                                                                                                                                                                            W09726010-A1
                                                                                                                                                                                                                                                                                                                                                                                                             Anti-Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                      27-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW24531;
                                 Example 7; Page 126; 150pp; English.
                                                                                                                                                Nichols
                                                                                                                                                                                   (UYVE-)
                                                                                                                                                                                             (SMIK )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSINPRTFGGGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ㅁ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101;
                                                                                                                                                ĄJ,
                                                                                                                                                                                   SMITHKLINE BEECHAM CORP.
UNIV VERMONT & STATE AGRIC COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                             Padlan
                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        relates to a method for treating an animal
                                                                                                                                              Church WR, Feo
Adlan EA, Patel
                                                                                                                                                                                                                       96US-0029119.
96US-0010108.
                                                                                                                                                                                                                                                             97WO-US00759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                             BC2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.6%;
                                                                                                                                                                                                                                                                                                                                                                                                             modified light chain.
                                                                                                                                                Feuerstein GZ,
tel AH, Sylves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ļ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              526; DB 23;
No. 1.8e-30;
                                                                                                                                                Sylvester
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٠,
                                                                                                                                                Grcss
er DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 induced
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This polypeptide sequence comprises a modified light chain variable region (see also AAW24520) of mouse anti-human factor IX monoclonal

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RESULT 6
AAU81001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Sim
Matches 101;
                   post-thromboembolic induced ischaemia or reducing a required dose of a thrombolytic agent in treatment of an animal post-thromboembolic induced ischaemia, comprising administering an anti-factor IX antibody or its fragment, optionally in combination with a plasminogen activator or thrombolytic agent. The method is useful for treating post-thromboembolic-induced ischaemia, for preventing thromboembolic stroke in an animal, and for reducing a required dose of a thrombolytic agent. Sequences AAU80972-AAU8104 represent antibodies and vector polypeptides used in the method of the invention.
                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; mouse; BC2; animal post-thromboembolic induced ischaemia; thrombolytic agent; anti-factor IX antibody; plasminogen activator; thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolyt. vasotropic; cardiant; anti-respiratory syncytial virus;
                                                                                                                                                          The
                                                                                                                                                                               Example 7; Page 153-154; 163pp; English.
                                                                                                                                                                                                                 administering anti-factor activator -
                                                                                                                                                                                                                                         Treating
                                                                                                                                                                                                                                                                                                                 Barone
                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                   15-MAY-2000; 2000US-0571434.
                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                             22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200187339-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine BC2 light chain modified variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU81001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU81001 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are useful in the treatment of thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody BC2. It is encoded by a DNA fragment (see AAT79899) produced by PCR amplification of BC2 cDNA. The modified BC2 VL region is incorporated into novel mouse-human chimeric light chain F9CHLC (see AAW24532). Claimed anti-Factor IX chimeric antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
                                                                                                                                                   invention relates to a method for treating an animal
                                                                                                                                                                                                                                                                     2002-082944/11.

DB; ABK24004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QTVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWIYATSNLASGVPAR
                                                                                                                                                                                                                                                                                                               3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 95.:
01; Conservative
                                                                                                                                                                                                                          post-thromboembolic ering anti-factor IX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 AA;
                                                                                                                                                                                                                                                                                                            Blackburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variable region;
                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-US27438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.6%;
                                                                                                                                                                                                                                                                                                               ž,
                                                                                                                                                                                                                                                                                                              Feuerstein GZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ۲,
                                                                                                                                                                                                                         induced ischaemia in an antibody in combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 526; DB 18;
Pred. No. 1.9e-30;
1; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽
                                                                                                                                                                                                                                                                                                            Toomey JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                         animal by with a pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thrombolytic;
                                                                                                                                                                                                                         plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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Sequence

112

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RESULT 8 AAB30694

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                                                                                                    RESULT 7
AAR55214
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Best Local S
Matches 101
                                                                   Matches
                                                                                   Query Match
                                                                                                                                                                   Treating B cell lymphoma with chimeric antibody - causing rapid depletion of peripheral B cells, all antibodies and hybridomas
                                                                                                    Sequence
                                                                                                                     See also
                                                                                                                             The sequence is the murine variable r murine anti-CD20 monoclonal antibody
                                                                                                                                                    Disclosure; Fig 4; 101pp; English.
                                                                                                                                                                                                               WPI; 1994-183162/22.
                                                                                                                                                                                                                                        Anderson
                                                                                                                                                                                                                                                                                                                                                                     B cell lymphoma cell lysis.
                                                                                                                                                                                                       N-PSBD; Q65630
                                                                                                                                                                                                                                                                          03-NOV-1993;
                                                                                                                                                                                                                                                                                                                                    WO9411026-A
                                                                                                                                                                                                                                                                                                                                                                                              Murine variable
                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1995
                                                                                                                                                                                                                                                                                 13-NOV-1992;
                                                                                                                                                                                                                                                                                                                    26-MAY-1994.
                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                AAR55214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR55214 standard;
                                                                                                                                                                                                                                                        (IDEC-) IDEC
                                                                                                                                                                                                                                                                                                   12-NOV-1993;
                                                                                                                                                                                                                                 Reffme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Sim
83
                61
                                 23
                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                         1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
        FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                 QIVLSQSPAILSASPGEKVTMTCRASSSVSYIHWFQQKPGSSPKPWIYATSNLASGVPVR
FSGSGSGTSYSLTISRVEAEDAATYYCQQWTSNPPTFGGGTKLEIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98; Conserv
                                                                                                                                                                                                                                        DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                    AAQ65629-35.
                                                                                                    128
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                         PHARM CORP
                                                                                                                                                                                                                                        Hanna N,
                                                                                                    AA;
                                                                                                                                                                                                                                                                         92US-0978891
93US-0149099
                                                                                                                                                                                                                                                                                                   93WO-US10953
                                                                                                                                                                                                                                                                                                                                                                             chimeric antibody; CD20;
                                                                                                                                                                                                                                                                                                                                                                                              region light chain from
                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
                                                                           93.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94.6%;
                                                                                                                                                                                                                                        Leonard JE,
                                                                  5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 128
                                                                 Score 521; DB 15;
Pred. No. 4.8e-30;
s. wismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 526; DB 23;
Pred. No. 1.9e-30;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₹
                                                                                                                            region light chain
y 2BS.
                                                                                                                                                                                                                                        Newman RA,
                                                                                                                                                                                                                                                                                                                                                                                              2BS
                                                                                                                                                                                                                                                                                                                                                                            peripheral blood
                                                                                                                                                                               also
                                                                                  Length 128;
                                                                                                                                                                                                                                        Rastetter WH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 112;
                                                                  Indels
                                                                                                                                                                                       against CD20
128
                                                                                                                                                                               new
                                                                                                                                     derived
                                                                                                                                                                                                                                                                                                                                                                              cells;
                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                     from
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
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Query Match
Best Local Similarity
                                                                                                                                       fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer, e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a
                                                                                                                                                                                                                                                                                                                                       The present sequence represents a fusion of an anti-CD20 single chain antibody (BBE9) streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin and a promoter, encoding a polypeptide to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with cancer, e.g. adenocarcinomas -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptavidin;
hematological
                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 11B; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-091213/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Goshorn SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NEOR-) NEORX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1999;
03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200075333-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
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                                                                                                                        target site
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249..253
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254..412
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Score 517;
Pred. No. 2
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                    Length 412;
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The present sequence represents a fusion of an anti-CD20 single chain antibody (B9E9) streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second
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03-DEC-1999;
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                                                                                                                                                                                                                                                                                                            Example 2; Fig 11C; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated or targeting tumour cells as the targeting tumour cells
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malignancy; B9E9.
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99US-0168976
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265..423
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260..264
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151..259
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127..150
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Pred. No. 2.9e-29;
3; Mismatches '
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RESULT 11
AAP94781
Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              light and heavy chain J regions useful in the design of oligonuclectides (UIGs) for use as primers or probes for cloning immunoglobulinlight or heavy chain mRNAs or genes. Depending on t nature of design of a particular UIG, it may be capable of hybridizing to all Ig mRNAs or genes containing a single specific sequence. UIG denotes universal immunoglobulin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ITGE-)
(ROBI/)
                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chains and 2 heavy chains, each comprising a constant human re and a variable non-human region. Coding sequences for the Ig are also claimed. The invention provides consensus sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prodn. of immunoglobulin chains and molecules - is by DNA procedures, with chimeric antibodies etc. related specific antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patentors claim chains and 2 heavy of
           Domain
                                                    Domain
                                                                        Domain
                                                                                              Domain
                                                                                                                  Peptide
                                                                                                                                                  Synthetic
                                                                                                                                                                       Antibodies;
                                                                                                                                                                                                                 06-JUL-1990
                                                                                                                                                                                                                                                            AAP94781 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Fig 22; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAN70972.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robinson RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-OCT-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Updated on 03-OCT-2002 to add missing OS field.)
                                                                                                                                                                                             H7 VL
                                                                                                                                                                                                                                                                                                               23
                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                       1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                         QIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPKPWIYAPSNLASGVPAR 82
                                                                                                                                                                                                                                                                                                                                                                                                      98;
                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INT GENETIC ENG INC ROBINSON R R.
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                128 AA;
                                                                                                                                                                       passive immunisation; pH3-12a; ss
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu AY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85US-0793980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86WO-US02269
                                                                         /label=FR1
50..55
                    /label=CDR2
                                                                                                                             location/Qualifiers
                                        'label=FR2
                                                                                                       label=Leader
                                                              label-CDR1
                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a chimeric antibody molecule comprising
           . 109
                                                                                                                                                                                                                                                                                                                                                                                                                92.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Horwitz
                                                                                                                                                                                                                                                               128
                                                                                                                                                                                                                                                                                                                                                                                                     Score 516; DB 8;
pred. No. 1.1e-29;
3; Mismatches 5
                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΑH,
                                                                                                                                                                                                                                                              A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to cancer
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n region
Ig chains
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AAW10589
ID AAW10
XX AW10
XX AW10
XX 21-OC
XX 21-OC
XX Inmun
KW Erame
XX Erm
Y Pepti
FT Pepti
FT Regic
FT Regic
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Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence carries the variable region of the chimeric immunoglobulin sequence. The antibodies are useful in passive immunisation avoidin negative immune reactions. They are also useful in assaying and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polynucleotide(s) encoding Immunoglobulin molecules used for efficient prodn. of chimeric human or non-l class switched antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
         Region
                                                                                                                      Immunoglobulin G; IgG; light chain; recombinant production; antibody; passive immunisation; serum sickness; anaphylactic shock; immunisasiug; reagent; complement mediated lysis; therapy; variable; region; complementarity determining; CDR;
                                                                                                                                                                                         21-OCT-1997
                                                                                                                                                                                                            AAW10589
                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; ; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Robinson RR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUL-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M-66600680M
                            Region
                                                                                            Mus spp
                                                                                                                                                                      2H7 antibody light chain variable region.
                                                                                                                                                                                                                               AAW10589 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ITGE-) INT
                                              Peptide
                                                                 Peptide
                                                                                                               ramework.
                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                  23
                                                                                                                                                                                                                                                                                                                1989-061144/08.
DB; AAN91147.
                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                            128
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                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu AY,
                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            δ
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                                   /label=
23..128
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label=CDR3
119..128
                                                                          Location/Qualifiers
'label= CDR_1
                  'label framework_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=FR4.
                                                                                                                                                                                                                               Protein; 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..118
                                                                                                                                                                                                                                                                                                                                                                 92.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Horw1tz
                                   mat_peptide
                                                       sig_peptide
                                                                                                                                                                                                                                                                                                                                                      Score 516; DB 10;
Pred. No. 1.1e-29;
3; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AΗ,
                                                                                                                                                                                                                              Ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wall
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-human
                                                                                                                                                                                                                                                                                                                                                                        Length 128;
                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                 avoiding
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        vitro
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RESULT 13
AAW16344
ID AAW16
                                                                                   Вþ
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The present sequence is the light chain variable region of the 2H7 antibody. The 2H7 cDNA was used in the preparation of a novel polynucleotide molecule encoding an Ig fragment. The DNA molecule comprises 2 DNA sequences encoding 2 pectate lyase secretion signal sequences respectively linked to a DNA sequence encoding an Ig fragment graduence single prokaryotic promoter so as to form a disistronic transcription unit, provided that the Ig fragment can bind an antigen and is produced and secreted by an E. coli host cell. The polynucleotide molecule is expressed in the host cell. The polynucleotide molecule is used for the production of recombinant antibodies, which can be used for passive immunisation without negative immune reactions (e.g. serum sickness and anaphylactic shock), in labelled forms as immunoassay or imaging reagents, in complement mediated lysis and for therapeutic agent.
                                                                                                                Query Match
Best Local S
                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAR-1990;
01-NOV-1985;
27-OCT-1986;
24-JUL-1987;
11-JAN-1988;
08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Better M,
Wall R, W
                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      Example; Fig 22; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encodinding immunoglobulin fragment - comprising discistronic transcription unit with pectate lyase signal sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-107579/10.
N-PSDB; AAT36317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JAN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (XOMA ) XOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
83
                         61
                                                   23
                                                                           \vdash
            FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEJR 106
                                                  QIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPKPW1YAPSNLASGVPAR
                                                               QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPNISATSNLASGVPAR
FSGSGSGTSYSLTISRVEAEDAATYYCQQWSFNPPTFGAGTKLELK
                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilcox GL;
                                                                                                                                                       128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Horwitz AH,
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90US-0501092.

85US-0793980.

86WO-US02269.

87US-0077528.

88US-0142039.

92US-0987555.

94US-0299085.
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/label= framework_2
71..77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119..128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- CDR_2
78..109
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                                                                                                                92.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lei
                                                                                                  Score 516; DB Pred. No. 1.1e 3; Mismatches
                                                                                                    ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY, Robinson RR;
                                                                                                                DB 18;
.1e-29;
                                                                                                     5,
                                                                                                                             Length
                                                                                                    indels
 128
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AAW16344 standard;

Protein; 128

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Gaps

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29-MAR-1990;
01-NOV-1985;
27-OCT-1986;
                                                                                                                                                                                                      11-JAN-1988;
17-APR-1992;
29-APR-1994;
      A polypeptide (AAW16344) comprises the light chain variable region of mouse monoclonal antibody 2H7, which recognises human B-cell surface antigen Bp35. It is encoded by a CDNA close (AAR70869) obtd. from a 2H7 cDNA library by PCR amplification. The 2H7 heavy chain variable sequence (AAW16343) is also provided. A novel human-mouse chimaeric antibody with specificity for the human B-cell antigen has been
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibody engineering; passive immunisation; 2H7; B-cell antigen; F
                                                                                        Secretable immunoglobulin heavy and light chain fragments - capable of assembling into chimeric antibodies, useful for e.g. passive immunisation, diagnosis, etc
                                                                                                                                                           Wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Peptide
                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
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constructed
                                                                        Example
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                                                                                                                                                                                     (XOMA) XOMA
                                                                                                                                                                                                                                   24-JUL-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW16344;
                                                                                                                               1997-225473/20.
DB; AAT70869.
                                                                                                                                                                  ,
                                                                        4; Fig
                                                                                                                                                         , Horwitz AH, Wilcox GL;
                                                                                                                                                                                      CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                                                                                                                                       86WO-US02269.
87US-0077528.
88US-0142039.
92US-0870404.
94US-0235225.
                                                                      22; 96pp;
                                                                                                                                                                                                                                                    90US-0501092.
85US-0793980.
                                                                                                                                                                                                                                                                                85US-0793980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Sig_peptide 23..46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
47..55
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110..1
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/note= "framework
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                                                                                                                                                                                                                                                                                                                                                                                   .118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;; heavy chain; light chain; chimaeric antibody;
;; diagnosis; hybridoma; monoclonal antibody;
Bp35.
                                                                                                                                                                                                                                                                                                                                     "framework region
                                                                                                                                                                                                                                                                                                                                                              "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                    "complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                "framework
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "complementarity
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                                                                        English.
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                                                                                                                                                                                                                                                                                                                                                                                         region
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                                                                                                                                                                    ΑY,
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RESULT 14
AAW10243
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Best Local S
Matches 98
                                                    29-MAR-1990;
01-NOV-1985;
27-CCT-1986;
24-JUL-1987;
11-JAN-1988;
08-DEC-1992;
22-FEB-1993;
09-DEC-1994;
N-PSDB; AAT51043
                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
        WPI; 1997-011254/01
                                                                                                                                                                                                                                                                                                                                     antibody;
                                                                                                                                                                                                                                                                                                                                             serum sickness;
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                       Better
                                                                                                                           01-NOV-1985;
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                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                               Mus musculus
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                                      (XOMA)
                                                                                                                                          19-NOV-1996
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98; Conser
                                      AMOX
                                                                                                                                                                                                                                                                                                                                cell
                                                                                                                                                                                                                                                                                                                                                     production; human
                                                                                                                                                                                                                                                                                                                                                           lyase; signal
                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                      Lei S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                      CORP
                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                    85US-0793980.

86WO-US02269.

87US-0077528.

88UUS-0142039.

92US-0987555.

93US-0020671.

94US-0357234.
                                                                                                                                                                                                                                                                                                                                      light-chain; hepatitis; mouse; lung carcinoma; cancer;
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                                                                                                           90US-0501092
                                                                                                                           85US-0793980
                                                                                                                                                                                                                                                                                                                                           signal sequence; Gram-negative backerium; immunoglobulin; ion; human; constant region; passive immunisation; toxin; anaphylaxis; sweetener; thaumatin; cytoplasm; periplasm;
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119..1
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47..55
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23..46
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1.1e-29;
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11-JAN-1988;
08-DEC-1992;
18-AUG-1994;
25-MAY-1995;
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N-PSDB; AAV18594.
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llcox GL;
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87US-0077528.

88US-014203.

92US-0987555.

94US-0299085.

95US-0450731.

95US-0466203.
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Pred. No. 1.1e-29;
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2002 Compugen Ltd.
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| | | 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 3 | 32 | 31 | 30 | |
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| | | 417 | 417 | 418 | 419 | 420 | 420 | 421 | 423 | 423 | 423 | 423 | 425 | 426 | 426 | 427 | 429 | |
| | | 75.0 | 75.0 | 75.2 | 75.4 | 75.5 | 75.5 | 75.7 | 76.1 | 76.1 | 76.1 | 76.1 | 76.4 | 76.6 | 76.6 | 76.8 | 77.2 | |
| | | 108 | 108 | 107 | 106 | 132 | 109 | 108 | 108 | 107 | 107 | 95 | 109 | 99 | 94 | 97 | 106 | |
| | | N | N | - | N | N | N | N | ນ | N | N | Ν | N | ν | N | N | N | |
| | | PL0277 | PL0276 | KVMSX4 | PS0070 | S05268 | PT0404 | PL0278 | S29581 | S11113 | S11112 | D33730 | PT0405 | D38601 | S26340 | PH1085 | G27887 | |
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ALIGNMENTS

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A; Cross-references: EMBL: M90690 A; Note: sequence extracted from NCBI backbone C; Superfamily: immunoglobulin V region; immunoglobulin C; Keywords: immunoglobulin F; 16-89/Domain: immunoglobulin homology < TMM> C:Species: Mus musculus (house mouse) C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change C:Accession: A42848; S33902 R:Fell, H.P.; Gayle, M.A.; Yelton, D.; Lipsich, L.; Schieven, G. J. Biol. Chem. 267, 15552-15558, 1992 A:Title: Chimeric L6 anti-tumor antibody. Genomic construction, A; Reference number: A42848; MUID:92348410; PMID:1639794 A; Accession: A42848 A; Molecule type: mRNA A; Residues: 1-106 <MEE> A; Residues: 1-106 <MEE> A; Experimental source: strain BALB/c A; Note: the sequence shown here is from the V C; Superfamily: immunoglobulin V region; immuno C; Keywords: heterotetramer; immunoglobulin F; 16-89/Domain: immunoglobulin homology <IMM> R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoui, M.; Urbain, J.; Exp. Med. 169, 519-533, 1989 A;Title: Structural characterization of antiidiotypic antibodies; evidence that Ab2s A;Reference number: PL0080; MUID:89094248; PMID:2492056 A;Accession: PL0082 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-107 <FEL> Ig kappa chain V region (2D3) - mouse C;Species: Mus musculus (house mouse) C;Date: 07-Jun-1990 #sequence_revision C;Accession: PL0082 Ig light chain V region - mouse (fragment) N;Alternate names: L6 anti-tumor antibody Local Similarity FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106 Conservative 94.1%; NCBI backbone (NCBIN:109958, NCBIP:109959) ω •• Score 523; Pred. No. 9 Mismatches 07-Jun-1990 #text_change 21-Jan-2000 the V kappa region of an antiidiotypic monocl immunoglobulin homology immunoglobulin homology : DB 2; | |.2e-38; |es 3; L.; Schieven, G.L.; Marken, J.S.; Length 106 Indels expression, and chara 21-Jan-2000 0; Gaps 60 60 <u>.</u>

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RESULT 3

If kappa chain V region (F3, anti-AFP) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 10-Nov-1997 #sequence_revision 23-Jan-1998 #text_cha
C; Accession: PC4405
R; Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
Chinese Biochem. J. 12, 648-653, 1996
A; Title: Generation of a phage display library of the immun.
A: Reference number: PC4405
                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-107 <51K>
A; Residues: 1-107 <51K>
C; Superfamily: immunoglobulin V region; immunoglobulin
C; Keywords: heterotetramer; immunoglobulin
F; 16-89/Domain: immunoglobulin homology <IMM>
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A; Status: preliminary
                                                                                                                                                                                                                                                                                           A;Title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-b A;Reference number: A30562; MUID:89110066; PMID:2464031
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A; Residues: 1-107 < DEN>
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Best Local
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                                                                         1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
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                            FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                           QIVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSGSGSGTSYSLAISRVEAEDAATYYCQQWNSNPLTFGAGTKLELK 106
FSGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPYTFGGGTKLEIK
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                                                                                                                                    85.3%;
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Pred. No. 4.1e-34;
6; Mismatches 9
                                                                                                                                    Score 474; DB 2;
Pred. No. 1.3e-33;
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Pred. No. 3.
                                                                                                                        Mismatches
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           Ig kappa chain V region (35.8.2H) - mot C;Species: Mus musculus (house mouse) C;Date: 23-Mar-1989 #sequence_revision C;Accession: G30560 R;Matsuda, T.; Kabat, E.A.
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S26338
R;Matsuda,
J. Immunol
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                                                                                                         RESULT 7
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Ig kappa chain V region (27.10.2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1989 #sequence_revision 23-Mar-1989 #text_change 21-Jan-2000
C;Accession: B30562
R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino A;Reference number: $26309; MUID:91341421; PMID:1908510
A;Accession: $26338
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C;Speciles: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26338
R;Stark, S.E.; Caton, A.J.
                                                                                                                                                                                                                                                                                                                                      C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;16-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Amino acid substitutions in V-H CDR2 change the A;Reference number: A30562; MUID:89110066; PMID:2464031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: immunoglobulin V region; imm C;Keywords: heterotetramer; immunoglobulin F;16-89/Domain: immunoglobulin homology <II
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A; Residues: 1-107 <SIK>
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A; Residues: 1-105 <STA>
A; Cross-references: EMBL:X59197; NID:g52328; PIDN:CAA41907.1; PID:g1334069
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
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89; Conserv
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85.7%;
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Pred. No. 3.5e
7; Mismatches
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Pred. No. 1.6e-33;
mouse (fragment)
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1989

23-Mar-1989 #text_change

21-Jan-2000

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Ig light chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C;Accession: S38720
R;Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A;Reference number: S38713
A;Reference number: S38713
A;Accession: S38720
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <CIMD
A;Cross-references: EMBL:X76023; NID:g416104; PIDN:CAA53610.1; PID:g1334265
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-89/Domain: immunoglobulin homology <IMM>
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H. Mol. Immunol. 25, 33-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies. A;Reference number: PL0011; MUID:88142863; PMID:3125424
A;Accession: PL0013
A;Accession: PL0013
A;Molecule type: mRNA
A;Residues: 1-140 CCHE>
A;Experimental source: cell line 4C11
C;Comment: This protein is an anti-idiotypic antibody that induces C:Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C:Keywords: heterote
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                                                                                                                                                                                                                                                                                                                                                                                                 PL0013

If kappa chain precursor V region (4C11) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C:Accession: PL0013

R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
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Pred. No. 5.8e-33;
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n,Armandola, E.A.; Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, Eur. J. Immunol. 22, 2893-2899, 1992
A; Title: Molecular analysis of anti-idiotypic monoclonal antibodies A; Reference number: A49049; MUID:93049629; PMID:1425914
A; Accession: B49049
A; Coression: B49049
                                                                                                                                                                                                                                                                                                                               Ig kappa chain V region (anti-idiotypic) - mquse (Species: Mus musculus (house monse) (Species: Mus musculus (house monse) (C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000 C;Accession: B49049 (Species: Mariani, S.M.; Zwickl, M.; Hardman, N.; Ferrone, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
B49049
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C;Keywords: heterotetramer; immunoglobulin
F;16-89/Domain: immunoglobulin homology <I
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A;Title: Functional immunoglobulin light chain A:Reference number: A92781; MUID:89310348; PMID A:Accession: PS0071
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F;38-111/Domain: immunoglobulin homology <IMM>
F;46-55/Region: complementarity-determining 1
F;71-77/Region: complementarity-determining 2
F;110-118/Region: complementarity-determining 3
F;130-140/Domain: constant region (fragment) #status predicted <COR>
                                                                C; Keywords: F; 16-89/Doma
                                                                                                         A; Note: sequence extracted from NCBI backbone (NCBIN:118298, NCBIP:118299) C; Superfamily: immunoglobulin V region; immunoglobulin homology
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PS0071
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                                                                                                                                                                         A; Molecule type: nucleic acid
A; Residues: 1-104 <ARM>
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A; Residues: 1-106
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                                                                                                                                                       A; Experimental source: BALB/c
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Query Match
Best Local
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Best Local
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                                                             immunoglobulin homology
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82.4%;
84.6%;
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Score
Pred.
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Pred. No. 2
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Pred. No. 1.8e-32;
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458; DB 2;
No. 2.9e-32;
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                    Length 104;
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Similarity

into

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A; Residues: 1-130 
A; Residues: 1-130 
A; Cross references: GB:M27792; NID:g197159
A; Cross references: mRNA clones for anti-phenyloxazolone antibody 6F6
A; Note: the authors translated the codon TTC for residue 8 as Pro and TTC for residue A; Note: the codon given for 1-Met (AGT) is inconsistent with the authors' translation R; M11stein, C.; Even, J.; Jarvis, J.M.; Gonzalez-Fernandez, A.; Gherardi, E.
Eur. J. Immunol. 22, 1627-1634, 1992
A; Title: Non-random features of the repertoire expressed by the members of one V kappa A; Reference number: A49044; MUID:92289826; PMID:1601044
A; Accession: A49044; MUID:92289826; PMID:1601044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig kappa chain precursor V region (anti-phenyloxazolone 6F6) - mouse C:Speciaes: Mus musculus (house mouse) C:Date: 31-Dec-1991 #sequence_revision 09-Aug-1996 #text_change 16-Jul-1999 C:Accession: JL0079; A49044; B49044 R:Kaartinen, M.; Rocca-Serra, J.; Maekelae, O. Mol. Immunol. 25, 859-865, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-107 <DEN>
C; Superfamily: immunoglobulin V region;
F; 16-89/Domain: immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q. Chinese Biochem. J. 12, 648-653, 1996
A;Title: Generation of a phage display library A;Reference number: PC4405
A;Contents: Spleen
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PD0011
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    A;Cross-references: GB:S37664; NID:g250215; PIDN:AAB22332.1; A;Experimental source: BALB/c germ-line A;Note: sequences extracted from NCBI backbone; partial nucle
                                                                      A; Molecule type: DNA
A; Residues: 114-116 <MIL2>
                                                                                                                     A; Note: sequence extracted A; Accession: B49044
                                                                                                                                        A;Cross-references: GB:S37663; NID:g250214; PIDN:AAB22331.1; A;Note: sequence extracted from NCBI backbone (NCBIN:106802,
                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-25 <MIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
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Pred. No. 3e-32;
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                                              PID:g250218
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NCBIP:106809)
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-100 <KAV>
A;Cross-references: EMBL:X59093; NID:g52225; PIDN:CAA41819.1;
C;Superfamily: immunoglobulin V region; immunoglobulin homolog
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                              s29590
If kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision
C:Accession: S29590
                                                                                                                                                                                    R; Kavaler, J. submitted to the EMBL
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A; Accession: S29590
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BL Data S26459

Library,

April 1991

PID:g52226

06-Jan-1995 #text_change

21-Jan-2000

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A;Gene: V(kappa)Oxl
A;Introns: 17/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical lig
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X59094; NID:952227; PIDN:CAA41820.1; PC:Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-88/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision
C;Accession: S29591
R;Kavaler, J.
submitted to the EMBL Data Library, App
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S29591
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A; Residues: 1-103 <KAV>
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Best Local Similarity
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                      SGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLE 104
                                                                                       IVLTQSPAIMSASPGEKVTMTCSASSSVSYMHWYQQKSGTSPKRWIYDTSKLASGVPARF
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SGSGSGTSYSLTISSMEAEDAATYYCQQWSSNPLTFGAGTKLE
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S26459
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85.4%;
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83.0%;
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Pred. No. 3.7e-32;
5; Mismatches 12
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Best Local S
Matches 85
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13-AUG-1987 (Rel. 0
13-AUG-1987 (Rel. 0
15-JUL-1999 (Rel. 3
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SEQUENCE FROM N.A.

MEDLINE-83271467; Pubmed-6877353;

Kaartinen M., Griffiths G.M., Markham A.F., Mil

"mRNA sequences define an unusually restricted
phenyloxazolone and its early diversification."

Nature 304:320-324(1983)

Nature 304:320-324(1983)
                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoqlobulin V region;
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                                                                                                                                                                                                                                                                                                                                                                               EMBL; K00735; AAA38680.1; -. HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Mammalia; Eutheria; Rodentia;
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COMPLEMENTARITY-DETERNINING-1.
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FRAMEWORK-4.
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GenCore version (c) 1993 - 2002

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                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
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COMPLEMENTARITY-DETERMINING-2
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COMPLEMENTARITY-DETERMINING-3.
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MEDLINE-83271467; PubMed-6877353;

MEDLINE-83271467; PubMed-6877353;

MEDLINE-83271467; PubMed-6877353;

MARYLORE M., Griffiths G.M., Markham A.F., Milstein C.

"mRNA sequences define an unusually restricted IgG resp
phenyloxazolone and its early diversification.";

Nature 304:320-324(1983).

-i- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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13-AUG-1987 (Rel. 05, Last sequence up
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15 kappa chain V-VI region NQ2-48.2.2.
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"mRNA sequences define an unusually restricted IgG
phenyloxazolone and its early diversification.";
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Pfam; PF00047; ig; 1.
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-I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY
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MEDLINE=83271467; PubMed=6877353;
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          InterPro; IPR003006;
InterPro; IPR003596;
Pfam; PF00047; 1g; 1.
                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a control of the swiss institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict the European Bioinformatics institute.
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MEDLINB-83271467; PubMed-6877353;

MEDLINB-83271467; PubMed-6877353;

Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.

"mRNA sequences define an unusually restricted IgG resp
phenyloxazolone and its early diversification.";

Nature 304:320-324(1983).
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                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Kaartinen M., Griffiths G.M., Markham A.F., Milstein
"mRNA sequences define an unusually restricted IgG ro
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Nature 304:320-324(1983).
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Similarity

Matches

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RESQUEY 7

KV6D_MOUSE
ID KV6D_M
AC P01678
AC P01678
DT 21-JUL
DT 21-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUL
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DT 21-JUL
DT 21-JUL
DT 11-JUL
RX MEDLIN
RX MEDLIN
RX MEDLIN
RA RUdiko
RT COMALIN
RA FIR; A
DR FIR; A
DR INTERP
DR INTERP
DR INTERP
DR INTERP
DR INTERP
DR SMART;
KW IMMUNC
FT DOMAIN
     RESULT 8
KV6A_MOUSE
ID V6A_M
AC P01675
DT 21-JUL
DT 21-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUL
OF 19 kap)
OS Mus mus
OC Eukary
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Best Local S
Matches 81
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P01678;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Daylor SAPC 10.
                                                                                                                                                                                                                                                                                                         DISULFID
NON_TER
SEQUENCE
                                                                                KV6A_MOUSE
P01675;
                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
15 kappa chain V-VI region XRPC 44.
                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
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Mammalia; Eutheria;
       Eukaryota; Metazoa;
                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; 1g; 1
SMART; SM00406; IGv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003006;
InterPro; IPR003596;
Pfam; PF00047; 1g; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Kappa Chain joining segments combining sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-81054757; PubMed-6776525; Rudikoff S., Rao D.N., Glaudemans
                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BIND GALACTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A01941
                                                                                                                                                      QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR
                                                                                                                                                                                                       FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPP--TFGGGTMLEIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P01679; ZFBJ.
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                                                                                                                                                                                                                                                        Similarity 76.4
31; Conservative
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                    (Mouse)
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56 87
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97 106
                                                                                             STANDARD;
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Rodentia;
   Chordata;
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76.48;
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                                                                                                                                                                                                                                                                                                           MW;
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                                                                                                                                                                                                                                                                  Score 419; DB 1;
Pred. No. 4.3e-33;
                                                                                                                                                                                                                                                                                                                                                                               FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                            COMPLEMENTARITY-DETERMINING-3 FRAMEWORK-4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mans C.P.J., Potter M.;
and structural diversity
      Craniata; Vertebrata;
                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77:4270-4274(1980).
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                                                       update)
                                                                                           107
                                          update)
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                                                                                                                                                                                                                                                                              Length 107;
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; Murinae; Mus
       Euteleostomi;
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       RESULT 9
KV6B_MOUSE
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Best Local S
Matches 81
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P01676;
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"k Chain v
                                                                                                                    PIR;
                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID-10090;
                             Immunoglobulin
DOMAIN 1
                                                                                                                                                      proteins.";
Biochemistry 17:5555-5559(1978)
                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last seq
15-JUL-1999 (Rel. 38, Last ann
15 kappa chain V-VI region XRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A01941; KVMSX4.
HSSP; P01679; 2FBJ.
       DOMAIN
                                                       SMART;
                                                                     Pfam;
                                                                                                                                                                                            Rao D.N.,
                                                                                                                                                                                                        MEDLINE=79082830; PubMed=103573;
                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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InterPro; IPR003596;
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BIND GALACTAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 17:5555-5559(1978).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
NCBI_TaxID=10090;
                   NIAMOC
                                                                                InterPro;
                                                                                          InterPro;
                                                                                                        HSSP;
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                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                ESGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                      Pro; IPR003006; Ig_MHC.
Pro; IPR003596; Ig_v.
Pr00047; ig; 1.
; SM00406; IGv; 1.
                                                                                                        P01679; 2FBJ
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107
Conservative
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                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                           THIS CHAIN WAS
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Rodentia;
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I9_v.
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76.48;
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 418;
Pred. No. 5
      COMPLEMENTARITY-DETERMINING-1. FRAMEWORK-2.
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                               FRAMEWORK - 1
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                                                                                                                                           A MYELOMA PROTEIN THAT
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KY6C_MOUSE STANDARD,

P01677;

P1-3UL-1986 (Rel. 01, Created)

T 21-3UL-1986 (Rel. 01, Last sequence update)

T 15-JUL-1999 (Rel. 38, Last annotation update)

IT 15-JUL-1999 (Rel. 38, Last annotation update)

E I kappa chain V-VI region TEPC 601/TEPC 191.

S Mus musculus (Mouse)

Mus musculus (Mouse)

S Mus musculus (Mouse)

Chordata; Craniata; Vertebr
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Best Local S
Matches 80
                      Query Match
Best Local S
Matches 79
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DOMAIN
                                                                        DISULFID NON_TER
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DOMAIN
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DOMAIN
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MEDLINE-79082830; PubMed-103573;
Rao D.N., Rudikoff S., Potter M.
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                                                                                                                                                                                                                                                                            combining sites.";
Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
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                                                               SEQUENCE
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                                                                                                                                                            Immunoglobulin
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SMART; SM00406; IGv; .
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MEDLINE=81054757; PubMed=6776525;
                                                                                                                                                                                                                                                                                                                                                                  proteins
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InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                 Kappa Chain joining segments
                                                                                                                                                                                                                                                                                                            Rudikoff S., Rao D.N., Glaudemans
                                                                                                                                                                                                                                                                                                                                                                          "k Chain variable regions from three
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
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                                                                                                                                                                                                                                                         MISCELLANEOUS: THESE CHAINS
                                                                                                                                                                                                                                                                  MISCELLANEOUS:
                                                                                                                                                                                                                                   THAT BIND GALACTAN.
A01941; KVMSX4.
 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
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                                                                                                                                                                                                                           P01679; 2FBJ
                       79;
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                               Similarity
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                       Conservative
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74.58;
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75.5%;
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                      11;
                              Score 411;
Pred. No. 2
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Pred. No. 1.
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BY SIMILARI'
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                                                                                            FRAMEWORK - 3.

COMPLEMENTARITY - DETERMINING - 3.

FRAMEWORK - 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
                                                               203CD752A5EC34D7 CRC64;
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                                                                                   SIMILARITY
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structural diversity
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                                                                                                                                                                                                                                                                    ARE IDENTICAL
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RESULT 11
KV4A_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
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SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J00577; AAA38780.1; -. EMBL; V00780; CAA24157.1; -. PIR; A01943; KVMS7B. HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
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21-JUL-1986 (Rel.
15-JUL-1999 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [mmunoglobulin
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                                                                                                      3 VLSQSPAILSASPGEKVTMTCRASSSV--NYMHWYQQKPGSSPKPHISATSNLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS: THIS PROTEIN, IN WHICH THERE IS A DELETION OF TWO AMINO ACIDS AT THE V-J RECOMBINATION SITE (AFTER POSITION 118), IS SYNTHESIZED BUT NOT SECRETED IN CELLS THAT EXPRESS AND SECRETE THE NORMAL KAPPA CHAIN S107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INE-82115300; PubMed-6799208;
S.-P., Max E.E., Seidman J.G.,
kappa immunoglobulin genes are
26:57-66(1981).
                     FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIk 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSGSGSGTSYSLTISSMEAEDAAIYYCQQWNYPLITFGAGTKLELK 106
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                                                                                VLTQSPAIMAASLGQKVTMTCSASSSVSSSYLHWYQQKSGASPKP1 | HRTSNLASGVPAR
FSGSGSGTSYSLTISSYEAEDDATYYCQQWSGYP--FGSGTKLEIK
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Rodentia;
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annotation update)
S107B precursor.
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Pred.
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FRAMEWORK-1
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                                                                                                                                                                                                                                                   E4BB73072DCF6BE4 CRC54;
                                                                                                                                                                  Mismatches
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in the myeloma
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RESULT 12

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P01679;
21-JUL-1986
21-JUL-1986
15-JUL-1999
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DOMAIN
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                                                                                           STRAND
NON_TER
SEQUENCE
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STRAND
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Interpro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; 3D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The galactan-binding immunoglobulin study at 2.6-A resolution."; Proteins 1:74-80(1986).
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Rudikoff S., Rao D
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Suh S.W., Bhat T.N.,
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Natl. Acad.
                                                     Similarity
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                                                                                             Conservative
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38, Last
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                                                                                                                                     11502 MW;
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                                        13;
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                                                   Score 396; DB 1;
Pred. No. 6.4e-31;
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                                                                                            EA30C9A3E903979C CRC64;
                                        Mismatches
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on update)
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RESULT 13
KV3J_MOUSE
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KV3T_MOUSE
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P01672;
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21-JUL-1986
15-JUL-1999
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MEDLINE-79012520; PubMed-99744;

MCKean D.J., Bell M., Potter M.;

"Mechanisms of antibody diversity: multiple genes

related mouse kappa variable regions.";

Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
                                                                                                                                                                                                                                          NON_TER
SEQUENCE
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-!- MISCELLANEOUS: THE AF PIR; A01935; KVMSM6.
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; 
                                                         KV3T_MOUSE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE (PC 9245).
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P01662;
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SMART; SM00406; IGv
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                                                                                                                                                                                                                                                                                                                                                                                 nterPro; IPR003596;
                                                                                                              62
                                                                                                                        57 VPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
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Rodentia;
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63.6%;
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Pred. No. 1.
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COMPLEMENTARITY-DETERMINING-2
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COMPLEMENTARITY-DETERMINING-1.
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BY SIMILARI
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COMPLEMENTARITY - DETERMINING - 3
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Sciurognathi; Muridae;
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SMARR; SM00406; ICv; 1.

Immunoglobulin v region.

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DOMAIN 54 60

DOMAIN 61 92

DOMAIN 93 101

DOMAIN 102 111

DOMAIN 102 111

DOMAIN 103 192

DOMAIN 103 193

DOMAIN 103 193
Immunoglobulin 1
DOMAIN 1
DOMAIN 24
DOMAIN 39
DOMAIN 54
                                                                                                                                         MEDIINE-79012520; PubMed-99744;
MCKean D.J., Bell M., Potter M.;
"Mechanisms of antibody diversity: multiple genes
related mouse kappa variable regions.";
Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; MuscBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                 RV3L_MOUSE STANDARD; PRT; 111 AA. P01664; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15 kappa chain V-III region CBPC 101.
                                                               Pfam; PF00047; 1g; SMART; SM00406; IGV
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HSSP; P80362; 1WTL.
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aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malla: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
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Pred. No. 1.0
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BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-2
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COMPLEMENTARITY-DETERMINING-1.
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 COMPLEMENTARITY - DETERMINING - 2.
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62.7%;
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BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-3.
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Q8r062 mus musculu
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ALIGNMENTS

Вp Ş Query Match Best Local Similarity Matches 89; Conserv Infect. Immun. 68:5803-5808(2000). EMBL; AF206030; AAF69328.1; -. HSSP; P01679; 2FBJ. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. Pfam; PF00047; 19; 1. SMART; SM00406; IGv; 1. Q9JL76 PRELIMINARY; PRT; 97 AA. Q9JL76; Q9JL76; Q1-OCT-2000 (TrEMBLrel. 15, Created) Q1-OCT-2000 (TrEMBLrel. 15, Last sequence update) Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update) Anti-myosin immunoglobulin light chain variable requestions. NON_TER MEDLINE=20448942; PubMed=10992488; Malklel S., Liao L., Cunningham M.W., Diamond B.; "T-(cell-dependent antibody response to the dominant streptococcal polysaccharide, N-acetyl-glucosamine, with cardiac myosin." Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; SEQUENCE FROM N.A. STRAIN-DBA/2; SEQUENCE (Fragment) 11 _ 1 97 97 / Conservative AA; 10542 81.9%; 91.8%; X X Score 455.5; DB 11; pred. No. 1.1e-38; 2; Mismatches 5; C9EE1FFE1F49DA1C CRC54; DB 11; Length region Indels epitope of is cross-reactive 97; 1; Gaps 70 ;

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Strausberg R.;
Strausberg R.;
Submitted (APR-2001) to the EF
Submitted (APR-2001)
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ANTI-MOG KAPPA.,
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
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                                                                                                                                                                                                                                                                     Unknown (protein for MGC:6582)
Mus musculus (Mouse)
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
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PF00047; ig; 1.
; SM00409; IG; 1.
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Last annotation update)
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7; Mismatches
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Sciurognathi;
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Sciurognathi; Muridae;
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01-OCT-2000
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SEQUENCE
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Submitted (NOV-1999) to the
EMBL; AF207620; AAF19434.1;
HSSP; P01679; 2FBJ.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 immunogloba
                                                                                                                                                                                                                                                                                                                                                                                                             Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., "Amplification, cloning and sequence analysis of the variable region gene of monoclonal anti-idiotypic anti-
                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Platyhelminthes; Schistosomatoidea; Schistosomatidae;
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Schistosoma japonicum (Blood fluke).
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NCBI_TaxID=10090;
                                          Mus musculus (Mouse)
                                                              Anti-myosin
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                                                                                                                                                                                                                                                                                               SEQUENCE
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SMART; SM00406; IGv; 1.
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                                                                                                                                                                               GSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR
                                                                                                                                                                                                              LTQSPAIMSASPGEKVTMTCSASSSVSYVYWYLQKPGSSPRLLIYDTSNLASGVPVRFS
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                                                                                                                                                                      GSGSGTSYSLTISRMEAEDAATYYCQQWTSYPFTFGSGTKLELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83;
                                                                                                                                                                                                                                                       82; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00290; IG_MHC; UNKNOWN_1.
235 AA; 26021 MW; 5FC73BDEBD5E8FEF CRC54;
                                                                                                                                                                                                                                                                                                                                                   IPR003596;
                                                                                                                                                                                                                                                                                               106
106 AA;
                                                            0 (TrEMBLrel. 15,
0 (TrEMBLrel. 15,
1 (TrEMBLrel. 19,
1 immunoglobulin 1
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                                                                                                                  PRELIMINARY;
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11478
                     Chordata;
Rodentia;
                                                                                                                                                                                                                                                                 76.8%;
78.8%;
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78.38;
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                                                            , Created)
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, Last annotation updat
light chain variable r
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                                                                                                                                                                                                                                                       Score 427; DB
Pred. No. 9.5e
11; Mismatches
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Pred.
                     Craniata; Ver
Sciurognathi;
                                                                                                                  PRT;
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No.
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.5e-36;
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                                 Euteleostomi;
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Best Local :
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Best Local :
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NON_TER
SEQUENCE
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NON_TER
SEQUENCE
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MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9UL78 PRELIMINARY; PRT; 109 AA.
Q9UL78:
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003596; Ig_v. Pfam; PF00047; Ig; 1. SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malkiel S., Liao L., Cunningham M.W., Diamond B.; "T-Cell-dependent antibody response to the dominant epitope of streptococcal polysaccharide, N-acetyl-glucosamine, is cross-re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01679; 2FBJ
                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF03503
HSSP; P80362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with cardiac myosin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20448942; PubMed=10992488; Malkiel S., Liao L., Cunningham M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003006;
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      61
                                              59
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ARFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                   SYSLTISRVEAEDAATYYCQQWSSNPP-TFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SYSLTIGTMEAEDVATYYCQQGSSIPRYTFGGGTKLEIK 101
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AF206028; AAF69326.1; -.
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AF035036; AAD56272.1; -.
                                                                                                                                                                                     66; Conserv
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IPR003596; Ig_v.
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101 AA;
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10778 MW;
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11646 MW;
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74.7%;
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                                                                                                                                                                                     19;
                                                                                                                                                                                Score 352; DB
Pred. No. 3.6e
19; Mismatches
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Pred. No. 7.2e-30;
8; Mismatches 1:
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                                                                                                                                                                                                                                                                        5F675C52EC7EE197 CRC64;
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                                                                                                                                                                                DB 4; I
3.6e-28;
hes 21;
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RESULT 7

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Best Local :
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NON_TER 111
SEQUENCE 111 F
                                                                                                                                                                                                                         fetus.";
Clin. Im
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"Definition of the Idiotope of Pterin-Mimickin
in Mammalian Cells.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ
EMBL, R307935; AALO9419.1;
Interpro; IPR003006; Ig_MHC.
Pfam, PF00047; ig; 1.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                         NON_TER
                                                                      InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
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(Fragment).
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                                                                                                                                                                         EMBL; AF035044; AAD56280.1; HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                Wu X., Liu B., Van Young D.C.;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                       "Myosin-reactive autoantibodies in rheumatic carditis
                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 VPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGIMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 VPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSRELPYTFGGGTKLEIK 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 IVLSQSPAILSASPGEKVTMTCRASSSV-----NYMHWYQQKPGSSPKPWISATSNLASG
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     108
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  AA;
108
11633 MW;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61.8%;
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diotope of Pterin-Mimicking
                                                                                                                                                                                                                                                                                                                       Merwe
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                                                                                                                                                                                                                                                                                                                    P.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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  B7BEDC3E41FCCA37 CRC64;
                                                                                                                                                                                                                                                                                                                    Kalis N.N., Berney
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Query Match

61.48;

Score 341.5;

DВ

Length 108;

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OCC MANOR SISTER AND REAL SIST
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Best Local S
Matches 64
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                                                                                                                                       Q96SA9 PRELIMINARY; PRT; 10/ AA.
Q96SA9;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa
variable region (Fragment).
Homo sapiens (Human).
Homo sapiens (Human).
                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wan der Merwe P.L.,
SEQUENCE FROM N.A.
MEDLINE=98375893; PubMed=9712075;
Adderson E.E., Shikhman A.R., Ward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003596; Ig_v. Pfam; PF00047; Ig; 1. SMART; SM00406; IGv; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosir-reactive immunoglobulin light chain variable
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Q9UL79;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64;
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Similarity 60.4%;
64; Conservative 2
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108 AA;
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                                                                                                               Chordata;
Primates;
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; Pred. No. 6.6e
22; Mismatches
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7; Mismatches 22;
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Catarrhini; Hominidae
                                                                                                               Craniata; Vertebrata;
Catarrhini; Hominidae
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    K.E.,
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                                                                                                                 Hominidae;
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Q9UL81
ID Q9UL8
AC Q9UL8
AC Q9UL8
DT 01-M
DT 01-M
DT 01-M
DT 01-M
OC Euk
OC Euk
OC Man
OC Euk
CO NC!
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RP SE
RX ME
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RESULT
Q9UL77
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AC Q9
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Best Local S
Matches 66
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Best Local S
Matches 66
Q9UL77
Q9UL77;
01-MAY-2000
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  (TrEMBLrel.
                                               PRELIMINARY;
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Created)

PRT;

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InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular analysis of polyreactive monoclonal antihodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin antibody v region genes";
J. Immunol. 161:2020-2031(1998).
EMBL; U96396; AAB68785.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                 Clin. Immunol. Immunopathol.
EMBL; AF035033; AAD56269.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable
                                                                                                                                                                                                                                                                                   HSSP; P01607; 1REI
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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               FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR
                                                       FSGSGSGTDFTLTISGLQAEDFATYYCQQ-SYSALTFGPGTKVDIR
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66; Conservative
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0047; ig; 1.
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107 AA;
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107 AA;
                                                                                                                     Conservative
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11520 MW;
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                                                                                                                                 58.8%;
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                                                                                                                  Score 327; DB 4;
Pred. No. 1.2e-25;
9; Mismatches 19
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Pred. No. 4.7e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Eutel
Catarrhini; Hominidae; Homo
                                                                                                                                                                             070549FDE0754748 CRC64
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MEDLINE-98277119; PubMed-9614934;
MEDLINE-98277119; PubMed-9814934;
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MEDLINE-98277119; PubMed-98277119; PubMed-981494;
MEDLINE-98277119; PubMed-981494;
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MEDLINE-98277139; PubMed-9614934;
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EMBL; AF035029; AAD56265.1;
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#FPO0047; Ig; 1.
#TI; $M00406; IGV; 1.
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57.4%;
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Pred. No. 2.
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SEQUENCE
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01-DEC-2001 (TrEMBLrel. 20, Last annotation update)
Pterin-mimicking anti-idiotope kappa chain variable
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                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
MCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF035028; AAI HSSP; P80362; 1WTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable
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  Submitted
                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                    (Fragment).
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Pro; IPR003596; Ig_v.
PF00047; 1g; 1.
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  (SEP-2000)
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  to
                                                            Jennings I.G.,
  the
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                                       of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created;
  EMBL/GenBank/DDBJ databases
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                                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                         PRT;
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                                     I.G., Horaitis O.
Pterin-Mimicking
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7.8e-25;
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                                         Antibodies
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Murinae; Mus
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Search completed: November 27, 2002, 07:22:55 Job time: 60.9344 secs
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                                                                                                                                                                                                                                                   EMBL; AF307938; AAL09422.1; -.
InterPro; IPR003006; I9_MHC.
Pfam; PF00047; 1g; 1.
NON_TER 1 1
NON_TER 109 109
SEQUENCE 109 AA; 11943 MW; DAD3F98E05DD1501 CRC64;
                                                            61 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR,106
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62 FSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPWTFGGGTKLEIK 107
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Minimum DB
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Perfect score:
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq
                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_AA:*
1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
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556
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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 US-08-783-853A-105
US-08-783-853A-11
US-08-783-853A-11
US-09-344-050-11
US-09-344-050-13
US-08-475-815B-7
US-08-475-815B-7
US-08-475-815B-7
US-08-475-815B-7
US-08-475-815B-7
US-08-489-18
US-09-423-439-18
US-09-423-439-18
US-09-423-439-18
US-09-423-439-10
US-08-459-310-4
US-08-459-310-4
US-08-459-310-4
US-08-459-310-4
US-08-459-658-57
US-08-668-772A-6
US-08-668-772A-6
US-08-668-772A-6
US-08-688-772A-6
US-08-688-772A-6
US-08-688-752-5
US-08-688-752-5
US-08-688-752-110
US-08-836-561-33
US-08-311-778E-2
US-08-438-562-2
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| 453 | 453 | 453 | 453 | 453 | 454 | 454 | 455 | 455 | 455 | 456 | 456 | 457 | 457 | 462 | 464 | 464 | 466 |
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| 81.5 | 81.5 | 81.5 | 81.5 | 81.5 | 81.7 | 81.7 | | 81.8 | • | | • | 82.2 | | • | • | | |
| | | 127 | | | | | | | | | 281 | 235 | 222 | 128 | 128 | 128 | 129 |
| US-08-483-932 | US-08 | 2 US-08-487-113D-80 | 2 US-08-483-389-80 | US-08-482 | 4 US-09-344-050-78 | | | 3 US-08-783-853A-99 | | 4 US-09-423-439-51 | 4 US-09-423-439-44 | 2 US-08-190-199A-61 | 2 US-08-190-199A-67 | 2 US-08-656-586-2 | 5 PCT-US95-07302-2 | 4 US-08-619-491-2 | 2 US-08-483-528B-92 |
| • | Sequence 80, Appl | Sequence 80, Appl | Sequence 80, Appl | Sequence 80, Appl | Sequence 78, Appl | Sequence 78, Appl | Sequence 99, Appl | Sequence 99, Appl | Sequence 9, Appli | • | Sequence 44, Appl | Sequence 61, Appl | • | • | • | Sequence 2, Appli | Sequence 92, Appl |

ALIGNMENTS

| | MOLECULE TYPE: protein | ٠. |
|--------------|--|----|
| | TOPOLOGY: linear | ٠. |
| | DEDNESS: | ٠. |
| | TYPE: amino acid | ٠. |
| | 1: 106 | ٠. |
| | CHARAC | ٠. |
| | INFORMATION FOR SEQ ID NO: 105: | ٠. |
| | TELEX: | ٠. |
| | | ٠. |
| | TELEPHONE: 610-270-5096 | ٠. |
| | TELECOMMUNICATION INFORMATION: | ٠. |
| | BER: | ٠. |
| | 굮 | ٠. |
| | NAME: Baumeister, Kirk | ٠. |
| | /AGENT I | ٠. |
| | Ţ- | ٠. |
| | APPLICATION NUMBER: 60/029,119 | ٠. |
| | PRIOR APPLICATION DATA: | ٠. |
| | FICATION | |
| • | N-1997 | ٠. |
| | APPLICATION NUMBER: US/08/783,853A | |
| | LICATION DATA: | ٠. |
| | FastSEQ | ٠. |
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| | PA | |
| | King of Prussia | ٠ |
| | 09 Swedeland Road | |
| | ADDRESSEE: SmithKline Beecham Corporation | |
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| | SEQUENCES: | |
| | OF INVENTION: OF THROMBOSIS | |
| IN TREATMENT | TITLE OF INVENTION: ANTICOAGHIANT AGENTS HEFFIH. | |
| | sylvester | |
| | APPLICANT: Pacial, Education | |
| | MICHOIS, | |
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| | CHUTCH | |
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| | Patent No. 6005091 | ٠. |
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US-09-344-050-105
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Best Local Similarity 95.3
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                    INFORMATION FOR SEQ ID NO: 105: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/78
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/19/344,050
FILING DATE: 24-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SmithKli
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ORIGINAL SOURCE:
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                           HYPOTHETICAL: I
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ORIGINAL SOURCE:
                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                RAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: King of Prussia
                                                                         TOPOLOGY:
                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                       LENGTH:
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                                                                                                                       106 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sylvester, Daniel VENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
                                                                    single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Padlan, Eduardo
Patel, Arunbhai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feuerstein, Giora
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                                       .. protein
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                                                                                                                                                                                                                                                                                                              08/783,853
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Pred. No. 1.
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.6e-42;
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US-08-783-853A-11
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Best Local Similarity
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             HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 95(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEPAX:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/0: FILING DATE: 24-OCT-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 60/029,119
                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
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                                                                                            TOPOLOGY:
                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                         NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/783,853A FILING DATE: 16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSINPRTFGGGTKLEIK 106
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                                                                                                                            amino acid
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Padlan, Eduardo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
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Church, William
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                                                                                            linear
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Pred. No. 1
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Query Match Best Local Similarity

94.6%;

Score 526; DB 3; Pred. No. 1.7e-42;

Length 107;

Matches

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                                         Matches
                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 950
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEPAX:
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344
                                                                                                        FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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                                                                                                                                  ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 2
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: King of Prussia
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                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                    Local
                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                              LENGTH:
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1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
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                                         101;
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                                                    Similarity
                                                                                                                                                                                                 amino acid
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                                                                                                                                                                    linear
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Patel, Arunbhai
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                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM Compatible
                                                                                                                                           NO peptide
                                                                                                                    internal
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                                                    94.6%;
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                                                  Score 526; DB 4; Pred. No. 1.7e-42;
                                       Mismatches
                                       4.
                                                             Length 107;
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; MOLECULE TYPE: pl
; HYPOTHETICAL; NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: 11
; ORIGINAL SOURCE:
US-08-783-853A-103
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US-08-783-853A-103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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APPLICATION NUMBER: US/0
FILING DATE: 16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
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APPLICANT:
                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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SOFTWARE: FastSE
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STREET: 7
                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                     Local Similarity 95.3
                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                 LENGTH:
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6005091
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                                                                                                                                                                                                         linear
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Feuerstein, Giora
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Padlan, Eduardo
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Church, William
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                                                                                                                                                            internal
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OF THROMBOSIS
                                                                                                  94.6%;
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                                                                                                                                                                                                                                                                          103:
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                                                                                  Score 526; DB Pred. No. 1.7e.
1; Mismatches
                                                                                                 526; DB 3;
No. 1.7e-42;
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                                                                                                           Length 112;
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RESULT 6
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                                                                                                                     Matches
                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                            HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 16-JAN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT TITLE OF INVENTION: OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                         MOLECULE TYPE:
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61
              61 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 24-JU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                       1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
                                                         QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWIYATSNLASGVPAR
                                                                                                                     101; Conservative
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                                                                                                                                                                                                                                                                                                     amino acid
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Patel, Arunbhai
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                                                                                                                                                                                                                                                                          linear
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                                                                                                                                                                                                                                                                                       single
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                                                                                                                                  94.6%;
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                                                                                                                                                                                                                                                                                                                                                     103:
                                                                                                                                   Score 526; DB 4;
Pred. No. 1.7e-42;
                                                                                                                   Mismatches
                                                                                                                                                 Length 112;
                                                                                                                     Indels
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                                                                                                                   Gaps
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RESULT

APPLICANT:

HANNA, NABIL LEONARD, JOH

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US-08-475-815B-7
, Sequence 7, Application US/08475815B
; Patent No. 6399061
; GENERAL INFORMATION:
, APPLICANT: ANDERSON, DARRELL R.
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                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein US-08-476-275-4
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                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                     Query Match
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INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
US 08/149,099 :--
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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                                                                                                                          Local Similarity 92.1 
les 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Teskin, Robin L
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 07-JUN
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Leonard, John L.
Newman, Roland A.
Reff, Mitchell E.
Reff, Mitchell E.
Reff, William H
                                                                                                                                                                                                                                                                                                                                                                                128 amino acids
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                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                    93.7%;
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Pred. No. 5.9e-42;
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                                                                                                                                                                                                                                                                                     Length 128;
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US-08-449-287-2
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                                                                                                                                                                                                    Sequence 2, Application US/08449287 Patent No. 5877293
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                   GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 7:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,815B
FILING DATE: 07-JUN-1995
                                                                    APPLICANT: MOUNTAIN, Andrew
APPLICANT: OWENS, Raymond John
TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
TITLE OF INVENTION: Their Production
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APPLICATION NUMBER: US 07
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
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                                    CORRESPONDENCE ADDRESS:
                                                       NUMBER OF SEQUENCES:
                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 03-NOV-1993
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ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
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                                                                                                                                                                                                                                                                                                                                   FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
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1100 New York Avenue, N.W., Ninth
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                                                                                                                                              ADAIR, John Robert
BODMER, Mark William
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         202-861-3000
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92.5%;
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Pred. No. 5.9e-42;
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RESULT 10
US-09-423-439-18
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT (FILING DATE: 21-DEC-1990 ATTORNEY/AGENT INFORMATION: NAME: SAXE, Bernhard D.
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                       91.28;
Local Similarity 91.58;
nes 97; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT OF FILING DATE: 05-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/449,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                        CORRESPONDENCE ADDRESS: Pillsbury Winthrop, L.L.P.
                                                                                                                                                                           TITLE OF INVENTION: CHEMICAL COMPOUNDS NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                           APPLICANT: EMERY, Stephen Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                          CITY: Washington
OPERATING SYSTEM:
                                                                             COUNTRY: U.S.A.
                                                                                              STATE: D.C
                                                                                                                            STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                             BLAKEY, David Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
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compatible
PC-DOS/MS-DOS
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Gaps

SOFTWARE: MS WORD CURRENT APPLICATION DATA:

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MOLECULE TYPE: protein
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SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-423-439-18
                                   US-09-423-439-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-423-439-58
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Patent No. 6339070
GENERAL INFORMATION:
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Query Match
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APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 58:
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nes 97; Conserv
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                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <Unknown>
                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
                                                      SEQUENCE
                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                             PRIOR
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                                                                                                                                                                               R APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: MS WORD
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FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pillsbury Winthrop, L.L.P. STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 235 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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91.5%;
91.2%;
                                                      SEQ
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Pred. No. 2.4e-40;
Score 507;
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                                                      <u>N</u>O:
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4.
Length 235;
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TOPOLOGY: linear;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-011-769A-23
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                                                                                                               Query Match
Best Local Similarity
Thes 97; Conserve
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US-09-011-769A-23
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                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/GB96/01975
APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-UN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
FILING DATE: 16-AUG-1995
INFORMATION FOR SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/09011769A ... Patent No. 6436691
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPAR 82
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APPLICATION NUMBER: US/09/011,769A
FILING DATE: 13-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro,
STREET: 1100 New York Ave., N.W.
                  FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 1.06
                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
 FSGSGSGTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEIK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSGSGSGTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEIK 128
                                                                                                                                                                                                                                                                   TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005
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                                                                                                                                  Conservative
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DOWELL, Robert I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HENNEQUIN, Laurent F.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAVIES,
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91.5%;
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David H.
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                                                                                                                                                  Score 507; DB 4; Pred. No. 2.4e-40;
                                                                                                                                  Mismatches
                                                                                                                                                                                                                     23:
                                                                                                                                                                 DB 4; Length 235
                                                                                                                                  Indels
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                                                                                                                                                                 RESULT 14
US-08-211-202-3
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                                                                                                                  Patent No. 5565332
GENERAL INFORMATION:
                                                                                                                                                 Sequence 3,
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                         TITLE OF INVENTION: Production of TITLE OF INVENTION: combinatorial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/100,963
ETLING DATE: 03-AUG-1993
APPLICATION NUMBER: DE P 422 58 53.7
FILING DATE: 05-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                           APPLICANT:
                                                                        APPLICANT:
                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
CORRESPONDENCE ADDRESS:
                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
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                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 02-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Wadler, Linda A. REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                        2 IVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPARF 61
                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                            SGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEI 105
                                                                                                                                                                                                                                                                                         IQLTQSPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPKPWIYATSNLASGVPARF 61
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                                                                                                                                                 Application US/08211202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 amino acids
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                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                  BAIER, Michael
                                                        WINTER, Gregory Paul
                                                                   JESPERS, Laurent Stephane Anne Therese
                                                                                                     HOOGENBOOM, Hendricus Renerus Jacobus Matteus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202-408-4000
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                                                                                                                                                                                                                                                                                                                                                                     88.1%;
91.3%;
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Pred. No. 3.8e-39;
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                                          chimeric antibodies -
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Best Local S
                                                                                                                                         Sequence 57, Application US/08469486 Patent No. 5739281
                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
                       TITLE OF INVENTION: Improved
TITLE OF INVENTION: proteins
NUMBER OF SEQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                         62 SGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 312-474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: GB 9
FILING DATE: 23-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 6300 :
CITY: Chicago
                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/GB92/00883 FILING DATE: 15-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 25-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                          2 IELTQSPAILSASPGGKVTMTCRASSSVSYMHWYQQKPGSSPKPWIYATSNLASGVPTRF
                                                                                                                                                                                                                                          SGTGSGTSYSLTISRVEAEDAATYYCQQWSRNPFTFGSGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                           93;
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                                                                                               Holtet, Thor Las
                                                                                                       Thoegersen, Hans Christian
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SYSTEM: PC-DOS/MS-DOS
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Fish & Richardson
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88.6%;
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                                                                               Michael
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Pred. No. 9.1e-39;
                                                              method for the refolding
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REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06363/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617 542 5070
TELEPHONE: 617 542 8906
TELEPAX: 617 542 8906
TELEPAX: 617 542 8906
TELEPAX: 617 542 8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acids
TYPE: amino acids
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-486-57
Search completed: November 27, 2002, 07:25:14 Job time: 21.2355 secs
                                                                                                                                                                                                                                   Query Match 87.4
Best Local Similarity 88.6
Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOTTWARE: PatentIn Release #1.0, Version

SOFTWARE: #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,486

FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 08/192,060
FILING DATE: Pebruary 4, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Paul T. Clark
                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225 Franklin Street
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88.68;
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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
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137.479 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:*
| //gn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
| //gn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| //gn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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Listing first 45 summaries
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: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
0: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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2: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
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/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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   US-09-144-886-90
US-09-144-886-91
US-09-144-886-91
US-09-965-099-99
US-10-051-852-99
US-09-965-099-78
US-09-965-099-78
US-09-965-099-62
US-09-965-099-62
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US-99-65-099-105
US-10-051-852-105
US-09-965-099-11
US-09-965-099-103
US-09-965-099-103
US-10-051-852-103
                 US-09-144-886-82
US-09-144-886-83
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                                           Sequence 89, Appl
Sequence 105, App
Sequence 11, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 103, App
Sequence 103, App
Sequence 90, Appl
Sequence 91, Appl
Sequence 99, Appl
Sequence 78, Appl
Sequence 78, Appl
Sequence 78, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 82,
Sequence 83,
Sequence 24,
                                                                                                                                                                                                                                                                                                              Description
                App1
App1
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(S-09-983-615-89)
; Sequence 89, Application US/09893615
; Patent No. US20020082395A1
; GENERAL INFORMATION:
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Fischer, Gerald W. Schuman, Richard F. Wong, Hing

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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | S | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
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| 420 | 420 | 422 | 427 | 434 | 437 | 437 | 437 | 441 | 441 | 443 | 444 | 445 | 446 | 446 | 447 | 447 | 447 | 447 | 448 | 448 | 448 | 448 | 448 | 448 | 448 |
| | | | | | | 78.6 | | | | | | | | | | | | | | | | | • | 80.6 | |
| 107 | 107 | 109 | 107 | 107 | 239 | 119 | 107 | 107 | 107 | 108 | 669 | 235 | 109 | 109 | 107 | 107 | 107 | 105 | 240 | 240 | 238 | 238 | 108 | 108 | 106 |
| 12 | 10 | φ | 9 | Q | 10 | 10 | 9 | 12 | 10 | 10 | 9 | 10 | 12 | 10 | 12 | 10 | 9 | 9 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| US-10-051-852-44 | US-09-965-099-44 | US-09-144-886-97 | US-09-144-886-75 | US-09-144-886-88 | US-09-808-037-6 | US-09-808-037-28 | US-09-144-886-78 | US-10-051-852-74 | US-09-965-099-74 | US-09-910-059-9 | US-09-807-721-2 | US-09-910-059-17 | us-10-051,-852-95 | US-09-965-099-95 | US-10-051-852-57 | US-09-965-099-57 | US-09-144-886-76 | US-09-982-107-12 | US-09-865-198-27 | US-09-976-787-28 | US-09-865-198-28 | us-09-976-787-29 | US-09-865-198-8 | us-09-976-787-8 | US-09-865-198-23 |
| Sequence 44, Appl | Sequence 44, Appl | | Sequence 75, Appl | | ~ | ~ | Sequence 78, Appl | Sequence 74, Appl | Sequence 74, Appl | Sequence 9, Appli | Sequence 2, Appli | Sequence 17, Appl | Sequence 95, Appl | Sequence 95, Appl | Sequence 57, Appl | Sequence 57, Appl | | 12, / | 27, | Sequence 28, Appl | • | • | Sequence 8, Appl1 | Sequence 8, Appli | Sequence 23, Appl |

ALIGNMENTS

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COUNTRY: USA
2IP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Unn-2001
AFTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REGISTRATION NUMBER: 32,220
REGISTRATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEG ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1300 I Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: FINNEGAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stinson, Jeffrey L. OF INVENTION: OPSONIC AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DUNNER, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPSONIC AND PROTECTIVE MONOCLONAL AND CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF
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RESULT 2
US-09-965-099-105
; Sequence 105, Application US/09965099
; Patent No. US20020136725A1
; GENERAL INFORMATION:
                                                                                                     ; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 105:
US-09-965-099-105
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Best Local Similarity
                                   Matches
                                                 Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                             TELEX: <Unknown> INFORMATION FOR SEQ ID NO: 105:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FSGSGGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
61 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beegham Corporation.
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ANTICOAGULANT AGENTS USEBUL IN
                                                                                                                                                     ANTI-SENSE: NO FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Blackburn, Michael
QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106;
                                   101;
                                                     Similarity
                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                             NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                               TELEFAX: <Unknown>
                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feuerstein, Giora
Patel, Arunbhai
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                                                   94.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                 1:
                                 Score 526; DB 10;
Pred. No. 2.8e-31;
1; Mismatches 4;
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Pred. No. 2.2e-33;
; Mismatches 0;
                                                                 Length 106;
                                 Indels
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                                 0;
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                                                                   ; SEQUENCE DESCRIPTION: SEQ ID NO: 105: US-10-051-852-105
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US-10-051-852-105
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                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 105,
   Matches
                                                                                                                                                                                                                                                      TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 105:
SEQUENCE CHARACTERISTICS:
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                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853-
FILING DATE: 16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                      FRAGMENT TYPE: internal
                                                                                                                                       HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Blackburn,
                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 19406
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                                                                                                                                                                                                                                                                                                        TELEFAX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                        LENGTH: 106 amino acids
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     Conservative
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Patel, Arunbhai
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                 94.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Michael
Score 526; DB 12;
Pred. No. 2.8e-31;
1; Mismatches 4;
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                                    Length 106
     Indels
     0;
   Gaps
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QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWIYATSNLASGVPAR 60

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RESULT 5
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Best Local S
Matches 101
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Patent No. US20020136725A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                            Local Similarity
mes 101; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister; Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
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CORRESPONDENCE ADDRESS:
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Patel, Arunbhai
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL
                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: internal
                                                                                  FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                     QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
                                                 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSINPRTFGGGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/09/965,099 FILING DATE: 26-Sep-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 107 amino acids
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blackburn, Michael
                                                                                                                                                                                                           94.6%;
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                                                                                                                                                                                        Score 526; DB 10;
Pred. No. 2.8e-31;
1; Mismatches 4;
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                                                                                                                                                                                            4.
                                                                                                                                                                                                                           Length 107;
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US-10-051-852-11
Sequence 11, Application U; Patent No. US20020146411A1; GENERAL INFORMATION:
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                                                                                                                                                  Matches 101;
                                                                                                                                                                                     Query Match
                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-199
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:

NAME: Baumeister; Kitk ...
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWJSATSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                           FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                               HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 19406
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 111 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                          QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWIYATSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/10051852
                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Blackburn, Michael
Church, William
Gross, Mitchell
Feuerstein, Giora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nichols, Andrew
Padlan, Eduardo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patel, Arunbhai
                                                                                                                                                                                                                                                                                                                  s: peptide
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                                                                                                                                                                  94.68;
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                                                                                                                                                                  Score 526; DB 12;
Pred. No. 2.8e-31;
                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P50438
                                                                                                                                                                                     DB 12;
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RESULT 6 US-09-965-099-103

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US-10-051-852-103
Sequence 103, Application US/10051852
Patent No. US20020146411A1
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           61
                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                         1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/346,487 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19406
COMPUTER READABLE FORM:
                                                                   APPLICANT: Blackburn, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 103:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                       FSGSGSGTSYSLTISRVEAEDAATYYCQQWSINPRTFGGGTKLEIK 106
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                                                                                                                                                                                                                                                                           QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWIYATSNLASGVPAR 60
                                                                                                                                                                                                                                         FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                             101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001
CLASSIFICATION: CUNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCES:
                Church, William
Gross, Mitchell
Feuerstein, Giora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Blackburn, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patel, Arunbhai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Feuerstein,
                                                                                                                                                                                                                                                                                                                                                              94.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTICOAGULANT AGENTS USEFUL TREATMENT OF THROMBOSIS,
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                                                                                                                                                                                                                                                                                                                                                         Score 526; DB 1(
Pred. No. 3e-31;
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                                                                                                                                                  RESULT 8
US-09-144-886-90
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                                                                                                   GENERAL INFORMATION:
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Best Local Similarity
CURRENT APPLICATION
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ANTI-SENSE: NO
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; SEQUENCE DESCRIPTION: SEQ ID NO: 103: US-10-051-852-103
                                                                                                                                                  Sequence 90, Application US/09144886 Patent No. US20020155114A1
                  APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Botulinum Neurotoxins
FILE REFERENCE: 2500.117USO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                   61 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                         61 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSINPRTFGGGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                        1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPW1%ATSNLASGVPAR 60
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APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 112 amino acids
TYPE: amino acid
TYPE: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 09/344,050 FILING DATE: 25-JUN-1999 APPLICATION NUMBER: 08/783,853 FILING DATE: 16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: King of Prussia
STATE: PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Padlan, Eduardo
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NUMBER: US/09/144,886
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Pred. No. 3e-31;
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                                                                                                                        Sequence 99, Application US/09965099 Patent No. US20020136725A1 GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 91, Application US/09144886 Patent No. US20020155114A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize TITLE OF INVENTION: Botulinum Neurotoxins FILE REFERENCE: 2500.117050 CURRENT APPLICATION NUMBER: US/09/144,886 CURRENT FILING DATE: 1998-08-31 NUMBER OF SEQ ID NOS: 98 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 10
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificia OTHER INFORMATION: 3H4 region VL epitope 2
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 CORRESPONDENCE ADDRESS:
                  NUMBER OF SEQUENCES:
                                                                                                      APPLICANT: Blackburn, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SGSGTSYSLTISRMEAEDAATYYCQQWSSYPPTFGGGTKLEIK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                RESGSGSGTSYSLTISRMEAEDAATYYCOOWSSYPPTFGGGTKLEIK 108
                                                                                                                                                                                                                                                                RFSGSGSGTSYSLTISRVEAEDAATYYCOOWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                   IELTQSPAIMSASPGEKVTMTCRASSSVSSSYLQWYQQKPGSSPRLWIYDTSNLASGVPV 61
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                                                                   Feuerstein, Gio
Patel, Arunbhai
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                                                                                                                                                                                                                                                                                                                                                                                                        83.5%;
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                                    TREATMENT OF
                                                                                       Giora
                                                                                                                                                                                                                                                                                                                                                                                                        Score 464; DB 9;
Pred: No. 6.7e-27;
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Pred. No. 1.8e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 109;
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US-10-051-852-99
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                                                                                                                                                                                                                                                              Sequence 99, Application US/10051852 Patent No. US20020146411A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                          61 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                       80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
              CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: p:
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
APPLICATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTERS Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                     FSGSGSGTDYTLTISSLQPEDFATYYCQQWSINPRTFGGGTKLEIK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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FILING DATE: 26-Sep-2001
CLASSIFICATION: <Unknown>
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: SmithKline STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                           Blackburn, Michael
Church, William
                                                                                                                   Padlan, Eduardo
Patel, Arunbhai
Sylvester, Daniel
                                                                                                                                                                                                         Church, William Gross, Mitchell
                                                                                                                                                                        Nichols, Andrew
                                                                                                                                                                                            Feuerstein, Giora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 455; DB 10;
Pred. No. 3.3e-26;
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Length 129; Indels

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Gaps

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RESULT 12
US-09-955-099-78
; Sequence 78, Application US/09965099
; Patent No. US20020136725A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 99:
US-10-051-852-99
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                       20 QIVLTQSPSSLSASVGDRVTITCRASSSVNYMHWYQQKPGKAPKPWIYATSNLASGVPSR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 QIVLSOSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
              STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-199
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                 Feuerstein, Giora
Patel, Arunbhai
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                 NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                         APPLICANT: Blackburn, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84;
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COUNTRY: US
ZIP: 19406
                                                                                                   CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/051,852 FILING DATE: 17-Jan-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
COMPUTER: IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Baumeister,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.8%; Score 455; DB 12; 79.2%; Pred. No. 3.3e-26;
                                                                                                                                                                                                    TREATMENT OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
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US-10-051-852-78
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Sequence 78, Application US/10051852 Patent No. US20020146411A1 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 78:
                                                                                                                                                                                                                                                                                Nichols, Andrew
Padlan, Eduardo
Patel, Arunbhai
Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AG
OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 QIVLTQSPATLSLSPGERATLSCRASSSVNYMHWYQQRPGQAPKPWIYATSNLASGVPAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity es 83; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWlSATSNLASGVPAR 60
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/346,487
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE: SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Blackburn, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FSGSGSGTDYTLTISSLEPEDFAVYYCOOWSINPRTFGGGTKVEIK 125
                                                                                                                                                                     CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 125 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: <Unknown>
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                                                                                                                            ZIP: 19406
                                                                                                                                                 COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                       Church, William
Gross, Mitchell
Feuerstein, Giora
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; Pred. No. 3.8e-26;
10; Mismatches 13;
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RESULT 14
US-09-753-436-80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 80, Application US/09753436 Patent No. US20010029293A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 78:
                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related Materials and
NUMBER OF SEQUENCES: 120
                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                      FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 FSGSGSGTDYTLTISSLEPEDFAVYYCQQWSINPRTFGGGTKVEIK 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 QIVLTQSPATLSLSPGERATLSCRASSSVNYMHWYQQRPGQAPKPWIYATSNLASGVPAR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
                                                                                                                          APPLICATION NUMBER: US/09/753,436
APPLICATION NUMBER: US 08/487,113 FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                       60606-6402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/783,853 FILING DATE: 16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 09/344,050 FILING DATE: 25-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCE CHARACTERISTICS:
LENGTH: 125 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/051,852 FILING DATE: 17-Jan-2002
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                                                                                                                                                                                                                                                                          United States of America
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.7%; Score 454; 78.3%; Pred. No.
                                                    09/382,289
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                                                                                                                                                                                                                                                                                                                           Gerstein, Murray & Borun
South Wacker Drive
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82
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RESULT 15
US-09-65-099-62
; Sequence 62, Application US/09965099
; Patent No. US20020136725A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-09-753-436-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 127 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Williams, Joseph A., REGISTRATION NUMBER: 38,65 REFERENCE/DOCKET NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07
FILING DATE: 05-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (312) 474-0448
TELEX: 25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 81.1 es 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                APPLICANT: Blackburn, Michael
                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSGSGSGASYSLTISIMEAEDAATYYCQQWKSIPLTFGAGTKLELK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                             ZIP: 19406
                                                                                                                                                COUNTRY: USA
                                                                                                                                                              CITY: King of Prussia
STATE: PA
FILING DATE: 26-Sep-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (312) 474-6300
                                                                                                                                                                                                                                                                                                  Feuerstein,
Patel, Arun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JAN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.5%;
                                                                                                                                                                                                                                                                                                    Arunbhai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 07/827,689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 08/286,754. . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 07/894,061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US 08/102,852
                                                                                                                                                                                                                                                                 ANTICOAGULANT AGENTS USEFUL TREATMENT OF THROMBOSIS
                                                                                                                                                                                                                                                 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                   Giora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 453; DB 10;
Pred No 4.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jr.
                                                                                                                                                                                               Beecham Corporation Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 127;
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Gaps

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INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPEE amino acids
TYPEE amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 62:
US-09-965-099-62
Search completed: November 27, 2002, 07:26:00 Job time : 12.278 \ \text{secs}
                                                                                                                                                                                                                      Query Match 81.1
Best Local Similarity 77.4
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <UNKnown>
                                                                        1 EIVLTQSPATLSLSPGERATLSCRASSSVNYMHWYQQRPGQAPKPWIYATSNLASGVPAR 60
                                                                                                                                                                                                                          81.1%; Score 451; DB 10; 77.4%; Pred. No. 5.5e-26; tive 11; Mismatches 13;
                                                                                                                                                                                                                                                                 Length 107;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                              Gaps
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Result
No.
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Maximum DB seq
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9::
                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
              259.6
                                                                                                                                      268.4
264.2
264.2
                                                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                    295.6
295.6
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295.6
                                                                                                                                                                                                                                                                300.4
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length: 2000000000
Gapop 10.0 , Gapext 1.0
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318
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                                                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341543 seqs, 192557720 residues
                                                                                                                                                                                                                                                                                                                              Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published_Applications_NA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAAATTGTTCTCCCCAGTC.......GGACCATGCTGGAAATAAGA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                 : /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
    /cgn2_6/ptodata/1/pubpna/US0B_NEW_PUB.seq:*
    /cgn2_6/ptodata/1/pubpna/US0B_NEW_PUB.seq:*
    /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
    /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
    /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
    /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
    /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
    /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
    /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                              DB
 10
11
10
11
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10
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10
10
    US-10-051-852-6
US-10-965-099-104
US-10-965-099-104
US-10-965-099-102
US-10-965-099-102
US-10-965-099-102
US-10-965-099-102
US-09-9808-037-27
US-09-9808-037-27
US-09-9865-198-26
US-09-976-787-27
US-09-976-787-31
US-09-982-107-11
US-09-982-107-11
US-09-982-107-11
                                                                                                                                                                                                                                                               US-09-893-615-88
US-09-965-099-6
                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (without alignments)
3349.042 Million cell updates/sec
                                                                                    Sequence 88 Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 104, App
Sequence 102, App
Sequence 102, App
Sequence 27, Appli
Sequence 27, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 26, Appli
Sequence 26, Appli
Sequence 16, Appli
                                                                                                                                                                                                                                                                                                            Description
                           Sequence
                                           Sequence
                                                          Sequence
                                                                          Sequence
                                           30,
            App1
App1
                                                        Appl
Appl
Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-09-893-615-88
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Sequence 88, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.

GR

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | ω S | 34 | 33 | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
|-------|----------|-------|----------|-------|------|-------------------|-------------|-------|-------------|-------------------|---------------|---------------|------|-------|------|-------------------|-------|-------------------|-----|-------------------|------------------|-------|-------------------|-------------------|-------------------|
| 152.2 | 154.6 | 154.6 | 156.4 | 156.4 | 166 | 166 | 169.8 | 169.8 | 9 | 193.8 | 94 | 94 | 99 | 195.2 | 95 | 195.4 | 197.8 | 198 | 198 | 36 | 198.6 | 241.8 | 248.2 | 251.4 | 251.4 |
| 47.9 | | | | 9 | 2 | 52.2 | ω. | ω | 60.9 | 0 | ٠. | | 61.4 | 61.4 | 61.4 | 61.4 | • | 62.3 | • | | • | | • | 79.1 | 79.1 |
| 321 | 705 | 321 | 705 | 321 | 321 | 321 | 280 | 280 | 321 | 321 | 401 | 401 | 330 | 330 | 321 | 321 | 357 | 412 | 412 | 321 | 321 | 5691 | 411 | 2059 | 717 |
| 10 | 10 | 10 | 10 | 10 | 12 | 10 | 12 | 10 | 12 | 10 | 12 | 10 | 12 | 10 | 12 | 10 | 10 | 12 | 10 | 12 | 10 | 10 | 10 | 9 | 80 |
| -059 | -910-059 | -059 | -910-059 | -059 | -852 | US-09-965-099-73 | -10-051-852 | 999 | -10-051-852 | US-09-965-099-43 | -10-051-852-7 | -09-965-099-7 | -852 | 999 | -852 | -099 | 1-436 | US-10-051-852-98 | 999 | -852-5 | US-09-965-099-56 | - | US-09-881-823-5 | US-09-807-721-1 | US-08-940-544-3 |
| • | 98, | 70, | | | | Sequence 73, Appl | 34, | | 43, | Sequence 43, Appl | • | 77, | 94, | 94, | | Sequence 61, Appl | | Sequence 98, Appl | 98 | Sequence 56, Appl | 56, | 11 | Sequence 5, Appli | Sequence 1, Appli | Sequence 3, Appl1 |

ALIGNMENTS

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Stinson, Hing
Stinson, Jeffrey L.
Stinson, Jeffrey L.
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC Compatible
OPERATING SYSTEM: 9C-DOS/MS-DOS
SOFTWARE: PACHOLIC NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION UNMBER: 32,20
REFERRNCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION UNMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-0000
TELEFAX: 202-408-0000
STRANDEDNESS: single
TOPOLOGY: linear
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NAME/KEY: CDS

LOCATION: 1..31;

SEQUENCE DESCRIPTION:
US-09-893-615-88
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US-09-965-099-6
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Patent No. US20020136725A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001
                                                                  APPLICATION NUMBER: 09/346,487 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                         CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                               ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL TREATMENT OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Blackburn, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCATGCTGGAAATAAGA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACCAATCAGCAGAGTGGAGGCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCCTCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCATGCTGGAAATAAGA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                  STREET: 709 Swedeland CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Feuerstein, Giora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA
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                                                                                                                                                                                                                                                                                                                                                                            Arunbhai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 318; DB 10;
Pred. No. 1.7e-88;
                                                                                                                                                                                                                                                                                              Road
                                                                                                                                                                                                                                                                                                         Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches .
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thes 0;
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US-10-051-852-6
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                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/10051852
Patent No. US20020146411A1
GENERAL INFORMATION:
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Matches
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                                                                                                                        NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline B
STREET: 709 Swedeland R
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity les 307; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE: SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
                                                                                                                                                                                                      Sylvester, Daniel TITLE OF INVENTION: ANTICOAGULANT OF THROMBOSIS
CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Blackburn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCATGCTGGAAATAAGA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GATGCTGCCACTTATTACTGCCAGCAGTGGAGTATTAACCCACGGACGTTCGGTGGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCAAGCTGGAAATCAAA 318
            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                STATE: PA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                              Nichols, Andrew Padlan, Eduardo Patel, Arunbhai
                                                                                                                                                                                                                                                                                                           Church, William Gross, Mitchell
                                                                                                                                                                                                                                                                                             Feuerstein, Giora
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Pred. No. 4.3e-83;
                                                                                                                                                           Beecham Corporation
                                                                                                                                               Road
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RESULT 4
US-09-965-099-104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: SMIthKline Beecham
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                       Feuerstein, Giora
patel, Arunbhai
Patel, Arunbhai
FITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL
TREATMENT OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                      ACCATGCTGGAAATAAGA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTÄCCAGCAGAAGCCAGGA 120
                                                                                                                                          APPLICANT: Blackburn, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCAGCAGAGTGGAGGCTGAA
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/051,852 FILING DATE: 17-Jan-2002 CLASSIFICATION: <Unknown>
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APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
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                    Corporation
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; LOCATION: 1..318
; OTHER INFORMATION:
; SEQUENCE DESCRIPTION: SE
US-09-965-099-104
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 RESULT 5
US-10-051-852-104
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Best Local
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INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAAATTGTTCTCTCCCAGTCTCCCAGCAATCCTGTATCTGCATCTCCAGGGGAAAAGGTCACA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CAGATAGTACTCCCCAGTCTCCCAGCAATCCTGTCTGCATCTCCAGGGGAGAAGGTCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 09/346,487 FILING DATE: <Unknown> ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                     TCCTCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC 180
                                                                                                                                                                                                                 TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCAGCAGAGTGGAGGCTGAA 240
                                                                                                                                                                  ACCAAGCTGGAAATCAAA 318
                                                                                                        ACCATGCTGGAAATAAGA 318
                                                                                                                                              GATGCTGCCACTTATTACTGCCAGCAGTGGAGTATTAACCCACGGACGTTCGGTGGAGGC
                                                                                                                                                                                                                                                                                                                                                               ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P50438-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Pred. No. 1.3e-81;
0; Mismatches 14;
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NAME/KEY: Coding Sequence;
LOCATION: 1...318;
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-10-051-852-104
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                                                                                                                   Query Match
Best Local Similarity 95.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 104:
 61
                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 318 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: ANTICOAGULANT OF THROMBOSIS
                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
               ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA 120
ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/344,050 FILING DATE: 25-JUN-1999 APPLICATION NUMBER: 08/783,853 FILING DATE: 16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Baumeister, Kirk REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patel, Arunbhai
Sylvester, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gross, Mitchell
Feuerstein, Giora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blackburn, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Padlan, Eduardo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nichols, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <Unknown>
                                                                                                                                                93.0%;
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                                                                                                                                 0
                                                                                                                               Score 295.6; DB 1
Pred. No. 1.3e-81;
0; Mismatches 14
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                                                                                                                                                                DB 12;
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                                                                                                                               Gaps
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RESULT 6
US-09-965-099-102
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SEQUENCE
US-09-965-099-102
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                                                                                                                                                                                                                                                                  TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 102:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301
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ADDRESSEE: SmithKline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Baumeister, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL TREATMENT OF THROMBOSIS
                                                                                  FEATURE:
                                                                                                  ORIGINAL SOURCE:
                                                                                                                 FRAGMENT TYPE: <Unknown>
                                                                                                                                  HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Blackburn, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCATGCTGGAAATAAGA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATGCTGCCACTTATTACTGCCAGCAGTGGAGTATTAACCCACGGACGTTCGGTGGAGGC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: King of Prussia STATE: PA
                              NAME/KEY: Coding Sequence LOCATION: 1...335
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                   LENGTH: 335 base pairs
                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                    fELEFAX: <Unknown>
                 DESCRIPTION: SEQ ID NO: 102:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patel, Arunbhai
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                                                                                                                                                                                                                                                                                                                                                                  33,833
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RESULT 7
US-10-051-852-102
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Patent No. US20020146411A1
GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 304;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAA 240
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                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
              REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                ATTORNEY/AGENT INFORMATION: NAME: Baumeister, Kirk
                                                                                                                                                                                       PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 111
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                                                                                                               APPLICATION NUMBER: 09/344,050 FILING DATE: 25-JUN-1999 APPLICATION NUMBER: 08/783,853 FILING DATE: 16-JAN-1997
                                                                                                                                                                                                     FILING DATE: 17-Jan-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                              CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                              ZIP: 19406
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
                                                                                                                                                                                     APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Blackburn, Michael
Church, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patel, Arunbhai
Sylvester, Daniel
NYENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nichols, Andrew
Padlan, Eduardo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feuerstein, Giora
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF THROMBOSIS
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US-09-753-436-79
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                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Gallatin, W. Mic
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-R
NUMBER OF SEQUENCES: 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: <Unknown>
INFORMATION FOR SEQ ID NO:
                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/753,43
                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole,
STREET: 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
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                                                                                                                                                   STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
                                                                                                                                                                                       STATE:
                                                                                                                                                                                                     STREET: 6300 (CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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CLASSIFICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CAAATTGTTCTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAAAAGGTCACA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATGCTGCCACTTATTACTGCCAGCAGTGGAGTATTAACCCACGGACGTTCGGTGGAGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCAAGCTGGAAATCAAA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Coding Sequence LOCATION: 1...335
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                            Gallatin, W. Michael
                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.08;
95.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 295.6; DB 1
Pred. No. 1.3e-81;
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                                                                                                                                                                                                                         Gerstein, Murray & South Wacker Drive
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PRIOR APPLICATION DATA: APPLICATION NUMBER:

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                                RESULT 9
US-09-808-037-27
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Sequence 27, Application US/09808037 Patent No. US20020052311A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Joseph A., Jr.
REGISTRATION NUMBER: 38,659
REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 33282
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/009,266
FILING DATE: 22-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 1
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 05-AUG-1994
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TELEX: 25-3856
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                                                                                                                              ACCATGCTGGAAATAAGA 318
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90.3%;
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Pred. No. 3.1e-73;
0; Mismatches 31;
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; LOCATION: (1)..(357)
US-09-808-037-27
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CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/473,653
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 60/152,417
PRIOR APPLICATION NUMBER: US 60/152,417
PRIOR FILING DATE: 1999-09-03
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Patent No. US20020052311A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.0
SEQ ID NO 27
LENGTH: 357
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APPLICANT: SOLOMON, Beka
APPLICANT: HANAN, Eilat
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS
TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
FILE REFERENCE: SOLOMON=2D
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Best Local Similarity
Matches 284; Conserv
APPLICANT: SOLOMON, Beka
APPLICANT: HANAN, Eilat
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS:
TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
TILE REFERENCE: SOLOMON-2D
CURRENT APPLICATION NUMBER: US/09/808,037
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 2000-07-31
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 33
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ORGANISM: synthetic
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Pred. No. 5.8e-72;
Pred. No. 5.8e-72;
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; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 27
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Mouse
US-09-976-787-27
                                                                                                                                                                                                                                                                                APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Use
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR APPLICATION NUMBER: US 09/17,726
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 1999-01-29
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; LOCATION: (1)..(717)
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Best Local S
Matches 284
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Best Local
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ORGANISM: HOMO :
FEATURE:
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3EQ ID NO 5
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                                                                                                                                 Local Similarity
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              TGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGGAT 121
                                                                        AAATTGTTCTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAAAAGGTCACAA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCATGCTGGAAATAAGA 318
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TAACCTGCAGTGCCAGCTCAAGTGTAAGTTACATGCACTGGTTCCAGCAGAAGCCAGGCA 121
                                                        ACATCGAGCTCACTCCAGCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCA 61
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ilarity 89.0%;
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                                                                                                                  Score 261; DB 10;
Pred. No. 5.3e-71;
0; Mismatches 35;
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; ORGANISM: Mouse
US-09-865-198-26
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Patent No. US20020103345A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins
FILE REFERENCE: 11245/47102
                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 26
LENGTH: 318
                                                                                                                                                                                                                                                                                                                           Query Match 82.1%;
Best Local Similarity 89.0%;
                                                                                                                                                                                                                                                                                                               Matches 282;
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
  302
             302 CCATGCTGGAAATAAGA 318
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                                                  TCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAG 241
                                                                                                                                                        CTTCTCCCAAACTCTGGATTTATAGCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGCT
                                                                                                                                                                  CCTCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGCT 181
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RESULT 13 US-09-976-787-16 ; Sequence 16, Application US/09976787 ; Patent No. US20020064528A1 ; GENERAL INFORMATION:

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TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Interpretation FILE REFERENCE: 11245/47102
CURRENT APPLICATION UNMBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 16
LENGTH: 324
TYPE: DNA
ORGANISM: Mouse
US-09-865-198-16
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; TYPE: DNA
; ORGANISM: Mus musculus
US-09-976-787-16
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TITLE OF INVENTION: Antibodies Specific to KD
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR TILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
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Best Local Similarity 89.0
Matches 282; Conservative
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Patent No. US20020103345A1
GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping
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SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 16
                                                                Query Match
                                   Matches
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   AAATTGTTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAAAAGGTCACAA
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                                   Conservative
                                             82.1%;
89.0%;
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                              Score 261; DB 10;
Pred. No. 5.4e-71;
0; Mismatches 35;
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; TYPE: DNA
; ORGANISM: Mouse
US-09-976-787-31
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US-09-976-787-31
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Matches 282;
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APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
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CCATGCTGGAAATAAGA 318
                                               TCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCACAATCAGCAGAGTGGAGGCTGAAG
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Pred. No. 7.1e-71;
0; Mismatches 35;
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Search completed: November 27, 2002, 05:31:02 Job time : $38.5677 \ \text{secs}$

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Result
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Listing first 45 summaries
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Perfect score:
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/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep:*
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Copyright (c) 1993 - 2002
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US-09-840-459-10
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US-09-881-823-16
US-09-835-087-8
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137.479 Million cell updates/sec
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Compugen Ltd.
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16, Appl
17, Appl
10, Appl
10, Appl
100, Appl
101, Appl
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US-09-893-615-87
US-09-893-615-87
Sequence 87, Application US/09893615
PATENT NO. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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Fischer, Gerald W. Schuman, Richard F.

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| | | 74.8 73.0 72.4 71.7 | 101 126 100 127 | 100 | US-09-840-459-34 US-09-840-459-74 US-09-840-459-35 US-09-840-459-71 |
|-------|---|--|--|--|---|
| 460.5 | | 71.3 | 120 | 12 | US-10-025-687-4 |
| 455 | | 70.5 | 126 | 10 | US-09-840-459-73 |
| 444 | 144.5 | 68.8 | 263 | 9 | US-09-956-086-3 |
| 444 | | | 263 | 9 | US-09-956-087-3 |
| 444 | | | 283 | 9 | US-09-985-442-6 |
| 444 | .5 | | 283 | 10 | US-09-983-580-6 |
| 4 | | | 123 | 10 | US-09-840-459-82 |
| 4 | 442 | | 140 | 10 | US-09-286-240-4 |
| 438 | | | 126 | 10 | TIC-00-040-450-73 |
| 4 | 438 | | | | 77-67-040-60-CD |
| 436 | 436.5 | 67.8 | 123 | 10 | US-09-840-459-91 |
| 4 | 1 | 67.8 67.6 | 123 124 | 10 | US-09-840-459-91 US-09-840-459-89 |
| 434 | 450 | 67.8 67.6 67.3 | 123 124 125 | 10 | US-09-840-459-89 US-09-840-459-89 US-09-840-459-84 |
| 4 | 4.5 | 67.8 67.6 67.3 | 123 124 125 298 | 10 10 10 | US-09-840-459-81 US-09-840-459-89 US-09-840-459-89 US-09-840-459-84 US-09-883-758-2 |
| 4 | 434 | 67.8 67.6 67.3 67.3 | 123 124 125 298 119 | 22222 | US-09-840-459-89 US-09-840-459-89 US-09-840-459-84 US-09-840-459-84 US-09-883-758-2 US-09-811-123-3 |
| 433. | 434 | 67.8 67.6 67.3 67.3 67.2 | 124 124 125 298 119 | 0101010 | US-09-840-459-89 US-09-840-459-89 US-09-840-459-84 US-09-883-758-2 US-09-811-123-3 US-09-840-459-92 |
| 433 | 344.5 | 67.8 67.6 67.3 67.3 67.2 | 123 124 125 298 119 121 | 0101010 | US-09-840-459-89 US-09-840-459-89 US-09-840-459-84 US-09-883-758-2 US-09-811-123-3 US-09-811-123-3 US-09-840-459-92 US-09-299-200A-28 |
| 4 | 33444 | 67.8 67.6 67.3 67.3 67.2 67.2 | 123 124 298 119 121 121 | 010101010 | US-09-840-459-89 US-09-840-459-89 US-09-8840-459-84 US-09-883-758-2 US-09-8811-123-3 US-09-840-459-92 US-09-829-200A-289 US-09-840-459-90 |
| 432 | 4444 | 67.8 67.3 67.3 67.2 67.2 | 123 124 125 298 119 119 121 121 124 473 | 10 10 10 10 10 10 10 10 | US-09-840-459-89 US-09-840-459-89 US-09-840-459-84 US-09-811-123-3 US-09-811-123-3 US-09-840-459-92 US-09-840-459-90 US-09-910-059-131 |
| 432 | 2 4 4 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 67.0 67.0 67.0 67.2 | 124 125 298 119 119 120 120 124 173 | 10 10 10 10 10 10 10 10 10 | US-09-840-459-89 US-09-840-459-89 US-09-840-459-84 US-09-883-758-2 US-09-811-123-3 US-09-810-459-92 US-09-840-459-90 US-09-910-059-131 US-09-756-301A-5 |
| 432 | 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 67.8 67.6 67.3 667.3 667.2 67.2 67.1 | 123 124 125 298 119 121 120 124 473 119 | 10 10 10 10 10 10 10 10 10 | US-09-840-459-89 US-09-840-459-89 US-09-8840-459-89 US-09-883-758-2 US-09-881-123-3 US-09-811-123-3 US-09-840-459-92 US-09-910-059-131 US-09-910-059-131 US-09-910-059-131 |
| 432 | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 | 67.8 67.3 67.3 67.3 67.2 67.2 67.1 67.0 | 123 125 298 119 121 120 120 124 473 119 | 10 10 10 10 10 10 10 10 10 | US-09-840-459-89 US-09-840-459-89 US-09-840-459-84 US-09-881-123-3 US-09-811-123-3 US-09-840-459-92 US-09-829-2200A-28 US-09-829-220-200A-28 US-09-910-059-131 US-09-9756-301A-5 US-09-756-535A-5 |

ALIGNMENTS

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INFORMATION FOR SEQ ID NO: 87:
                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Un-2001
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN,
                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DUNNER, LLP
STREET: 1300 I Street, N
CITY: Washington
STATE: DC
COUNTY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wong, Hing
Wong, Hing
Stinson, Jeffrey L.
OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID
POSITIVE BACTERIA
                                              TYPE: amino acid
                                                                                                                                                                                                     NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HENDERSON, FARABOW, GARRETT
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                                                                                                                                                     US-09-835-087-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Murine US-09-881-823-16
                                                                                                                                                                   RESULT 3
Sequence 8, Application US/09835087
Patent No. US20020042370A1
GENERAL INFORMATION:
APPLICANT: Wayne W. Hancock
TITLE OF INVENTION: Method of Treating Graft Rejection Using
TITLE OF INVENTION: Inhibitors of CCR2 Function
FILE REFERENCE: 1855.2008-003
CURRENT APPLICATION NUMBER: US/09/835,087
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Method for the Treatment and Prevention of Dental Caries FILE REFERENCE: 22851-032
CURRENT APPLICATION UMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 143
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Best Local Similarity
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APPLICANT: ANDERSON, MAXWELL
APPLICANT: MORRISON, SHERIE
APPLICANT: TRINH, RYAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WIMS, LETITIA APPLICANT: CHEN, LI
                                                                                                                                                                                                                      137 VTVSS 141
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                                                                                                                                                                                                                                                                                    61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYA--MDYWGQGTS 118
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                                                                                                                                                                                                                                                                                                                                                     20 EVQLVETGGGLVQPKGSLKLSCAASGFTFNTNAMNWVRQAPGKGLEWVARIRSKSNNYAT
                                                                                                                                                                                                                                                                                                                                                                 1 EVMLVESGGGLVQPKGSLKLSCAASGFTFUNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                   106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 532.5; DB 1
Pred. No. 3.9e-42;
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Pred. No. 1.5e-52;
; Mismatches 0;
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                                                                                                                                  ; NAME/KEY: SITE
; LOCATION: (101)...(106)
; OTHER INFORMATION: CDR3
; OTHER INFORMATION: Mouse
US-09-809-739-12
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: Sequence 12, Application US/09809739

; Patent No. US20020106369A1
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APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia E.
APPLICANT: Rao, Patricia E.
TITLE OF INVENTION: Method of Inhibiting Stenosis and
TITLE OF INVENTION: Restenosis
FILE REFERENCE: 1855.1069-003
                                                                             Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
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                                                           Matches
                                                                                            Query Match
                                                                                                                                                                                                                           NAME/KEY: SITE
LOCATION: (31)...(35)
OTHER INFORMATION: CDR1
NAME/KEY: SITE
LOCATION: (50)...(68)
OTHER INFORMATION: CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/809,739
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US 09/528,267
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/549,448 PRIOR FILING DATE: 2000-04-14 NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mus Musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: DOMAIN
LOCATION: (1)...(117)
OTHER INFORMATION: Murine mab 1D9 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)...(117)
OTHER INFORMATION: Murine mAb
                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Unknown FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                         Local Similarity 80.5 nes 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 YYADSVKDRYTISRDDSESMLFLQMNNLKTEDTAMYYCVTFYGNGV-----WGTGTTVT 114
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1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT
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                                                     ; Score 519; DB 10;
; Pred. No. 5.4e-41;
11; Mismatches 7:
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Pred. No. 5.4e-41;
1; Mismatches 7;
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GENERAL INFORMATION:
APPLICANT: LAROSA, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
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: Sequence 100, Application US/09840459

: Patent No. US20020150576A1
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US-09-840-459-10
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SOFTWARE: FastSEQ for
SEQ ID NO 10
LENGTH: 117
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Best Local 9
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APPLICANT: O'Brien, Slobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES
TITLE OF INVENTION: METHODS OF USE THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1998-07-23
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND TITLE OF INVENTION: METHODS OF USE THEREFOR
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Newman, Walter
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80.5%; Pred. No. 5.4e-41;
tive 11; Mismatches 7;
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CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR TILING DATE: 2001-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
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LENGTH: 148
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/835,087
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/549,448
PRIOR FILING DATE: 2000-04-14
NUMBER OF COLUMBER OF C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 117
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial
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121 VSS 123
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                                                                                                                                                                                                   Local Similarity
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                                                                   YYADSVKDRYTISRDDSKNTLYLQMNSLKTEDTAVYYCVTFYGNGV---
                                                                                                                                          FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
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Pred. No. 6.9e-41;
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GENERAL INFORMATION:

APPLICANT: Horvath, Christopher J.

APPLICANT: Rao, Patticia E.

TITLE OF INVENTION: Method of Inhibiting Stenosis and TITLE OF INVENTION: Method of Inhibiting Stenosis FILE REFERENCE: 1855.1069-003

CURRENT FILING DATE: 2001-03-15

CURRENT FILING DATE: 2001-03-15

PRIOR APPLICATION NUMBER: US 09/528,267

PRIOR APPLICATION NUMBER: US 09/528,267

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 23
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Best Local Similarity
SEQ ID NO 20
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 20, Application US/09840459 Patent No. US20020150576A1
                                                                                                                                                                                                                                                        APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LaRosa,
APPLICANT: Horvat
APPLICANT: Newman
                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
                                            SOFTWARE:
                                                                                                                                               PRIOR APPLICATION NUMBER: 09/359,193
                                                                  NUMBER OF SEQ ID NOS:
                                                                                    PRIOR FILING DATE:
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                     FILING DATE: 1999-07-22
APPLICATION NUMBER: 09/121,781
                                                                                                                                                                      APPLICATION NUMBER: 09/497,625
FILING DATE: 2000-02-03
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                                            FastSEQ for
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                                                                                      1998-07-23
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                                            Windows Version 3.0
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76.4%;
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; OTHER INFORMATION: Humanized sequence US-09-840-459-20
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US-09-809-739-22
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           GENERAL INFORMATION:
APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricla E.
TITLE OF INVENTION: Method of Inhibiting Stenosis
TITLE OF INVENTION: Restenosis
FILE REFERENCE: 1855.1069-003
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APPLICANT: Wayne W. Hancock
TITLE OF INVENTION: Method of Treating Graft Rejection Using
TITLE OF INVENTION: Inhibitors of CCR2 Function
FILE REFERENCE: 1855,2008-003
CURRENT APPLICATION NUMBER: US/09/835,087
CURRENT FILING DATE: 2001-09-24
CURRENT FILING DATE: 2001-09-24
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 117
                                                                                                      Sequence 22, Application US/09809739 Patent No. US20020106369A1
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Best Local Similarity
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PRIOR FILING DATE: 2000-04-14
NUMBER OF GEN.
CURRENT APPLICATION NUMBER: US/09/809,739
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94; Conserv
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75.6%;
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Pred. No. 1.3e-38;
.4; Mismatches 9,
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Pred. No. 3e-38;
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CURRENT FILING DATE: 2001-03-15 PRIOR APPLICATION NUMBER: US 09/528,267

PRIOR FILING DATE:

2000-03-17

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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 117
TYPE: PRT
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Best Local
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Best Local :
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
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PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
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CURRENT FILING DATE: 2001-02-02
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APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
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APPLICANT: Newman, Walter
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OTHER INFORMATION: Humanized sequence
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 61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
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                                       EVQLVESGGGLVKPGGSLRLSCAASGFSFNAYAMNWVRQAPGKGLEWVARIRTKNNNYAT
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75.6%; Pred. No. 3e-38;
rative 14; Mismatches
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75.6%;
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; Pred. No. 3e-38;
14; Mismatches
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US-09-835-087-11
                                 ; OTHER INFORMATION: Humanized sequence US-09-809-739-21
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                                                                                                                                                                                                                                                                                                   Sequence 21, Application US/09809739
Patent No. US20020106369A1
GENERAL INFORMATION:
APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia E.
APPLICANT: Rao, Patricia E.
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Matches
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Patent No. US200
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Query Match
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                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/809,739
CURRENT FILLNG DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US 09/528,267
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                 TITLE OF INVENTION: Method of Inhibiting Stenosis TITLE OF INVENTION: Restenosis FILE REFERENCE: 1855.1069-003
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                                                                                                                                                                     NUMBER OF SEQ ID NOS:
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ORGANISM: Artificial Sequence
                                                                                                 LENGTH: 117
TYPE: PRT
                                                                   ORGANISM: Artificial Sequence FEATURE:
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93; Conservative
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S20020042370A1
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75.6%;
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Pred. No. 3.7e-38;
.3; Mismatches 11;
 Score 488;
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 10;
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Length 117;
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Patent No. USZUWZUJSYWAL

GENERAL INFORMATION:
APPLICANT: LAROSA, Gregory J.
APPLICANT: LAROSA, Gregory J.
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Steefe, Theresa
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1090-07-22
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
SOFTWARE: FastSEQ ID NOS: 107
SOFTWARE: FastSEQ ID NOS: 107
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18
LENGTH: 117
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Humanized sequence
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Search completed: November 27, 2002, 07:26:00 Job time : 15.2471 \text{ secs}
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                                                                                                                                                                                                                                                                                                Query Match 75.5%; Score 488; DB 10; Length 1 Best Local Similarity 75.6%; Pred. No. 3.7e-38; Matches 93; Conservative 13; Mismatches 11; Indels
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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        of hits satisfying chosen parameters:
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1: /cgn2_6/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*

2: /cgn2_6/ptcdata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptcdata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptcdata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptcdata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptcdata/1/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptcdata/1/pubpaa/US07_PUBCOMB.pep:*

8: /cgn2_6/ptcdata/1/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptcdata/1/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptcdata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptcdata/1/pubpaa/US09_PUBCOMB.pep:*

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14: /cgn2_6/ptcdata/1/pubpaa/US09_PUBCOMB.pep:*

15: /cgn2_6/ptcdata/1/pubpaa/US09_PUBCOMB.pep:*

16: /cgn2_6/ptcdata/1/pubpaa/US09_PUBCOMB.pep:*

17: /cgn2_6/ptcdata/1/pubpaa/US09_PUBCOMB.pep:*

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US-09-893-615-23
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US-09-893-615-37
US-09-893-615-65
US-09-893-615-31
US-09-893-615-31
US-09-893-615-31
US-09-893-615-31
US-09-728-721-4
US-09-728-721-4
US-09-728-721-2
US-09-771-61A-184
US-09-771-61A-184
US-09-771-61A-184
US-09-771-161A-184
US-09-771-161A-184
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US-10-133-780-1
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1, Appli 29, Appl 33, Appl 35, Appl 65, Appl 65, Appl 44155, Appl 11, Appl 12, Appl 13, Appl 14, Appl
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ALIGNMENTS

US-09-893-615-1

Sequence 1, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:

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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
                                                                                                                   NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN,
                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Einaudi, Carol P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fischer, Gerald W. Schuman, Richard F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DUNNER, LLP
STREET: 1300 I Street,
TOPOLOGY: line
                                       TYPE: amino acid
                                                          LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wong, Hing
Stinson, Jeffrey L.
STINSON, Jeffrey L.
INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC
                     <Unknown>
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Sequence

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US-09-99-615-29
US-09-99-615-29
Sequence 29, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
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US-09-893-615-27
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                                                                                                                                                                                                                      Query Match
Best Local :
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Best Local 9
                                                                                                                                                                                                      Matches
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                                                                                                                                                                    1 WRMYFSHRHAHLRSP 15
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APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS: HENDERSON, FARABOW, GARRETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO:
APPLICANT:
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                                                                                                                                                                                                      15;
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15; Conserv
                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Einaudi, Carol P. REGISTRATION NUMBER: 32,220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1300 I Street, NW CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 04995.0041-00000
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INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOT
   Fischer, Gerald W.
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                                                                                                                                                                                                                                                                                       SEQ ID NO:
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                                                                                                                                                                                                                      Score 91;
Pred. No.
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Pred. No.
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Query Match
Best Local Similarity
Watches 15; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-893-615-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WRMYFSHRHAHLRSP 15
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ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P
REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC POSITIVE BACTERIA
                                                                                                                                                                                            NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                          TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 04995.0041-00000 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/893,615 FILING DATE: 29-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: DC
                                                                                      COUNTRY:
                                                                                                         STATE: DC
                                                                                                                      CITY: Washington
                                                                                                                                           STREET: 1300 I Street,
                                                                                                                                                                          ADDRESSEE: FINNEGAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005-3315
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                                                                                                                                                                                                                                                                                                                                 Fischer, Gerald W.
                                                                                                                                                                                                                                                                                                                  Schuman,
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                                                                                    USA
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Pred. No.
                                                                                                                                                                            HENDERSON, FARABOW,
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TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 33:
US-09-893-615-33
TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ
US-09-893-615-35
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Patent No. US20020082395A1
GENERAL INFORMATION:
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                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 35:
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Local Similarity 100.0%;
es 15; Conservation
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: OPSONIC AMPIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1300 I Street, NW
                                                                                               LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005-3315
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LENGTH: 19 amino acids
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Pred. No. 3.7e-08;
; Mismatches 0;
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                    <u>N</u>O:
                    35:
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RESULT 6
US-09-893-615-37
: Sequence 65, Application US/09893615 ; Patent No. US20020082395A1 ; GENERAL INFORMATION:
                                                             US-09-893-615-65
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                       NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEPAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENCTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Un-2001
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Stinson, Jeffrey L.
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONCCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOT
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 37:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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Pred. No. 3.7e-08;
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Fischer, Gerald W. Schuman, Richard F.

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US-09-893-615-31; A
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Patent No. US20020082395A1
GENERAL INFORMATION:
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REGISTRATION NUMBER: 32,220
REFERRECE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
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les 15; Conserv
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC
POSITIVE BACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 9
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Fischer, Gerald W. Schuman, Richard F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                   NUMBER
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                                                                                                                                                                     CITY: Washington
                                                                                                                                                                                         STREET: 1300 I Street, NW
                                                                                                                                                                                                                              ADDRESSEE: FINNEGAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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DUNNER, LLP
STREET: 1300 I Street, NW
                                                                                                                                  COUNTRY: USA
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                                                                                                                                                                                                                                                                   OF SEQUENCES:
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CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
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Pred. No.
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3.7e-08;
                   Version
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                     #1.30
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                 PRIOR
                                                                                                                                                                                                                                                                                                     PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/864,761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-408-4400 INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
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                                                                                                                                     APPLICATION NUMBER: PCT/US01/00663 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: GB 24263.6 FILING DATE: 2000-10-04 APPLICATION NUMBER: US 60/236,359 FILING DATE: 2000-09-27
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REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-08-4000
APPLICATION NUMBER: US 60/234,687
                                     APPLICATION NUMBER: PCT/US01/00670
                                                                           APPLICATION NUMBER:
                                                                                                                    APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                            FILING DATE: 2001-01-30
                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00668
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                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US01/00665
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                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US01/0066
                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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Chen, Wensheng
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Hanzel, David K.
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73.3%;
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Pred. No. 0.00
1; Mismatches
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; Sequence 4, Application US/09728721
; Patent No. US20020061845A1
                                     RESULT 11
US-09-728-721-4
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                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 87
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PRIOR APPLICATION NUMBER: 60/195,150
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,099
PRIOR APPLICATION NUMBER: 60/195,151
PRIOR APPLICATION NUMBER: 60/195,151
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
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CURRENT FILING DATE: 2001-04-06
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PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
NOSTYMARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/230,149 PRIOR FILING DATE: 2000-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: 60/195,098
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                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
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                                                                                                               123 WKAYFSKSYVHL 134
                                                                                                                                                                                     Local Similarity 50.0%; ses 6; Conservation
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EXPRESSED IN PLACENTA, SIGNAL = 0.72

EXPRESSED IN ADULT LIVER, SIGNAL = 0.62

EXPRESSED IN LUNG, SIGNAL = 0.71

EXPRESSED IN BRAIN, SIGNAL = 0.79

EXPRESSED IN BONE MARROW, SIGNAL = 1.5

EST_HUMAN HIT: AM502362.1, EVALUE 5.00e-40
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Pred. No. 14;
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US-09-748-537-1
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US-10-105-931-4
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                                                                                             Sequence 1, Application US/09748537 Patent No. US20020061833A1 GENERAL INFORMATION:
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Best Local
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Matches 5; Conservative
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CURRENT APPLICATION NUMBER: US/10/105,931
CURRENT FILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER: 09/099,041
PRIOR EPILICATION NUMBER: 09/099,041
PRIOR FILING DATE: 1998-06-17
                   APPLICANT: Bertin, John APPLICANT: Chao, Moses V. THE CARD-RELATED PROTEIN FAMILE AND USES THE TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILE AND USES THE FILE REFERENCE: 07334-316001
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PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
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CURRENT FILING DATE: 2000-12-01
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TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES
FILE REFERENCE: 07334-124001
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TYPE: PRT
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CURRENT APPLICATION NUMBER: US/09/748,537
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TYPE: PRT
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nes 5; Conserv
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Pred. No.
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Pred. No. 32;
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APPLICANT: LEVINE, et al.
TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
FILE REFERENCE: 802620-2005.1;
CURRENT APPLICATION UMBER: US/09/771,161A
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 09/724,676
PRIOR FILING DATE: 2000-11-28
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 135619
PRIOR APPLICATION NUMBER: 135619
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US-09-771-161A-184
Sequence 184, Application US/09771161A
Patent No. US20022110811A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQ ID NO 2
, LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-728-721-2
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SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
US-09-748-537-1
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US-09-728-721-2
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PRIOR FILING DATE: 1999-66-28
PRIOR PELICATION NUMBER: US 09/207,359
PRIOR FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US 09/09,041
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEO ID NOS: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 33.3
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 44.0%;
Best Local Similarity 33.3%;
Matches 5; Conservative
                                                                                                                                                                                                                     GENERAL INFORMATION:
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APPLICANT: Bertin, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2000-12-26
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: US 09/019,942
PRIOR FILING DATE: 1998-02-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: MOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE FILE REFERENCE: 07334-124001 CURRENT PROLICATION NUMBER: US/09/728,721 CURRENT FILING DATE: 2000-12-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                      40 WRVQVAVKHLHIHTP 54
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Pred. No. 57;
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; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 184
; LENGTH: 540
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-184

Query Match
Pest Local Similarity 33.3%; Pred. No. 57;
Matches 5; Conservative 5; Mismatches 5; Indels 0; Gaps
| 1 WRMYFSHRHAHLRSP 15
| Db 40 WRVQVAVKHLHIHTP 54
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Search completed: November 27, 2002, 07:25:58 Job time: 1.73745 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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// cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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                                                                                                                                                                       Sequence 2, Appli
Sequence 9, Appli
Sequence 17, Appl
Sequence 19, Appl
Sequence 41, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 37, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 33, Appl
Sequence 81, Appl
Sequence 41, Appl
Sequence 41, Appl
Sequence 4166, App
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                                                                Sequence
Sequence
Sequence
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40505, A
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RESULT 1 US-09-893-615-2

ALIGNMENTS

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | ω ω | 32 | 31 | 30 | 29 | 28 | 27 | 26 | 25 | 24 | 23 | 22 | 21 | 20 |
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| 39.6 | 40.1 | 40.1 | 40.7 | 40.7 | 40.7 | 40.7 | 40.7 | 41.2 | 41.2 | 41.2 | 41.8 | 41.8 | 41.8 | 41.8 | 41.8 | 41.8 | 42.3 | 42.9 | 42.9 | 42.9 | 43.4 | 44.0 | 44.0 | 44.0 | 44.0 |
| 11 | 557 | 295 | 610 | 178 | 178 | 79 | 73 | 417 | 264 | 189 | 824 | 797 | 577 | 133 | 58 | 25 | 343 | 338 | 253 | 96 | 557 | 1074 | 802 | 136 | 136 |
| 10 | 10 | 10 | 10 | ø | 9 | 10 | 10 | 10 | 10 | 10 | ဖ | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 9 | 10 | 10 |
| US-09-780-070-21 | US-09-798-743A-3 | US-09-815-242-10104 | US-09-748-107-2 | US-09-966-545-2 | US-09-966-546-2 | US-09-867-550-860 | US-09-764-887-288 | US-09-815-242-10165 | US-09-815-242-13980 | US-09-815-242-11799 | US-09-932-145-3 | US-09-815-242-5071 | US-09-815-242-11760 | us-09-867-550-372 | US-09-864-761-48958 | US-09-864-761-43467 | US-09-985-694A-2 | US-09-318-271-8 | US-09-815-242-11842 | US-09-864-761-45697 | US-09-798-743A-1 | US-09-509-196A-2 | US-09-964-899-41 | US-09-263-689-13 | US-09-728-479-9 |
| Sequence 21, Appl | Sequence 3, Appli | Sequence 10104, A | Sequence 2, Appli | Sequence 2, Appli | Sequence 2, Appli | Sequence 860, App | Sequence 288, App | Sequence 10165, A | Sequence 13980, A | Sequence 11799, A | Sequence 3, Appli | Sequence 5071, Ap | Sequence 11760, A | Sequence 372, App | Sequence 48958, A | Sequence 43467, A | Sequence 2, Appli | Sequence 8, Appli | Sequence 11842, A | Sequence 45697, A | Sequence 1, Appli | Sequence 2, Appli | Sequence 41, Appl | Sequence 13, Appl | Sequence 9, Appli |

Sequence 2, Application US/09893615 Patent No. US20020082395A1 GENERAL INFORMATION: APPLICANT: Fischer, Gerald W. Schuman, Richard F. Wong, Hing Stinson, Jeffrey L. TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF NUMBER OF SEQUENCES: 89 CORRESPONDENCE ADDRESS: ADDRESSE: FINNEGAN, HENDERSON, FARABOW, GARRETT 6

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CORRESSEE: FINNEGAM, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: «Unknown»
TOPOLLOGY: linear

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RESULT 3
US-09-893-615-17
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US-09-893-615-9
         Sequence 17, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                          Matches
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ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDJUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
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                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT
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TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: DC
                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-408-4400
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Stinson, Je
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Pred. No.
                                                                                                                                                                                                       Score 91; DB 10;
Pred. No. 9.6e-08;
                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                    Length 19;
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TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-893-615-17
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 17:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER:
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTENTIAL CHIMERICAL SPECIFIC FOR LIPOTENTIAL CHIMERICAL SPECIFIC FOR LIPOTENTIAL 
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FILING DATE: 29-Unn-2001
ATTORNEY/AGENT IMPORMATION:
NAME: Einaudi, Carol P.
                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
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                                                                                                                                                                                                                        CITY: Washington
STATE: DC
                                                                                                                                               COUNTRY: USA
ZIP: 20005-3315
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COMPUTER: IBM PC of OPERATING SYSTEM:
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Stinson, Jeffrey L.
STINVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
INVENTION: OPTMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF
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Wong, Hing
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   compatible
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Pred. No. 9.6e-08;
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COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P
REGISTRATION UNMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acids
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MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-893-615-41
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US-09-893-615-41
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Patent No. US20020082395A1
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
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les 15; Conservarion
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Stinson, Jeffrey L.
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
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CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT
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TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
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Pred. No. 9.6e-08;
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                                                                       US-09-893-615-15
Sequence 15, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
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RESULT 6
US-09-993-615-57
; Sequence 57, Application US/09893615
; Patent No. US20020082395A1
; GENERAL INFORMATION:
                                                                                                                                                  US-09-893-615-57
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Best Local Similarity
Matches 15; Conserv
                                                                                        Query Match
Best Local :
                                                                          Matches
                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/893,615
APPLICATION UNMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elinaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
                                                                      Match 100.0%; Score 91; D)
Local Similarity 100.0%; Pred. No. 9.0
Local Similarity 0; Mismatches
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1 WHWRHRIPLOLAAGR 15
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Wong, Hing
Stinson, Jeffrey L.
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF A
                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1300 I Street,
CITY: Washington
STATE: DC
                                                                                                                                                                                                                         TYPE: amino acid
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ZIP: 20005-3315
                                                                                                                                                                                                                                            LENGTH: 19 amino acids
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Pred. No. 9.6e-08;
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hes 0;
                                                                                                               DB 10;
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APPLICANT: Fischer, Gerald W. Schuman, Richard F. Wong, Hing

Stinson, Jeffrey L.

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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-x-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
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                                                                                 APPLICATION NUMBER: GB 24263.6
FILING DATE: 2000-10-04
APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
                                                                                                                                                                         APPLICATION NUMBER: US 09/632,366 FILING DATE: 2000-08-03
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OPERATING SYSTEM: PC-DOS/MS-DOS.
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                         APPLICATION NUMBER: PCT/US01/00666 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: 9
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LENGTH: 19 amino acids
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REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 202-408-4000
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, David K.
    2001-01-30
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100.0%; Pr
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Pred. No.
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4e-06;
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Query Match
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; ORGANISM: Rattus norvegicus US-09-816-087-4
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Best Local
Matches
                                                                                                                                  GENERAL INFORMATION:
APPLICANT: WEI, MING-HUI
APPLICANT: WEI, MING-HUI
TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUDLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO00749-CID
CURRENT APPLICATION NUMBER: US/09/816,087
CURRENT FILING DATE: 2001-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: Annomax Sequ
SEQ ID NO 33721
LENGTH: 139
                                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 4
                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09816087 Patent No. US20020064822A1
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                                      LENGTH: 32
TYPE: PRT
                                                                                                                NUMBER OF SEQ ID NOS:
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APPLICATION NUMBER: US 09/608,408
FILING DATE: 2000-06-30
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8; Conserv
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EXPRESSED IN BONE PROPRESSED IN ADULT
EXPRESSED IN PLACES
EXPRESSED IN FETAL
EXPRESSED IN LUNG,
EXPRESSED IN HELA,
EXPRESSED IN HELA,
EXPRESSED IN HELA,
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72.7%;
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ED IN BY474, SIGNAL = 5.3
ED IN FETAL LIVER, SIGNAL = 5.3
ED IN LUNG, SIGNAL = 4.3
ED IN HELA, SIGNAL = 3.5
ED IN HELA, SIGNAL = 3.5
ED IN HELAO, SIGNAL = 3.5
ED IN HELAO, SIGNAL = 3.5
ED IN HEART, SIGNAL = 3.5
ED IN HEART, SIGNAL = 3.5
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ADULT LIVER, SIGNAL -
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48.98;

Score 44.5;

В 10;

Length 323;

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APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: ACOMICA-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 9/632,366

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR APPLICATION NUMBER: PCT/US01/00669
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Best Local Similarity
Tatches 8; Conserve
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; ORGANISM: human
US-09-985-694A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1 SEQ ID NO 9
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CURRENT APPLICATION NUMBER: US/09/985,694A
CURRENT FILING DATE: 2001-11-05
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PRIOR EILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: PCT/US94/13296
PRIOR FILING DATE: 1994-11-18
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               150 WYWRRR-PKRLSAG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 WYWRRR-PKRLSAG 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank, David R.
Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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57.1%;
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Pred. No. 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: MAP TO AL049594.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.9
; OTHER INFORMATION: EST_HUMAN HIT: BF338634.1, EVALUE 4.00e-21
; OTHER INFORMATION: SWISSPROT HIT: P42128, EVALUE 5.20e-01
US-09-864-761-42937 .
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PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PRIOR DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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SEQ ID NO 42937
LENGTH: 51
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Best Local
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
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                                        ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYDE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/982,610
FILING DATE: 17-Oct-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICATION NUMBER: 08/446,648 FILING DATE: 1996-MAY-23
                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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Wood, William I
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Goeddel, David
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Pred. No.
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FILING DATE: 04-APR-1994 ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy

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RESULT 14
US-09-925-297-466
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US-09-220-920-81
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US-09-220-920-81
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                                                                                                  Sequence 466, Application US/09925297
Patent No. US20020081659A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 81
LENGTH: 68
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APPLICANT: Baloh, Robert H.
TITLE OF INVENTION: Artemin, A No. US20020002269Alel Neurotrophic Factor
FILE REFERENCE: 6029-7996
CURRENT APPLICATION NUMBER: US/09/220,920
CURRENT FILING DATE: 1998-12-24
EARLIER APPLICATION NUMBER: 09/163,283
EARLIER FILING DATE: 1998-09-29
EARLIER APPLICATION NUMBER: 60/108,148
EARLIER APPLICATION NUMBER: 60/108,148
EARLIER FILING DATE: 1998-11-12
EARLIER APPLICATION NUMBER: 09/218,698
EARLIER APPLICATION NUMBER: 09/218,698
EARLIER FILING DATE: 1998-12-22
                                   CURRENT APPLICATION NUMBER: US/09/925,297
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 68
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INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                     1 WHWR--HRIPLQLA 12
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FILING DATE:
APPLICATION |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WHWRPWTPCKMFAQR 472
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                    2000-03-08
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Query Match
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NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence
SEQ ID NO 40505
LENGTH: 99
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NUMBER OF SEQ ID NOS: 928
SOFTWARE: PATENTIN VEr. 2.0
SEQ ID NO 466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                         PRIOR APPLICATION NUMBER: US 09/774,203
                                                                                                                                             PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: Aeomica-X-1
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                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/234,687
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TYPE: PRT
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                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00670
                                                                                                                                                                                                                                                       FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                          FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US01/00665 FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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Hypothetical 38.6 kDa p
YMR144W OR YM9375.13.
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01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
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"Structure of the dnaA region of Pseudomonas
"mona three bacteria, Bacillus subtilis, Esci
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P13455;
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FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA. THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY. THE BETA CHAIN IS REQUIRED FOR INITIATION OF REPLICATION ONCE IT IS CLAMPED ONTO DNA, IT SLIDES FREELY (RITHERFOTTONNAT AND ARCH.)
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Fritz
Ghim S.Y., Gir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GARL BACULT PA(2241; P4(2240); P4(2240); P4(2241); 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 39, Last sequence upd/30-MAY-2000 (Rel. 39, Last annotation ullowed the complex of the
                         Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Ermerson P.T.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger'D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Transferase; DNA-directed DNA
SEQUENCE 367 AA; 40718 MW;
                                                                                                                                                                                                                                                                            MEDLINE=98044033; PubMed=9384377;
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  + {DNA}(N).
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FE65ABBAD685FEAD CRC64;
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     Harwood C.R., Henaut A.
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RESULT 5
CBP8_HUMAN
ID CBP8_H
AC P22792
DT 01-AUG
DT 16-OCT
DE CARDOX
DE SUBUNIT
GN CPN2.
OS HOMO S
OC EUKARTY
OC MAMMAI
AN NCBI_T
RN [1]
RP SEQUEN
RC TISSUE
RA RONINS
RA RONINS
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Rurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,

Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,

None D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,

Sato T., Scanian E., Schleich S., Schroeter R., Scoffone F.,

Sakiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

Sorokin A., Tanakoshi A., Tankadi T., Takahashi H., Takamaru K.,

Takeuchi M., Tamakoshi A., Tankada T., Terpstra P., Tognoni A.,

An Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
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Best Loc
Matches
                                                                                                                                                                  P22792;
01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
Carboxypeptidase N 83 kDa chain (Carbo
Subunit) (Fragment).
MEDLINE=9094386; PubMed=2378615;
Tan F., Weerasinghe D.K., Skidgel R.A.,
Roninson I.B., Schilling J.W., Erdoes E.
"The deduced protein sequence of the hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D30808; BAA06472.1; ALT_FRAME. EMBL; D30808; BAA06473.1; ALT_FRAME. EMBL; D30905; CAB12045.1; -... EMBL; Z93105; CAB12045.1; -... SubtiList; BG11163; garD.
                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                           Homo sapiens (Human)
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                                                          TISSUE=Liver;
                                                                       SEQUENCE FROM
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aramata D., Kasahara Y., Klaerr-Blanchard
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F.1 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO
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Primates;
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Catarrhini;
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              Tamei H.,
E.G.;
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                             Kaul R.K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 154:1323-1329(1988).
-- FUNCTION: THE 83 KDA SUBURIT BINDS AND STABILIZES THE SUBURIT AT 37 DEGREES CELSUIS AND KEEPS IT IN CIRCUL SOME CIRCUMSTANCES IT MAY BE AN ALLOSTERIC MODIFIER
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MEDLINE-88309120; PubMed-3408501;
MEDLINE-88309120; PubMed-3408501;
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InterPro; IPR000372; LRR
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PTM: WHETHER OR NOT ANY CYS RESIDUES PARTICIPATE IN INTRACHAIN
BONDS IS UNKNOWN, BUT THEY DO NOT FORM INTERCHAIN DISULFIDE BON
WITH THE 50 KDB CATALYTIC SUBUNIT.

DISEASE: A COMPLETE ABSENCE OF THE ENZYME IS NOI CONSIDERED TO
COMPATIBLE WITH LIFE.
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SUBUNIT: TETRAMER OF TWO CATALYTIC
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15-DEC-1998
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Proc. Natl. Acad. Sci. U.S.A. 92:1941-1944(1995).

-I- FUNCTION: Involved in bacteriochlorophyll biosynthesis; introduces -I- FUNCTION: Involved in ba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95199269;
Gibson I C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hansson M., Kannangara C. "Rhodobacter sphaeroides magnesium chelatase.";
                                                                                                                                             EMBL; AJ010302; CAB38736.1; -. EMBL; AF017642; AAB97157.1; -. EMBL; AF195122; AAF24286.1; -.
                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE-20115911;
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                                   SEQUENCE
                                                  DOMAIN
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                                                                              Photosynthesis; Bacteriochlorophyll biosynthesis
                                                                                               InterPro; IPR002035; VWF_A.
SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hunter C.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sphaeroides 2.4.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "DNA sequence analysis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
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PubMed=7892204;
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RESULT
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                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
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MEDLINE=20089027; PubMed=10620777;
Machida M., Yamazaki S., Kunihiro S
Haikawa Y., Yamazaki J., Yamamoto S
Sakai M., Aoki K., Ogura K., Kudoh
Yanagida M.;
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15-DEC-1998 (Rel. 37, Last sequence up
15-DEC-1998 (Rel. 41, Last annotation
Hypothetical protein C30B4.06 in chrom
SPBC30B4.06C OR PIO79.
                                                                                                                                                                                                                                                                           Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Pot: Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.; The genome sequence of Schizosaccharomyces pombe."; Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21848401;
Wood V., Gwilliam
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Eukaryota; Fungi; Ascomycota;
Schizosaccharomycetales; Schi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic DNA and cDNAs
Yeast 16:71-80(2000).
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                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                            tatement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
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Sekine M., Og
, Kikuchi H.,
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, Oguchi A., N
H., Zhang M.Q.
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RESULT 8
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ProDom; PD003738; GIDA; 1.
PROSITE; PS01280; GIDA_1; 1.
PROSITE; PS01281; GIDA_2; 1.
                                                                                                                                                                                                                                                                                                                                       EMBL; x75627; CAA53289.1; -. InterPro; IPR002543; FtsK_SpoIIIE. Pfam; PF01580; FtsK_SpoIIIE; 1.
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Coxiella group; Coxiella.
NCBI_TaxID=777;
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                                                                                                                                                                                                                                                                                                                     Cell division;
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J. Vet. Med. B 40:366-370(1993).
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MEDLINE=94055499; PubMed=82
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FTSK OR SPOILIE.
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                                            9 LQLAAG 14
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666 AA; 74230 MW;
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Pubmed=8237209;
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DE DNA POLYMER;
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InterPro; IPR003141; PHP_N.
InterPro; IPR004365; PALC, alpha.
InterPro; IPR004365; tRNA_anti.
Pfam; PF02136; tRNA_anti; 1.
Pfam; PF02211; PHP_N; 1.
Pfam; PF02211; PHP_C; 1.
SMART; SM00481; PHP_C; 1.
TIGREMAS; TIGR00594; POLITIO:; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
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"Complete DNA sequence of a serogroup A strain of Neisseria"
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MEDLINE=20222556; PubMed=10761919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               meningitidis Z2491.";
Nature 404:502-506(2000)
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9JVX8;
16-OCT-2001
                                                                                                                                                                                                                                                                     Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL162753; CAB83921.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
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16-OCT-2001 (Rel.
15-JUN-2002 (Rel.
                                                                                                                  Local Similarity
les 6; Conserv
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SUBGURIT: CONTAINS A CORE (COMPOSED OF ALPHA, EPSILON, AND THET CHAINS) THAT ASSOCIATES WITH A TAU SUBGURIT HICH ALLOW THE CORD DIMERIZATION TO FORM THE POLITI' COMPLEX. POLITI' ASSOCIATES WITH B GAMMA, DELTA, DELTA', PS AND CHI) AND WITH THE BETA CHAIN GAMMA, DELTA, DELTA', PS AND CHI) AND WITH THE BETA CHAIN (BY SIMILARITY).

SUBCELLULAR LOCATION: Cytoplasmic (By Similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME
RESPONSIBLE FOR MOST OF THE RETLEATIVE SYNTHESIS IN BACTERIA.
THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXCHUCLEASE ACTIVITY.
THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY).
CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphosphate
RIPLOL 1102
                                                         RIPLQL 11
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                                                                                                                     Conservative
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40, Last sequence update)
41, Last annotation update)
I alpha subunit (EC 2.7.7.7)
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                                                                                                                                                  Score 6;
                                                                                                                     Mismatches
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5. 63;
                                                                                                                                                                               Length 1144;
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RESULT 10 DP3A_NEIMB

DP3A_NEIMB

STANDARD;

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Best Local
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
NAA bolymerase III alpha subunit (EC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K. Elsen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B., Haft D.H., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B. Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J., Glail J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.; "Complete genome sequence of Neisseria meningitidis serogroup B st."
   1097
                                                                                                                                                          Pfam; PF02231; PHP_N; 1.
Pfam; PF02811; PHP_C; 1.
SMART; SM00481; PHPCC; 1.
TIGRFAMS; TIGR00594; Polc; 1.
Transferase; DNA-directed DNA polymerase; DNA replication;
                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN-MC58 / Serogroup B;
MEDLINE-20175755; PubMed-10710307;
                                                                                                                                            Complete proteome.
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                                                                                                                                                                                                                                                                                            InterPro;
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SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C FAMILY. DNAE CHERNATITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: DNA POLYMERASE III IS A COMPLEX, MULTICHAIN ENZYME RESPONSIBLE FOR MOST OF THE REPLICATIVE SYNTHESIS IN BACTERIA. THIS DNA POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY. THE ALPHA CHAIN IS THE DNA POLYMERASE (BY SIMILARITY). CATALYTIC ACTIVITY: N deoxynucleoside triphosphate - N diphospha
                                                                                                                                                                                                            srPro; IPR003141; PHP_N.
srPro; IPR004805; PolC_alpha.
srPro; IPR004365; FCNA_ant1.
n; PF01336; FCNA_ant1; 1.
n; PF02231; PHP_N; 1.
n; PF02811; PHP_C; 1.
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RIPLOL
                                RIPLQL 11
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6; Conser
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Proteobacteria; beta sul
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                                                                Conservative
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PolC_alpha
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                                                                Mismatches
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2.7.7.7).
                                                                       DB 63;
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                                                                                             Length 1144
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RESULT 11 HOXY_RHOOP

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Best Local S
Matches
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01-NOV-1988
01-NOV-1988
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01-AUG-1991
01-AUG-1991
16-OCT-2001
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                 Kim K., Meyer R.J.;
"Copy-number of broad host-range plasmid
small RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identical subunits of the NAD-linked hydrogenases Ib and Alcaligenes eutrophus H16.";
Eur. J. Biochem. 181:175-180(1989).
-i- CATALYTIC ACTIVITY: H(2) + NAD(+) = H(+) + NAT-1-CATALYTIC ACTIVITY: H(2) + NAD(+) = H(+) + NAD(+) = H(
                                                                                                                      Nucleic Acids Res. 14:8027-8046(1986).
-I- FUNCTION: THIS PROTEIN IS INVOLVED IN REGULATING THE PLASI COPY-NUMBER. INCREASING THE LEVEL OF THIS PROTEIN RESULTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase;
NON_TER 29
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NCBI_TaxID=37919;
                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE-87040771; PubMed-2430262.
                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
{1]
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Plasmid R1162
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SUBUNIT: TETRAMER OF AN ALPHA AND A
CONTAINING DIMER), AND A DELTA AND
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SUBCELLULAR LOCATION: Cytoplasmi
SIMILARITY: TO OTHER [NIFE] OR [
                                                                                                       HIGHER PLASMID COPY-NUMBER.
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5; Conser
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protein repI (Fragment).
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Conservative
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26;
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SEQUENCE
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Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella
Loeffelhardt W., Stirewalt V.L., Michalowski C.B., Annarella
Farley J.Y., Schluchter W.M., Chung S., Newmann-Spallart C.,
Steiner J.M., Jakowitsch J., Bohnert H.J., Bryant D.A.;
The complete sequence of the cyanelle genome of Cyanophora p
the genetic complexity of a primitive plastid.";
(In) Schenk H.E.A., Herrmann R., Jeon K.W., Mueller N.E.,
Schwemmler W. (eds.);
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01-MAY-1991 (Rel.
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MEDLINE=90346172; PubMed=2116981;
Neumann-Spallart C., Brandtner M., Kraus M., Jakowitch ,
Bayer M.G., Maier T.L., Schenk H.E.A., Loeffelhardt W.;
"The petFI gene encoding ferredoxin I is located close operon on the cyanelle genome of Cyanophora paradoxa.";
FEBS Lett. 268:55-58(1990).
Stevanovic S., Bayer M.G., Troger W., Schenk H.E.A.; "Cyanophora paradoxa korsch.: ferredoxin partial amino-terminal amino acid sequence, phylogenetic/taxonomic evidence."; Endocyt. Cell Res. 6:219-226(1990).
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Stevanovic S.,
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Stirewalt V.L.,
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                                                 HSSP; P00246; 4FXC.
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InterPro; IPR001041; Ferredoxin.
Pfam; PF00111; fer2; 1.
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                                                                                                                                                                     implications.";
J. Biochem. 83:761-770(1978).
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component). Structural characteristics and e
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15-JUL-1998 (Rel. 36, Last sequence upda
16-OCT-2001 (Rel. 40, Last annotation up
Hypothetical protein yair.
Hypothetical protein yair.
FACTY OR B0379 OR 20475 OR ECS0429.
Escherichia coli ol57:H7.
Bacteria, Proteobacteria; gamma subdivis
                                                                                               STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino E., Ohnishi M., Kurokawa K., Tanaka M., Tobe 1 Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli Ol17:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                                                       STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Melch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Duncan M., Allen E., Araujo R., Aparicio A.M., Chung E., Davis Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12 / MG1655;
MEDLINB=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., Rc
Gregor J., Davis N.W., Kirkpatrick H.A., Goe
Mau B., Shao Y.;
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STRAIN=0157:H7 / F
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[4]
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                                                                                                                                                                                                                                                                "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
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Search completed: November 27, 2002, 07:28:46 Job time : 5.44788 secs

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| Q8viv5 mycobacteri | Q9x4h6 streptomyce | Q8rhy2 fusobacter1 | | | staphy | | mycob | ~ | orycto | Q28666 oryctolagus | Q28665 oryctolagus | | | O57434 fugu rubrip | O54764 mus musculu | O9ve32 drosophila | 09rwf7 deinococcus | Q92uk3 rhizobium m | | Q9fbw3 streptomyce | Q8yfh0 brucella me | 0 | Q9njv2 haemonchus | O8r3s2 mus musculu | Q9csq7 mus musculu | Q56187 streptomyce | Q8zza7 pyrobaculum | Q9kws4 pseudomonas |

ALIGNMENTS

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RESULT 1
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                                                                     Query Match
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                                                                                                            STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1.
clone:P0482C06.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AP002863; BAB16919.1;
EMBL; AP002863; BAB16919.1;
EMBL; AP002863; BAB1610.1;
EMBL; AP002863; BAB1610.1;
SEQUENCE 160 AA; 16198 MW; 86560C2B6AC8F777 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               OPFIM6 PRELIMINARY; PRT; 160 AA.

OPFIM6;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
P0005A05.23 protein (P0482C06.6 protein).
P0005A05.23 OR P0482C06.6.
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                      STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA,
clone:P0005A05.";
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RESULT 2

Q988K1

ID Q988K1

Q988

AC Q988

DT Q1-C

DT Q
RESULT

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Best Local
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01-OCT-2001 (TrEMBLrel. 18, La
01-JUN-2002 (TrEMBLrel. 21, La
Hypothetical protein mll6708.
MLL6708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPRO01633; EAL.
InterPro: IPRO0163; EAL.
Pfam; PF00563; EAL.; 1.
Pfam; PF00950; GGDEF; 1.
Pfam; PF00990; GGDEF; 1.
SMART; SM00267; DUF1; 1.
SMART; SM00267; DUF1; 1.
TIGRFAMS; TIGR00254; GGDEF; 1.
Hypothetical protein; Complete prepared to the protein protein protein; Complete prepared to the protein protein
                                                                               "K6irs, a new cytokeratin in the human hair follicle."; Submitted (WAR-2001) to the EMBL/GenBank/DDBJ databases EMBL; AJ308599; CAC43429.1; -. InterPro; IPR001664; IF. Pfam; PF00038; filament; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q96DU2;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-21082930; PubMed-11214968; Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasa Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimot Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                                                                                                                                   Rogers M.A., Langbein L., Schweizer J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 7:331-338(2000).
EMBL; AP003009; BAB52949.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobact
Phyllobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; alpha subd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q988K1
SEQUENCE
                                            PROSITE; PS00226; IF;
                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-SCALP;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome structure Mesorhizobium loti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-MAFF303099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q988K1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 LQLAAGR 15
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7; Conserv
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Primates;
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100.0%;
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19,
20,
        ME.
                                                                                                                                                                                                                                                                                                                                          Winter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Catarrhini; Hominidae;
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ED3361CD737C363E CRC64;
797F5655EE3A62D7 CRC64;
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                                                                                                                                                                                                                                                                                                                                          Η.,
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30;
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RESULT
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Best Local
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01-MAY-2000 (
01-MAY-2000 (
01-MAR-2002 (
                                                                               Q9P4A3;
01-OCT-2000 (
01-OCT-2000 (
01-DEC-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Type .

KRT2-6G.

Mus musculus (Mouse).

Mus musculus (Mouse).

Mus musculus (Mouse).

Musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                           Porter R.M., McLean W.;
"Keratin K6irs is specific to the inner root sheath of hair in mouse and humans.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                      Coiled coil; in
                                                                                                                                                                                                                                                                        PRINTS; PRO1248; TYPE1KERATIN PRINTS; PRO1276; TYPE2KERATIN PROSITE; PS00226; IF; 1.
SEQUENCE FROM N.A. MEDLINE-21258791; PubMed-11361337;
                                      Eurotiales; Trichocomaceae; Er
                                                                                                                                                                                                                                                                                                        InterPro; IPR002957; Keratin_I.
InterPro; IPR003054; Keratin_II.
Pfam; PF00038; filament; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-C57BL/6;
                           NCBI_TaxID=162425;
                                                                      Campothecin
                                                                                                                       Q9P4A3
                                                                                                                                                                                                                                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and characterization of a novel mouse type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aoki N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001664; IF.
                                                                                                                                                                                                                                                                                                                                               MGD; MGI:1861586; Krt2-6g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 LQLAAGR 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytokeratin
                                                                                                                                                                                                              h 46.7%;
Similarity 100.0%
7; Conservative
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                                                           nidulans.
                                                                    (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
resistance conferring protein rcaA.
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                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                       Intermediate filament.
24 AA; 57382 MW; 45FF0C44B440A72A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Keratin
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Last annotation update)
n protein K6irs).
                                                                                                                                                                                                                         Score 7;
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                                         Emericella
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Pred. No.
                                                  Pezizomycotina; Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleosto
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                 Mismatches
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31;
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5. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                           root sheath of hair follicles
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RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Beyraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Gebrya D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Gebry J.M., Cawley S., Dahke G., Davenport I.B., Davies P.,
RA Gebabios B., Delcher A., Dong Z., Mays A.D., Dew I., Dietz S.M.,
RA Gebabios B., Delcher A., Dong Z., Mays A.D., Dew I., Dietz S.M.,
RA Godson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Godson K., Doup L.E., Downes M., Dugan Rocha S., Pleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Hamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Hamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Weiden M., Weiberson D.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D.A., Nelson D.L.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D.A., Nelson D.L.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D.A., Nelson D.L.,
RA Kimmel B.E., Kodira C.D., Kraft C., Weiden B., Weiberson D.,
RA Merkilvo G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Palazzolo M., Pittman G. S., Pan S., Pollard J., Puri Y.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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EMBL: AF228504; AAF81094.1; -
SEQUENCE 594 AA; 67513 MW; 19C4BE8E3DBD4505 CRC64;
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Morris N.F
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A Boistard P., Becker A., Boutry M., Cadleu E., Dreano S., Gloux S.,
A Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
A Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
A Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
"Analysis of the chromosome sequence of the legume symbiont
"Sinorhizobium meliloti strain 1021.",
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
EMBL; AL591792; CAC47576.1; -.
R EMBL; AL591792; CAC47576.1; -.
R InterPro; IPR000425; MIP_family.
R PROSITE; PS00221; MIP_family.
R Hypothetical protein; Complete proteome.
9 SEQUENCE. 1869 AA; 191305 MW; 32B51E6878708F9B CRC64;
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Pfam; PF00651; BTB; 1.

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SMART; SM00258; BTB; 1.

PROSITE; PS50098; ANK_REP_REGION; 1.

PROSITE; PS50097; BTB; 1.

PROSITE; PS50097; BTB; 1.

PROSITE; PS50098; LIPASE_GDSL_SER; UNKNOWN_1.

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SEQUENCE 1549 AA; 166717 MW; ED837D9A83114DX
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NCBI_TaxID=382;
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Q1-NOV-1996 (TrEMBLrel. 01, C1
01-NOV-1996 (TrEMBLrel. 21, La
01-JUN-2002 (TrEMBLrel. 21, La
Potential molybdenum-pterin-b:
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Bacillus halodurans.
Bacteria; Firmicutes; Facillaceae; Bacillus.
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MEDLIND-21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe Tida T., Tanaka M., Tobe Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaa Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(201).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis nucleic Acids Res. 28:4317-4331(2000).

EMBL; AP001509; BAB044411.; -
Hypothetical protein; Complete proteome.

SEQUENCE 82 AA; 8895 MW; 2747633A66928A81 CRC64;
                                                                                                                                                                                                                                                                                                                     Hypothetical protein. SEQUENCE 111 AA; 1
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MEDLINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G.
Fuji F., Hirama C., Nakamura Y., Ogasawara
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T., Tanaka M., Tobe T.,
Ogasawara N., Yasunaga T.,
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N., Kuhara
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Q9VIO3;
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                                                                                                                                                                                                                                                                           MEDLINE-21145866; PubMed-11248100; May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam "Complete genomic sequence of Pasteurella multocida Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001). EMBL; AE006164; AAK03339.1; ...
            Drosophila
                                                                                                                                                                                                                                                         Hypothetical protein; Complete SEQUENCE 158 AA; 18065 MW;
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NCBI_TaxID=747;
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Azotobacter vinelandii.
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32 QLAAGR
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RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barndon R.C., Rogers Y.H.C., Blazej R.G., Change M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Bascadaie J., Baltaker R.G., Bladwin D.,
RA Ballew R.M., Basu A., Bascadaie J., Bayraktaroglu L., Besaley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA Borson K.N., Boup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahike C., Davenport L.B., Davies R.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann R.,
Fosler C., Gabrielian A.E., Garg N. S., Gelbart W.M., Glasser K.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann R.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kednid T.J., Wei M.H., Ibeywam C.,
Jalai N., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Hount S.M., May M., Hurphy B., Murphy L., Mazny D.M., Netson D.L.,
RA Mental N., Mattei B., McIntosh T.C., McLeod M.P., Moshreil A.,
RA Mental N., Mattei B., McIntosh T.C., McLeod M.P., Moshreil A.,
RA Mental N., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Palazzolo M., Hurphy L., Mazny D.M., Netson D.L.,
RA Palazzolo M., Mary M., We
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Conserved hypothetical transmembrane protein.
AF0350.
                                                                                                                                                                                                             029897;
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NCBI_TaxID-7227;
                                                       Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobaceae; Archaeoglobus.
                                                                                           Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20196006; PubMed=10731132;
 SEQUENCE FROM N.A
                                     NCBI_TaxID-2234;
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6; Conser
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100.0%;
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Pred. No. 1.1
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No. 1.1e+02;
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                                                                           Archaeoglobales
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RESULT 15
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ID O56309
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Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Kichardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; x84791; CAA59262.1; -.
InterPro; IPR000711; ATPsynt_
Pfam; PF00213; OSCP; 1.
PRINTS; PR00125; ATPASEDELTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Micrococcus luteus (Micrococcus lysodeikticus).
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Micrococcineae; Micrococcaceae; Micrococcus.
NCBI_TaxID=1270;
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pfam; pr01925; DUF81; 1.
Hypothetical protein; Transmembrane; Complete proteome.
SEQUENCE 211 AA; 23303 MW; 927825BC1EFC1B46 CRC64;
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Nature 390:364-370(1997),
EMBL; AE00180; AAB90884.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-ATCC 4698;
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nes 6; Conserv
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(TrEMBLrel. 03, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
orting ATP synthase (EC 3.6.1.34) (Fragment).
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tive 0;
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enes H and A from Microco
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PRELIMINARY;

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AC 0.56309;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-1998 (TrEMBLrel. 19, Last annotation update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cyclin homolog:
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Sequence:

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Title:
Perfect score:
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length: 2000000000
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Query
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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        US-08-592-646A-28
US-09-165-422-48
US-09-165-422-48
US-09-165-422-48
US-09-165-422-59
US-08-592-646A-27
US-08-592-646A-27
US-08-592-646A-20
US-08-592-646A-30
US-09-165-422-27
US-09-165-422-30
US-08-592-646A-31
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59, Appl
27, Appl
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31, Appl
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                     WHWRHRIPLQLAAGR 15
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Result No.

Minimum Maximum

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Word size

Database :

ALIGNMENTS

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; SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
; TYPE: amino acid
STRANDEDNESS: not releva
; TOPOLOGY: Linear
; MOLECULE TYPE: peptide
US-08-592-646A-28
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GENERAL INFORMATION:
Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 15; Conservative (
                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEFHONE: 703 836-2787
TELEFAX: 703 836-2787
                                                                                                                                                                                                                               TELEFAX: 703 836-2787 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYTEPTIDES (
TITLE OF INVENTION: GONDII AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. Box CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.O. Box 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                            not relevant
      0;
                     Score 15; DB 2;
Pred. No. 2.1e-09
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      Mismatches
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                                        Length 15;
      Indels
    0;
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RESULT 3
US-09-165-422-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 6372897
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, COLETTE
APPLICANT: JOLIVET-REYNAUD, COLETTE
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
TOWNST AND APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 28, Application US/09165422 Patent No. 6372897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 48, Application US/08592646A Patent No. 5851535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: JOLIVET-
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703 836-2787 INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS: LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11
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CORRESPONDENCE ADDRESS:
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CITY: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: /UJ L. TELEPHONE: /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Berridge, William P. REGISTRATION NUMBER: 30,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 WHWRHRIPLQLAAGR 15
                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WHWRHRIPLQLAAGR 15
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APPLICATION NUMBER: US/09/165,422
                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۷A
                                                                                                                                                                                                             ZIP: 22320
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JENTION: MIMOTOPIC POLYPEPTIDES
JENTION: GONDII AND APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLYPEPTIDES OF TOXOPLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                      US-09-165-422-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 6372897
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOLLYET-REYNAUD, Colette
APPLICANT: JOLLYET-REYNAUD, COLETTE
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 48,
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Best Local Similarity
                                                        Query Match
                                                                                                                                                                                                                                                                                                    TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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TELEPHONE: 703 836-6400
TELEPAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
Local Similarity hes 15; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-0ct-1998
CLASSIFICATION: <Unknown>
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopp
                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WP.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
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                                                                                                                                                  MOLECULE TYPE: peptide SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
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TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
                                                                                                                                                                                                                                         STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Alexandria
STATE: VA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Berridge, William P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09165422
100.0%; Score 15; DB 4; ilarity 100.0%; Pred. No. 2.1e-09; Conservative 0; Mismatches 0;
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Pred. No. 2.1e-09;
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Length 15; indels

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RESULT 6
US-09-165-422-59
; Sequence 59, Application US/V.
; Patent No. 6372897
; PATENT INFORMATION:
   APPLICANT: JOLIVET-REYNAUD, Colette
   APPLICANT: JOLIVET-REYNAUD, COLETTE
   GONDII AND APPLIC
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US-08-592-646A-59
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 59, Application US/08592646A Patent No. 5851535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 703 836-2787 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
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TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
TITLE OF INVENTION: GONDII AND APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: OLIFF & BERRIDGE, PLC STREET: P.O. Box 19928
CITY: Alexandria
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COMPUTER READABLE FORM:
                                                                                      NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
CORRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
                                                                                                                                                                                   TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
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               COUNTRY: USA
ZIP: 22320
                                                    STATE: VA
                                                                     CITY: Alexandria
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TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 59:
US-09-165-422-59
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; Sequence 27, Application US/08592646A

; Patent No. 5851535
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Best Local Similarity
Thehes 15; Consert
                                                                                              APPLICATION NUMBER: US/08/592
FILING DATE: 26-7AN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION UMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB
FILEOMHUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEPAX: 703 836-2787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                              TELEFAX: 703 836-2787 INFORMATION FOR SEQ ID NO:
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TELEPHONE: 703 836-6400
TELEPAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JOLIVET-
TITLE OF INVENTION:
TITLE OF INVENTION:
                                     SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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ADDRESSEE: OLIFF & BERRIDGE, PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
TYPE: amino acid
STRANDEDNESS: no
                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: P.O. Box CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 WHWRHRIPLQLAAGR 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,02
REFERENCE/DOCKET NUMBER: W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       22320
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P.O. Box 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOLIVET-REYNAUD, COLETTE
JENTION: MIMOTOPIC POLYPEPTIDES OF TOXOFLASMA
ENTION: GONDII AND APPLICATIONS
not relevant
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100.0%; Pred. No. 4.7
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                    Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                               US/08/592,646A
                                                                                                                                                              WPB 36923
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TOPOLOGY: 1

linear

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RESULT 8
US-08-592-646A-29
; Sequence 29, Application US/08592646A
; Patent No. 5851535;
                                                                                                                                                                                                                                                                           RESULT 9
US-09-165-422-27
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                                                                                                                             Sequence 27, Application US/09165422
PATENT NO. 6372897
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
APPLICANT: JOLIVET-REYNAUD, COLETTE OF TOXOPLASMA
TITLE OF INVENTION: MIMOTOPIC POLYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
TITLE OF INVENTION: GONDII AND APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: not relevant TOPOLOGY: linear MOLECULE TYPE: peptide
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CORRESPONDENCE ADDRESS:
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CITY: Alexandria
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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FILING DATE: 26-JAN-1996
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CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
                                                                              GONDII AND APPLICATIONS
NUMBER OF SEQUENCES: 63
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P.O. Box 19928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 amino acids
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100.0%; Pr
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Pred. No.
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Pred. No.
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. 2.2e-08;
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2.2e-(
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MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-165-422-27
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US-09-165-422-29
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Patent No. 6372897
Patent No. 6372897
Patent No. 6372897
GENERAL INFORMATION: MIMOTOPIC POLYPEPTIDES OF "CXUPLASMA GONDII AND APPLICATIONS
ON TITLE OF INVENTIONS
ON THE STATE OF THE STATE
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Best Local (
  TELEPHONE: 703 836-64
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 27:
                                                                              APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-Oct-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 63
CORRESS:
ADDRESSE: OLIFF & CAPPY: Box 19:
CTTY: Alexandria
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
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14; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 22320
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Pred. No.
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Length 15; Indels

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TOPOLOGY: Inear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-165-422-29
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                             Sequence 30, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bertidge, William P.
RECISTRATION NUMBER: 30,024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                  Matches
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TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
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                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET WHBER: WP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
                                                                                                                                                                                                                                                        TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: JOLIVET-REYNAUD, COLETTE
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
TITLE OF INVENTION: GONDII AND APPLICATIONS
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                      LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not rele
                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                      1 WHWRHRIPLQLAA 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 HWRHRIPLQLAAGR 15
                                                                                                                     WHWRHRIPLQLAA 15
                                                                                                                                                                                  13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: OLIFF & BERRIDGE, PLC
VI: P.O. Box 19928
Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: not relevant
                                           Application US/08592646A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08592646A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 15 amino acids
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JOLIVET-REYNAUD, Colette
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                        peptide
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                                                                                                                                                                                                86.7%; Score 13; 100.0%; Pred. No.
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Pred. No.
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                                                                                                                                                                                                DB 2; L
2.2e-07;
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2.2e-08;
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US-09-165-422-26
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                                                                                                                                                                                                                                                                                      Sequence 26, Applicated Sequence 26, Applicated Sequence 26, Applicated Sequence 26, Application: Patent No. 6372897

Patent No. 6372897

Patent No. 6372897

PATENTIAL OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA GONDII AND APPLICATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 703 836-2787 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: WP TELECOMMUNICATION INFORMATION: 703 836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: VA
COUNTRY: USA
COUNTRY: USA
ZIP: 22320
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/165,422
FILING DATE: 02-0ct-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
DAME: BOTTAGE US/1014E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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STRANDEDNESS: no
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ZIP: 22320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Berridge, William P. REGISTRATION NUMBER: 30,02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WRHRIPLQLAAGR
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ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.7%; Score 13; 100.0%; Pred. No.
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NAME: Berridge, William P. REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 36923

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TOPOLOGY: linear;

MOLECULE TYPE: peptide;
SEQUENCE DESCRIPTION: S
US-09-165-422-30
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US-09-165-422-30
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                                                    Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/165,422

FILING DATE: 02-Oct-1998

CLASSIFICATION: <UDKnown>.

ATTORNEY/AGENT INFORMATION:

NAME: Berridge, William P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 36923

TELEPHONE: 703 836-6400

TELEPHONE: 703 836-6400

TELEPHONE: 703 836-2787

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Application US/09165422
Patent No. 6372897
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, COLETTE
APPLICANT: JOLIVET-REYNAUD, COLETTE
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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les 13; Conservative
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                 3 WRHRIPLQLAAGR 15
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ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 703 836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 703 836-64 TELEFAX: 703 836-2787
                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: VA
                                                                                                                                                                                                                                         LENGTH: 15 amino acids
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                                                                  Conservative
                                                         86.7%; 500
100.0%; Pr
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100.0%; Pr
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                                                                                                                                                    SEQ ID NO: 30:
                                                              Score 13; DB; Pred. No. 2.2 0; Mismatches
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Pred. No.
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                                                                                DB 4; L
. 2.2e-07;
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. 2.2e-07;
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Search completed: November 27, Job time: 3.08494 secs
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US-08-592-646A-25
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GENERAL INFORMATION:
                                                                                                                           Matches
                                                                                                                                                       Query Match
                                                                                                                        Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                 TELEPHONE: 703 836-64
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                              NAME: Berridge, William P. REGISTRATION NUMBER: 30,024 REFERENCE/DOCKET NUMBER: WPI TELECOMMUNICATION INFORMATION: TELEPHONE: 703 836-6400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                  STRANDEDNESS: not rel
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: GO
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 22320
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 26-JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: P.O. Box CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                           1 WHWRHRIPLQLA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                           4 WHWRHRIPLOLA 15
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VERWION: MIMOTOPIC POLYPEPTIDES OF TOXOPIASMA
VERWION: GONDII AND APPLICATIONS
EQUENCES: 63
                                                                                                                          Conservative
                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JAN-1996
                                                                                                                                         100.0%;
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              2002, 07:32:09
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                                                                                                                                         Score 12;
Pred. No.
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                                                                                                                           Mismatches
                                                                                                                                         DB 2; Le
                                                                                                                                                       Length 15;
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Result
No.
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Maximum DB seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                              Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PUT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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Match
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171.849 Million cell updates/sec
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0 US-09-893-615-9
0 US-09-893-615-19
0 US-09-893-615-17
0 US-09-893-615-41
0 US-09-893-615-57
0 US-09-893-615-15
0 US-09-893-737-142
0 US-09-815-242-1325
0 US-09-815-242-11923
0 US-09-815-242-11923
0 US-09-8162-172-16
0 US-09-8162-172-16
0 US-09-8164-761-46783
0 US-09-864-761-46783
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Compugen Ltd
sequence 15, Appl
Sequence 12356, A
Sequence 12356, Ap
Sequence 1923, A
Sequence 11923, A
Sequence 16, Appl
Sequence 16, Appl
Sequence 215, Appl
Sequence 45173, A
Sequence 45173, A
Sequence 48053, A
Sequence 48053, A
Sequence 48053, Appl
Sequence 48054, Appl
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Sequence
Sequence
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Sequence
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Sequence
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9, Appli
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US-09-893-615-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09893615 Patent No. US20020082395A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fischer, Gerald W. Schuman, Richard F.
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| 33.3 | | 33.3 | Ψ | ω. | ω. | 33.3 | ω. | ω. | ω. | ω. | | ω. | 33. 3 | ω. | 33.3 | ω. | ω. | ω. | ω. | ω. | 33.3 | 33.3 | 33.3 | 33.3 | 33.3 |
| 218 | 218 | 218 | 216 | 216 | 216 | 216 | 215 | 203 | 202 | 193 | 190 | 184 | 180 | 155 | 140 | 133 | 111 | 97 | 97 | 97 | 92 | 88 | 83 | 80 | 62 |
| 12 | 12 | 12 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 9 | 10 | 10 | 10 | 10 | 10 | 10 | 12 | 12 | 10 | 10 | 8 | 10 | 10 | 10 |
| US-10-011-033-10 | US-10-011-033-6 | US-10-011-033-2 | US-09-747-155-427 | US-09-771-730-146 | US-09-771-730-143 | US-09-771-730-50 | | US-09-912-020-338 | US-09-811-284-151 | US-09-941-936A-2 | US-09-895-913A-132 | US-09-764-864-827 | US-09-771-730-131 | | US-09-864-761-43849 | -09- | -09-764-898- | US-10-052-586-468 | -10-036 | US-09-864-761-43414 | US-09-867-550-494 | US-08-424-550B-275 | US-09-726-643-84 | -761- | US-09-864-761-33340 |
| 10, | Sequence 6, Appli | Sequence 2, Appli | Sequence 427, App | Sequence 146, App | 143, | Sequence 50, Appl | ~ | 338, | 151 | Sequence 2, Appli | 132, 🌶 | 827, | Sequence 131, App | • | ₹. | • | • | Sequence 468, App | Sequence 16, Appl | Sequence 43414, A | Sequence 494, App | Sequence 275, App | • | Sequence 48387, A | Sequence 33340, A |

ALIGNMENTS

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Wong, Hing
Stinson, Jeffrey L.

Stinson, Jeffrey L.

Stinson, Jeffrey L.

OFSONIC AND PROTECTIVE MONOCLONAL AND
CHAPERC OPSONIC AND PROTECTIVE MONOCLONAL AND
CHAPERCE SERVENCES: 89

CORRESPONDENCE ADDRESS:
ADDRESSE: FINNEGAN, HENDERSON, FARABOW, GARRETT &

STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION NUMBER: US/09/893,615

FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acids
TYPE: anino acids
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
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RESULT 3
US-09-893-615-17
US-09-893-615-17
Sequence 17, Application US/09893615
Patent No. US20020082395A1
PATENT INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
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US-09-893-615-9
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; SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-893-615-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
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                                                                                                                                                                              Matches
                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100 nes 15; Conservative
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                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Elhaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 049
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: US/09/893,615 FILING DATE: 29-Jun-2001
                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: DC
                                                                                                                                                                                                                                                                                                                LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                              Conservative
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Pred. No. 1.8e-09;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HENDERSON, FARABOW, GARRETT &
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US-09-893-615-19
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                                                                  COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wong,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schuman, Richard F.
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TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-893-615-17
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19, Application US/09893615 Patent No. US20020082395A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEPAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615

FILING DATE: 29-Jun-2001

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 WHWRHRIPLQLAAGR 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WHWRHRIPLQLAAGR 15
              ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                  Wong, Hing
Stinson, Jeffrey L.
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
POSITIVE BACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stinson, Jeffrey L.

TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Fischer, Gerald W. Schuman, Richard F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                       DUNNER, LLP
STREET: 1300 I Street, LP
CITY: Washington
STATE: DC
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                ADDRESSEE: FINNEGAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Einaudi, Carol P. REGISTRATION NUMBER: 32,220
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STREET: 1300 I Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: FINNEGAN,
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Pred. No. 1.8e-09;
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TYPE: amino acid
; TOPOLLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-893-615-19
; MOLECULE TYPE: Protein; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-893-615-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
US-09-893-615-41
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Patent No. US20020082395A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local :
                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEPAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 100.0%;
Local Similarity 100.0%;
nes 15; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS;
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WONG, HANGE L.
STINSON, JEffrey L.
STINSON, JEFFREY L.
OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GRAM
POSITIVE BACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fischer, Gerald W. Schuman, Richard F.
                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1300 I Street, NW CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Einaudi, Carol P. REGISTRATION NUMBER: 32,220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 29-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/893,615
                                                                  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: DC
                                                                                                       LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 19 amino acids
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Pred. No. 1.8e-09;
Mismatches 0;
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TYPE: amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
US-09-893-615-57
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                                                                   US-09-893-615-15
US-09-893-615-15
Sequence 15, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
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US-09-893-615-57
; Sequence 57, Ap
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Best Local Similarity
Matches 15; Conserve
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Patent No. US20020082395A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                         Best
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEPAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                Match 100.0%;
Local Similarity 100.0%;
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                                                                                                                                                                                                                                 1 WHWRHRIPLQLAAGR 15
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ZIP: 2005-3315
ZIP: 2005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaud1, Carol P.
REGISTRATION NUMBER: 32,220
REGISTRATION NUMBER: 32,220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCIONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fischer, Gerald W. Schuman, Richard F.
                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
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: Fischer, Gerald W. Schuman, Richard F. Wong, Hing Stinson, Jeffrey L.
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Pred. No. 1.8e-09); Mismatches 0.
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Pred. No. 1.8e-09
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TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-893-615-15
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                                                                                                                                ; ORGANISM: Homo sapiens
US-09-893-737-142
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                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 142
LENGTH: 228
                                                                Matches
                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 329
                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/893,737 CURRENT FILING DATE: 2001-06-28
                                                                                                                                                                                                                                                                                                                APPLICANT: Sheppard, Paul O.
APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
200
                               10 QLAAGR 15
                                                            Local Similarity
les 6; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/893,615 FILING DATE: 29-Jun-2001 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF POSITIVE BACTERIA

NUMBER OF SEQUENCES: 89
QLAAGR 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 19 amino acids
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                                                                Conservative
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                                                         40.0%; 5cc
100.0%; Pr
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100.0%;
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Pred. No.
                                                                               Score 6;
Pred. No
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                                                                                                                                                                                                                                                                                                                                             Sequence 5746, Application Patent No. US20020061569A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ
SEQ ID NO 12356
LENGTH: 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR PELICATION NUMBER: 60/191,078 PRIOR PILING DATE: 2000-03-21 PRIOR PILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848 PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21 PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: APPLICANT:
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PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, APPLICANT: Ohlsen, K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/253,625 PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                              Trawick, John D.
                                                                                                                                                                                                                                                               Wall, Daniel
                                                                                                                                                                                                                                                                                    Ohlsen, Kari L.
Zyskind, Judith W.
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Yamamoto, Robert T
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Yamamoto, Robert T.
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Zyskind, Judi
                                                                                                                                                                                                                                                                                                                                                                                        Application US/09815242
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                                                                                                                                                                                                                                                                                                                               Robert
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Pred. No.
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APPLICATION NUMBER: 60/207,727 FILING DATE: 2000-05-26

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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASISEQ for Windows Version 4.0
SEQ ID NO 5746
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                                                                                                                 US-09-815-242-11923
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/243,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 11923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Best Local
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APPLICANT:
APPLICANT:
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                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L. APPLICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 411
TYPE: PRT
                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quence 11923, Application US/09815242 tent No. US20020061569A1
                                                                                                                                                                      ENGTH: 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 IPLQLA 376
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nes 6; Conserv
                                     Local Similarity
nes 6; Conserv
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   9 LQLAAG 14
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Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto, Robert T.
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                                       Conservative
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100.0%; Pred. No.
                                                       100.0%;
                                                         40.0%; Score 6; 1
100.0%; Pred. No.
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                                   Mismatches
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5. 27;
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US-09-891-762-2
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                                                                          RESULT 14
US-09-982-172-215
; Sequence 215, Application (
; Patent No. US20020137119A1
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; OTHER INFORMATION: Computer generated synthetic peptide
US-09-982-172-16
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: Sequence 16, Application US/09982172

: Patent No. US20020137119A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LENGTH: 741
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-762-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SQ TD NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: CUITLIS, ROIY A.J.
APPLICANT: SILOS-Santiago, Inmaculada
TITLE OF INVENTION: 48000 AND 52920, NOVEL HUM
TITLE OF INVENTION: CHANNELS AND USES THEREOF
FILE REFERENCE: MNI-170
GENERAL INFORMATION:
APPLICANT: Emil Israel Katz
APPLICANT: EMIL ISRAEL KATZ
TITLE OF INVENTION: PEPTIDES REPRESENTATIVE OF POLYPEPTIDES OF INTEREST AND ANTIBO
TITLE OF INVENTION: DIRECTED THEREAGAINST, AND METHODS, SYSTEMS AND KITS FOR GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
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SEQ ID NO 16
LENCTH: 29
TYPE: PRT
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APPLICANT: Emil Israel Katz
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                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
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CURRENT FILING DATE: 2001-06-26
PRIOR APPLICATION NUMBER: US 60/214,176
PRIOR FILING DATE: 2000-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial sequence
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                                                                                                    Application US/09982172
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100.0%; Pred. No.
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100.0%; Pred. No.
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o. 24;
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US-09-864-761-45173
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US-09-982-172-215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches 5
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CURRENT APPLICATION NUMBER: US/09/982,172
CURRENT FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 253
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 215
LENGTH: 29
LENGTH: 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 45173, Application US/09864761 Patent No. US20020048763A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/180,312 PRIOR FILING DATE: 2000-02-04
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                OR APPLICATION NUMBER: US 60/207,456
OR FILING DATE: 2000-05-26
OR APPLICATION NUMBER: US 09/632,366
OR FILING DATE: 2000-08-03
OR APPLICATION NUMBER: US 09/632,366
OR FILING DATE: 2000-08-03
OR APPLICATION NUMBER: US 60/236,359
OR APPLICATION NUMBER: US 60/236,359
OR APPLICATION NUMBER: PCT/US01/00666
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: PCT/US01/00667
OR APPLICATION NUMBER: PCT/US01/00667
OR APPLICATION NUMBER: PCT/US01/00666
OR APPLICATION NUMBER: PCT/US01/00666
OR APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                    DR APPLICATION NUMBER: PCT/US01/00665
DR FILING DATE: 2001-01-30
DR APPLICATION NUMBER: PCT/US01/00668
DR FILING DATE: 2001-01-30
DR APPLICATION NUMBER: PCT/US01/00663
DR APPLICATION NUMBER: PCT/US01/00662
DR FILING DATE: 2001-01-30
DR FILING DATE: 2001-01-30
DR APPLICATION NUMBER: PCT/US01/00661
DR APPLICATION NUMBER: PCT/US01/00661
DR FILING DATE: 2001-01-30
DR FILING DATE: 2001-01-30
DR FILING DATE: 2001-01-30
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                                                                          APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30 APPLICATION NUMBER: US 60/234,687 FILING DATE: 2000-09-21
                      APPLICATION NUMBER: US 09/608,408 FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h. 33.3%; S
Similarity 100.0%;
5; Conservative 0;
NUMBER: US 09/774,203
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ORGANISM: Homo sapiens

ORGANISM: Homo sapiens

FEATURE:

FEATURE:

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.52

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.52

OTHER INFORMATION: EXPRESSED IN BOME MARROW, SIGNAL = 0.51

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.48

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.46

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.46

OTHER INFORMATION: SWISSPROT HIT: P25109, EVALUE 7.00e-17

OTHER INFORMATION: SWISSPROT HIT: P25109, EVALUE 8.30e+00

US-09-864-761-45173
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                                     δõ
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 45173
LENGTH: 41
                                                                                 Matches
                                                                                                   Query Match
Best Local :
24 IPLQL
                                       7 IPLQL 11
                                                                             l Similarity
5; Conserv
28
                                                                             33.3%;
ilarity 100.0%;
Conservative
                                                                                   0;
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Pred. No.
                                                                                   Mismatches
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o. 33;
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                                                                                                                      Length 41
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Search completed: November 27, 2002, 07:32:52 Job time : 1.38996 secs

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369
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Score Query Match Length DB IJ SUMMARIES Description

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| 251 | 760 | 357 |) L | 231 | 663 | 322 | 333 | | 185591 | 663 | 475 | 351 | 200 | 76/T | 357 | 332 | 360 | 348 | 337 | 301 | 375 | 421 | ب ا ا ا | ر ا ا | 7 | 330 | 242 | 360 | 299 | 663 | 300 | 474 | 360 | 357 | 337 | 312 | 366 | 366 | 366 | 316 | \$ | |
| 10 | - t | 10 | 10 | 10 | 10 | 10 | 10 | 10 | N | 10 | 10 | 10 | 3 6 | 5 | 0 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | | • | > | | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 5 | 10 | 10 | . B | |
| AF133813 | MDIGGVAT | MUSIGH339A | AF030229 | S60842 | AF064444 | AF118987 | MMU55544 | AF006574 | AC073561 | AF064443 | MUSIGHAAAC | AF006586 | AF073799 | | I73737 | · UT | MDIGMVAR | AF468835 | MMU55545 | MMU55465 | S63182 | MMIGGIHV | AF321939 | MMII55466 | 38380184 | AR108680 | AF023222 | MDIGMVAQ | AF072804 | AF064445 | MMIGH1 | MUSIGKCLT | MUSIHCVRA | MUSIGHXT | MMU55546 | MUSIGHACT | AF178596 | AF178595 | AF178591 | AF118969 | ID | |
| 81 | 7.22093 M.domesticu | Mus Muscu | AF030229 Mus muscu | . ≥ | AF064444 Mus muscu | 7 140 | 4 Mus mu | 574 Mus | Musin | 443 Mus | esu | AF006586 Mus muscu | | o sequence 1/ | Sequence 1 | 55520 Mus musc | 2082 M. | 35 Mu | Mus | U55465 Mus musculu | | 3 | w | US5466 Mus musculu | · | Sequence | 2 Mus mu | . dome | 72804 Mus | 64445 Mus | X59104 M. musculus | 9 Mouse | 76 Mouse | 470 | 6 Mus muscu | 1735 Mouse | 178596 Mus | 178595 Mus | 178591 Mus | 969 Mus mu | iption | |

ALIGNMENTS

| <pre>seidl, K.J., Wilshire, J.A., MacKenzle, J.D., Kantor, A.B.,</pre> | AUTHORS S |
|--|--------------|
| Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus | |
| Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | Ħ |
| Mus musculus | ORGANISM M |
| Mus musculus. | SOURCE |
| | KEYWORDS . |
| AF118969.1 GI:4633367 | VERSION A |
| AF118969 | ACCESSION A |
| mRNA, partial cds. | 3 |
| Mus musculus AE0203 immunoglobulin heavy chain VH10-JH4 region | DEFINITION M |
| AF118969 316 bp mRNA linear ROD 22-APR-1999 | LOCUS A |
| | AF118969 |
| | RESULT 1 |
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Herzenberg, L.A. and Herzenberg, L.A.

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2 (bases 1 to 366)
Putterman, G., Deocharan, B. and Diamond, B.
Direct Submission
Submitted (17-AUG-1999) Rheumatology/Medicine,
                                                                            J. Immunol.
20143847
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 366)
Putterman, C., Deocharan, B. and Diamond, B.
Molecular analysis of the autoantibody re
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Seidl.K.J., Wilshire, J.A., MacKenzie, J.D.,
Herzenberg, L.A. and Kantor, A.B.
Direct Submission
                                                                                                                                                                                                    Mus musculus
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                                                                                                            autoimmunity
                                                                                                                                                                                                                     Mus musculus.
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/cell_line="AE0203"
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thi; Muridae;
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AF178595
                                                                                      2 (bases 1 to 366)
Putterman, C., Deocharan, B. and Diamond, B.
Direct Submission
Submitted (17-AUG-1999) Rheumatology/Medicine, Albert
College of Medicine, 1300 Morris Park Ave., Bronx, NY
                                                                                                                                                                                   J. Immunol.
20143847
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LEWVARIRSKSNNYATYYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRHS
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99.58;
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Rodentia;
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Pred. No. 3.6e-77;
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195; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus 39-9 immunoglobulin
                                                                                                                                                                                                        Submitted (17-AUG-1999) Rheumatology/Medicine, Albert College of Medicine, 1300 Morris Park Ave., Bronx, NY
                                                                                                                                                                                                                                   Putterman, C., Deocharan, B. and Diamond, B. Direct Submission
                                                                                                                                                                                                                                                                                                    autoimmunity
J. Immunol. 164 (5), 2542-2549 (2000)
                                                                                                                                                                                                                                                                                                                               Putterman, C., Deocharan, B. and Diamond, B. Molecular analysis of the autoantibody re
                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 366)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      partial cds.
AF178596
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82 c 99 g 86 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="from peptide-immunized mouse"
<1. .>366
              /product="immunoglobulin heavy
/protein_id="AAD54352.1"
/db_xref="GI:5853182"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="immunoglobulin heavy chain variable region"
/protein_id="AAD54351.1"
/db_xref="GI:5853180"
                                                       /codon_start-]
                                                                   /note="anti-peptide antibody"
                                                                                              /note="from peptide-immunized mouse"
                                                                                                              /cell_type="hybridoma"
                                                                                                                         /organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/cell_line="39-9"
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translation="DVKVVESGGGLVQPKGSLKLSCAASGFTFNTYAMNWVRQAPGKG/
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Pred. No. 3.6e-77;
0; Mismatches 1;
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Best Local Similarity
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                                                                                                    106 TGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGT 165
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                     AATAATTATGCAACATTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGAT 225
  AATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGAT
                                                                                 TGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V region gene usage and somatic mutation in the primary and secondary responses to influenza virus hemagglutinin J. Immunol. 144 (7), 2795-2801 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clarke, S.H., Staudt, L.M., Kavaler, J., Schwartz, D., Weigert, M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 312)
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D-region; J-region; V-region; immunoglobulin heavy
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LGRYWYFDVWGAGTTVTVSS"
8 82 c 98 g 86 t
                                                                                                                                                                                                                                                                                                              /protein_id="AAA38022.1"
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/translation="pkgszkuscaasgetentnamnwvrqapgkglemvarirsksnn
/translation="pkgszkuscaasgetentnamnykvrqapykglemvarirsksnn
yatyyadsvkdretisrddsqsmlylqmnnlktedtamyycvraayyamdymgqgtsv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Ig H-chain VDJ-region"
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                                                                                                                                                                                    Score 144; DB 10;
Pred. No. 1.5e-76;
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Pred. No. 3.6e-77;
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Matches 194; Conserv
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                         GATTCACAAAGCATGCTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATG 285
                                                                                                                                                  TGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGT 165
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TATTACTGTGTGAGA 300
                                                                                            AATAATTATGCAACATTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGAT 225
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                                                                                AATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (18-APR-1996) Dept: of Microbiology/Immunology. University of Tennessee, 858 Madison Ave., Memphis, TN 38 Location/Qualifiers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Correlation between the amino acid position of arginine in VH-CDR3 and specificity for native DNA among autoimmune antibodies J. Immunol. 157 (6), 2430-2439 (1996)
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                                                                                                                                                                                                                                                           96
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                     /product="anti-DNA immunoglobulin heavy chain IgG"
/protein_id="AAB49145.1"
/db_xref="GI:1872413"
/translation="vQxeGSLKLSCAASGFSFNTNAMNWVRQAPGKGLEWVARIRSKS
NNYATYYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVREGYSTLYWYXDVW
GAGXTYTYSS"
<1..>337
                                                                                                                                                                                                                                                                                                                                                                                          /cell_line="452p.108"
/cell_type="hybridoma"
/note="mouse number-452; clonally
452p.119 and 452p.84"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/strain="(NZB x NZW) F1"
/db_xref="taxon:1000"
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99.5%;
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Rodentia;
                                                                                                                                                                                      Score 144; DB 10;
Pred. No. 1.5e-76;
D; Mismatches 1
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Sciurognathi; Muridae;
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Murinae; Mus
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RESULT 8
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                                                                                                                                                                                                                      286 TATTACTGTGTGAGA 300
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                                                                                                                                                                                                                                                                         GATTCACAAAGCATGCTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATG
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3131427
                              D50376
D50376.1 GI:804892
D50376.1 GI:804892
immunoglobulin heavy chain variable region.
Mus musculus (strain BALB/c) hybridoma producing anti-human procollagenase antibody, cell-line K1E6 cDNA to mRNA.
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 357)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M21470.1 GI:196220
C-region; V-region;
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                                                                                                              sequence.
                                                                                                                            Mouse mRNA
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J. Immunol. 140
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                     Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Ig heavy chain V-region signal 58. .>357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="aaa38634.1"
/db_xref="G1:196721"
/tanslation="MLIGLKWVFEVVEYQGVHCEVQLVETGGGLVQPKGSLKLSCPAS
GESENTNAMNWVRQAFGKGLEWVARIRSKSNNYATYYADSVKDRFTISRDDSQSMLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="Ig heavy
65 c 92 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Ig heavy chain MRL-DNA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus
        Eutheria;
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                     Metazoa;
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99.5%;
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Rodentia;
                    Chordata;
        Rodentia;
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Pred. No. 1.5e-76;
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      Sciurognathi;
                     Craniata;
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y chain
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        Muridae;
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                     Euteleostomi;
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         Murinae;
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RESULT 9
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96104992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-APR-1995) Hachiro Yamanaka, New Drug Research Laboratories, Kanebo Ltd.; 5-90 Tomobuchi-cho 1-chome, Miyakojima-Ku, Osaka, Osaka 534, Japan (Tel:06-921-1281(ex.3609),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yamanaka, H.I., Kirii, Y. and Ohmoto, H. An improved phage display antibody cloning designed PCR primers optimized for Pfu DNA J. Blochem. 117 (6), 1218-1227 (1995)
             Mouse (strain MRL/Mp cDNA to mRNA.
                       V-region; autoantibody; immunoglobulin heavy chain mouse (strain MRL/Mp -lpr/lpr) spleen hybridoma ce
                                                                            Mouse IgG2ak rearranged anti-DNA autoantibody.
                                                     M20829.1 GI:196951
                                                                                                     MUSIGKCLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax:06-923-3381)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="PCR primer"
complement(339. .360)
/note="PCR primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="immunoglobulin heavy chain variable region"
/db_xref="IMGT/LIGM:D50376"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="hybridoma producing anti-human procollagenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_line="KlE6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sub_species="domesticus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="BALB/c"
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Pred. No. 1.5e-76;
0; Mismatches 1;
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heavy-chain mRNA variable
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JOURNAL
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Best Local Similarity 99.5%;
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                                     286 TATTACTGTGTGAGA
TATTACTGTGTGAGA
                                                                        GATTCACAAAGCATGCTCTATCTGCAAATGAACAACTTGAAAAACTGAGGACACAGCCATG
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Kofler,R., Strohal,R., Balderas,R.S., Johnson,M.E., Noonan,D.J., Duchosal,M.A., Dixon,F.J. and Theofilopoulos,A.N.

Immunoglobulin kappa light chain variable region gene complex organization and immunoglobulin genes encoding anti-DNA autoantibodies in lupus mice
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R.Kofler
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Ig heavy chain"
52. .111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mllGlkwvffvvffyOGvhCEvOLvETGGGLVQPKGSLKLSCPAS
GFSFNTNAMNWVRQAPGKGLEWVARIRSKSNNYATYYADSVKDRFTISRDDSQSMLYL
QMNNLKTEDTAMYYCVRDAANWSAWFAYWGQGTLVTVSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="IgG2ak mRNA" 52. .>474
                                                                                                                                                                                                                                                                                                                                                                                                   /note="Ig heavy chain signal peptide"
95 c 119 g 140 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAA38849.1"
/db_xref="GI:196952"
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/db_xref="taxon:10090"
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Pred. No. 1.5e-76;
0; Mismatches 1;
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661 bp DNA linear ROD Mus musculus immunoglobulin heavy chain variable region gene, Vh10.3a allele, partial cds.
AF064446

ROD 04-JAN-2000

(Vh10.3)

Germline structure and differential utilization $VH10\ genes$

Whitcomb, E.A., Haines, B.B., Parmelee, A.P.,

Pearlman, A.M.

of.

Igha and

Ighb

Brodeur, P.H.

Immunol.

162

(3),

1541-1550 (1999)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 661)

Mus musculus

AF064446.1 c . Mus musculus.

GI:3420274

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MEDLINE
PUBMED
REFERENCE
AUTHORS
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ORIGIN
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JOURNAL
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Best Local
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                            TATTACTGTGTGAGA 300
TATTACTGTGTGAGA
                                                                                                                                                             GATTCACAAAGCATGCTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATG
                                                                                                                                                                                                                                         AATAATTATGCAACATTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGAT 225
                                                                                                        GATTCACAAAGCATGCTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATG
                                                                                                                                                                                                                   AATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGAT
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Direct Submission
Submitted (08-MAY-1998) Pathology,
MA 02111, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99138834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whitcomb, E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 99.9
94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="variable region 623, .661
623, .661
/gene="vh10.3"
/note="recombination signature of the following signature of the follow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="lader exon"
join(221,310...>622)
/gene="vhi0.3"
310...622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="milglkwvffvvffyOgvhcevolveTggglvopkgsikiscaas
GfTfNTNAMNWvRQAPGKGLEWVARIRSKSNNYATYYADSVKDRFTISRDDSQSMLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QMNNLKTEDTAMYYCVR"
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/gene="Vh10.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="immunoglobulin heavy
/protein_id="AAC31898.1"
/db_xref="GI:3420275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="immunoglobulin heavy join(176. .221,310. .>622) /gene="Vh10.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  υυπ(<176. .221,310. .>622)
/gene="Vh10.3"
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/chromosome="12"
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/strain="BALB/cByJ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="liver"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'allele="Vh10.3a"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 144; DB 10;
Pred. No. 1.5e-76;
0; Mismatches 1
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BASE COUNT
ORIGIN
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AUTHORS
JOURNAL
                                                              SOURCE
ORGANISM
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KEYWORDS
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DEFINITION
                                                                                                                                                                   RESULT 12
AF064445
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AUTHORS
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ORGANISM
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           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                       142
                                                                                                                                                                                                                                                                                                                                               166
                                                                                                                                                                                                                                                                     202
                                                                                                                                                                                                                     262
                                                                                                                                                                                                                                             286
                                                                                                                                                                                                                                                                                              226
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                     AATAATTATGCAACATTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGAT 225
                                                                                                                                                                                                                                    TATTACTGTGTGAG
                                                                                                                                                                                                                                                                     TATTACTGTGTGAG
                                                                                                                                                                                                                                                                                              GATTCACAAAGCATGCTCTATCTGCAAATGAACAACTTGAAAACTGAGGCACACCAGCCATG
                                                                                             Mus musculus immunoglobulin heavy chain gene, Vh10.2a allele, partial cds. AF064445.1 GI:3420272
           1 (bases 1 to 663) Whitcomb, E.A., Hain
                                    Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-APR-1991) J. Kavaler, Street, Philadelphia PA 19104, USA 2 (bases 1 to 300)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 300)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain; house mouse.
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X59104
Brodeur, P.H
                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kavaler, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kavaler, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X59104.1
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                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Codon_start=1
//codon_start=1
//product="IgH heavy chain V region"
/protein_igH heavy chain V region"
/protein_igH heavy chain V region"
/protein_igH heavy chain V region"
/db_xref="GI:3980166"
/translation="MVDPKGSLKLKLSCAASGFTFNTNAMNWVRQAPGKGLEWVARIR
SKSNNYATYXADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVSDFSHWCQG"
a 67 c 69 g 73 t
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chain; Ig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="BALB/c"
/db_xref="taxon:10090"
/cell_type="B cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="hybridoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocation/Qualifiers
                                                                                                                                                                                                                     275
                                                                                                                                                                                                                                             299
                                                                                                                                                                                                                                                                                                                                                                                                                                    38.8%;
             Haines, B.B.,
                                    Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 143; DB 1
Pred. No. 6e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
             Parmelee, A.P.,
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                                   Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wistar Institute,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunoglobulin;
                                                                                                                                          linear
variable r
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 300;
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                                                                                                                                          region
                                      Euteleostomi;
; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ROD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3601 Spruce
                                                                                                                                          04-JAN-2000
(Vh10.2)
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JOURNAL
                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 193; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                                                     428 TGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGT
286 TATTACTGTGTGAG
                                          548
                                                                    226 GATTCACAAAGCATGCTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATG
                                                                                                                                                                                105 TGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGT 165
                                          GATTCACAAAGCATGCTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATG
                                                                                                AATAATTATGCAACATATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGAT
                                                                                                               AATAATTATGCAACATTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGAT
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99138834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (08-MAY-1998) Pathology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Germline structure and differential utilization of Igha and Ighb
                                                                                                                                                                                                                                                                                 182
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                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                 D
                                                                                                                                                                                                                                                                                                                         /note="variable region 625, .663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MLLGLKWVFFVVFYQGVHCEVQLVESGGGLVQPKGSLKLSCAAS
GFTFNTYAMNWVRQAPGKGLEWVARIRSKSNNYATYYADSVKDRFTISRDDSQSMLYL
                                                                                                                                                                                                                                                                              /note="recombination signal sequence RSS" 129 c 159 g 193 t
                                                                                                                                                                                                                                                                                                                                                                   /gene="Vh10.2"
                                                                                                                                                                                                                                                                                                                                                                                               /note="leader exon"
join(223,312. .>624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OMNNLKTEDTAMYYCVS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="immunoglobulin heavy chain variable
/protein_id="AAC31897.1"
/db_xref="GI:3420273"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="immunoglobulin heavy chain variable region"
join(178. .223,312. .>624)
gene="Vh10.2"
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/produc+="
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="BALB/cByJ"
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                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="Vh10.2"
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                                                                                                                                                                                                                        38.8%;
                                                                                                                                                                                                                                                                                                                       . 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /h10.2"
                                                                                                                                                                                                         Score 143; DB 10;
Pred. No. 6.1e-76;
0; Mismatches 1;
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ORGANISM
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AF072804
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ACCESSION
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                                                                                RESULT 14
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TITLE
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Best Local Similarity
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                                                                                                                                               246
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                                                                                                                                               TATTACTGTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Krishnan,M.R. and Marion,T.N. Comparison of the frequencies of arginines antibodies expressed in the primary B cell autoimmune-prone and normal mice
Z22080
Z22080.1 GI:288685
anti-DNA antibody;
                                                MDIGMVAQ
M.domesticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Tennessee, Memphis, 858 Mi
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-JUN-1998) Microbiology and of Tennessee, Memphis, 858 Madison Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krishnan, M.R. and Marion, T.N. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 299)
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AF072804.1
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                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAC26043.1"
/db_xref="GI:3309239"
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/translation="KGSLKLSCAASGFTENTNAMNWYRQAPGKGLEWVARIRSKSNNY
ATYYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVASYYGNFHAYWGQG"
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ATYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVASYYGNFHAYWGQG"
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                GI:288685
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/cell_line="B.143"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain-"BALB/c"
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 IgM gene; IgM variable region; immunoglobulin.
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Pred. No. 1e-74;
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                                                            linear.
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Matches 188;
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                                                                                                                                  TATTACTGT
                                                                                                                                                                TATTACTGT 294
242 bp mRNA linear ROD 30-OCT-1 Mus musculus clone 185b, family VH10 anti-fluorescein monoclonal IgM heavy chain mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tillman,D.M., Jou,N., Hill,R.J. and Marion,T.N. Both IgM and IgG anti-DNA antibody are the products selective B cell stimulation in (NZB x NZW)FI mice J. Exp. Med. 176 (1992) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-MAR-1993) Tony N. Marion, Microbiology and Immunology, University of, Tennessee, Memphis, 858 Madison Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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Similarity 99.5%;
88; Conservative
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                                                                                                                                  294
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/strain="(NUB x NZW)F1"
/isclate="mouse #17"
/db_xref="taxon:10092"
/chromosome="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /function "heavy chain variable region for IgM anti-DNA antibody; vh558 family related to the IgM hybridoma 1/p.80 and the IgG hybridoma 17s.161 in the 17ps-c7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="IgM"
<1. .>360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YVAWFAYWGQGTLVTVSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="immunoglobulin variable
/protein_id="CAA80054.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="EVQLYETGGGLVQPKGSLKLSCAASGFSENTNAMNWVRQAPGKG
LEWVARIRSKSNNYATYYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCMRDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 to 360)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="hybridoma"
/tissue_type="spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Female"
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Best Local Similarity
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Gene family use and somatic mutation in primary fluorescein-specific IgM antibody responses Immunol. Cell Biol. 74 (3), 245-254 (1996) 96392936
8799724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (08-SEP-1997) Biology, Haverford College, 370 Lancaster Ave., Haverford, PA 19041, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         van der Keyl, H. a
Direct Submission
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/protein_id="AABB2170.1"
/db_xref="GI:2570571"
/translation="APGKGLEWVARIRSKSNNYATYYADSVKDRFTISRDDSQSMLYL
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/strain="BALB/c"
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Anti-Her2neu singl
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Anti-Staph (HAY) 9
3B1 heavy chain va
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| AAZ31388 AAT43738 AAT43740 AAT58252 | AAV03848 AAH21995 AAH22024 AAZ31376 | AAZ31379 AAH22042 AAV18537 AAV18573 | AAZ21887 AAX06031 AAZ31384 | AAV12531 AAT70515 AAT73465 | AAQ/9930 AAQ23444 AAQ44176 AAT37234 | o 5 4 7 6 | AAA40202 AAZ31382 AAT39561. AAV22074 | AAD13178 AAX05580 AAX05581 AAN90301 AAD13179 |
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ALIGNMENTS

AAT58261 standard; cDNA; 330 Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic; pharmaceutical; health care; skin treatment; pesticide; herbicide; Lead binding MAb 6F5 heavy chain variable region encoding cDNA. Location/Qualifiers "no stop codon given"

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 05-JUN-1996;
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                                                                                                                                                        Mus musculus
                                                                                                                                                                                 heavy metal;
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               CDS
                                                                          Retroviral vector; Spleen Necrosis Virus; SNV;
antibody-envelope fusion protein; retroviral envelope prote
gene therapy; antigen binding site; single chain antibody;
Her2neu cell surface marker; cell specific gene transfer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 88; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding heavy metal binding polypeptide sequences - used fetecting, removing, adding or neutralising heavy metals, such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-1995;
05-JUN-1995;
                                                                                                                                       Anti-Her2neu
                                                                                                                                                               05-JUN-2000
                                                                                                                                                                                         AAZ51115;
                                                                                                                                                                                                                 AAZ51115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes the heavy chain variable region for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lead cations
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                                                                                                                                                                                                                                                                                                                                          1997-043140/04
                                                 sapiens
                                                                                                                                                                                                                                                                                                                             CTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAGACG
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                                                                                                                                                                                                                standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murray PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                      single chain antibody gene
                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0541373.
95US-0462798.
Location/Qualifiers
14..1015
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wylie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 130; DB 18;
Pred. No. 2.4e-57;
0; Mismatches 1;
                                                                                                  s Virus; SNV; retroviral envelope protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   especially in gene therapy. The invention overcomes the restricted host range limitation of retroviral vectors. The present sequence is a gene encoding anti-Her2neu single chain antibody (scA). This sequence was used in the construction of plasmid pAJ7 which contains a tagetting vector comprising the anti-Her2neu scA fused to the SNV-Env(envelope)-TM(transmembrane) coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The patent discloses a novel retroviral vector, particularly Spleen Necrosis Virus (SNV) vector, having target cell specificity. The vector has a targetting envelope which is a chimeric protein consisting of an antigen binding site of an antibody (e.g. anti-DNP-scFv) or another peptide that binds to a specific cell surface protein, fused to the carboxy terminal part of the retroviral envelope protein. The presence of the wild type envelope protein serves as a helper molecule to improve or supplement a functional membrane fusion domain. The antigen binding site replaces the natural viral receptor binding site. The retroviral vector is used for cell specific gene transfer,
                                                                                                                                                        Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria; immunoglobulin; phagocytosis; infection; epitope; peptide mimic; MAb 96-110; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell specific gene transfer using retroviral vectors containing antibody-envelope fusion proteins and wild type envelope proteins
                                                                                                                                                                                                                                                        Anti-Staph (HAY) 96-110 heavy chain variable region encoding DNA
                                                                                                                                                                                                                                                                                                                 22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                    AAX05582
                                                                                                                                                                                                                                                                                                                                                                                                                    AAX05582 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                     Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATGCTCTATCT
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DB; AAY70111.
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                                                                                                                                                                                                                                                                                                              (first entry)
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                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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Pred. No. 5.7e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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RESULT 5
AAX05579
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Best Local
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                                                   Mus
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacterial infections. Sequences AAX05579-83 represent gene fragments encoding the heavy chain variable regions of the anti-lipoteichoic antibody 96-100.
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P-PSDB; AAW94738.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antibodies to lipoteichoic acid of gram positive bacteria - used to develop products for the diagnosis, prevention and treatment of infections caused by gram positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUN-1998;
                                                                                      immunoglobulin;
mab 96-110; ss.
                                                                                                                                                          Anti-Staph (HAY) 96-110 heavy chain variable region encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 96
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                                                                                                      Monoclonal antibody: MAb; lipoteichoic acid; gram positive; bacteria; immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
                                                                                                                                                                                               22-APR-1999
                                                                                                                                                                                                                                AAX05579;
                                                                                                                                                                                                                                                               AAX05579 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                          265
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                                                   sp.
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                                                                                                                                                                                                                                                                                                                                                       AAAACTGAGGACACAGCCATGTATTACTGTGTGAGA
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              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.0%; 5c.
100.0%; Pr
                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                   90
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                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 G; 23 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 96;
Pred. No.
                                                                                           infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.1e-39;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 96
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RESULT 6
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacterial infections. Sequences AAX05579-83 represent gene fragments encoding the heavy chain variable regions of the anti-lipoteichoic antibody 96-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
20-JUN-1995;
                            11-JAN-1996
                                                      WO9600783-A1
                                                                                 Insecta
                                                                                                           antibody; ss
                                                                                                                       delta endotoxin; Bacillus thuringiensis; western corn rootworm; WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;
                                                                                                                                                               3B1 heavy chain variable region DNA from pCIB4613
                                                                                                                                                                                             25-JUN-1996
                                                                                                                                                                                                                        AAT15725;
                                                                                                                                                                                                                                                 AAT15725 standard; cDNA; 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     constant region and at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acid of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antibodies to lipoteichoic acid of gram positive bacteria - to develop products for the diagnosis, prevention and treatment infections caused by gram positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fischer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-1997;
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DB; AAW94735.
                                                                                sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 BP; 20
                                                                                                                                                                                                                                                                                                                                                                                                                              24.4%; Score 90; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                                                                                                                                                          (first entry)
95WO-IB00497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; 17 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stinson JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 G;
                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                1.4e-36;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 90
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RESULT 7
AAT15733
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolating the fused cells, culturing them and cloning positive hybrid cells; and screening the hybrid cells for prodn. of the required MAbs. The MAbs bind to the gut of a target insect but do not bind to mammalian BBMs. The DNA sequence can be operably linked to a toxin molety, esp. selected from e.g. Bacillus toxins, Pseudomonas exotoxin and phytolaccin, etc. The Abs are useful for control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and Lepidoptera. The pesticidal compsn. is pref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fragment. MAbs were produced by using insect guts, partic. insect brush border membranes (BBMs), esp. corn rootworm, as antigen; immunising a donor animal with the antigen; isolating immunocompetent B cells from the immunised animal; fusing B cells with a tumour cell line;
                                                                                                                                                                                                                        delta endotoxin; Bacillus thuringiensis; western corn rootworm; WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; Page 50-51; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New monoclonal antibodies which bind insect gut proteins - used partic. with toxin moieties for the control of insect pests, partic.
                                                                    28-JUN-1994;
                                                                                              20-JUN-1995;
                                                                                                                                                    WO9600783-A1
                                                                                                                                                                                 Insecta
                                                                                                                                                                                                           antibody; ss
                                                                                                                                                                                                                                                               3B1 single chain antibody DNA from pCIB4631
                                                                                                                                                                                                                                                                                            25-JUN-1996
                                                                                                                                                                                                                                                                                                                         AAT15733;
                                                                                                                                                                                                                                                                                                                                                   AAT15733 standard; cDNA; 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    applied to a plant, e.g. maize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT15725-35 are DNA mols. encoding a monoclonal antibody or a binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAR90829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1996-077494/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carozzi NB,
                                       (CIBA ) CIBA GEIGY AG
                                                                                                                         11-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                .75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 GGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCTCATGTGCAGCCTC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15 GGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCTCATGTGCAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                         75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          TGGATTCACCTTCAATAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGATTCACCTTCAATAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 08
                                                                                                                                                                               sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Koziel MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP;
                                                                                                                                                                                                                                                                                            (first entry)
                                                                  94US-0267641
                                                                                               95WO-IB00497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94US-0267641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; 76 C; 91 G; 88 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                         94
                                                                                                                                                                                                                                                                                                                                                                                                                                                94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17;
. 2.1e-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74
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Carozzi NB,

Koziel MG

WPI; 1996-077494/08

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RESULT 8
AAA44338
ID AAA44338
AC AAA4
XX AAA AAA
XX Huma
DE Huma
XX Huma
KW Huma
KW Liram
KW Liram
KW Antil
KW Antil
KW Cere
KW Insu
KW Lymp
KW Ocare
KW Lymp
KW Ocare
KW O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                              antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; mouse; chicken; rat; secreted expressed sequence tag; sEST; expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antinilammatory; cytostatic; antibacterial; antifungal; antiviral; antidabetic; antiasthmatic; vulnerary; antiparkinsonian; antiviral; antidabetic; antiasthmatic; vulnerary; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; Page 68-72; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA44338 standard; cDNA; 359 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1797 BP; 455 A; 488 C; 452 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT15725-35 are DNA mols. encoding a monoclonal antibody or a binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New monoclonal antibodies which bind partic, with toxin moieties for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAR90837
                                   15-OCT-1998;
                                                                                                      15-OCT-1999;
                                                                                                                                                                                                                                         WO200021991-A1
                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    477 GGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCTCATGTGCAGCCTC 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 GGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCTCATGTGCAGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 21.7%;
Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed sequence
                                   98US-0104436
                                                                                                      99WO-US24206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tag SEQ ID NO:913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       d insect gut proteins - used control of insect pests, partic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17; I
. 2.1e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          402 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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RESULT 9
AAX05583
ID AAX

AAX05583 standard; DNA; 69

MAb

sp.

Anti-Staph 22-APR-1999 AAX05583;

(first entry)

Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria; immunoglobulin; phagocytosis; infection; epitope; peptide mimic;

(HAY) 96-110 heavy chain variable region encoding DNA.

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CDS Mus

Location/Qualifiers

W09857994-A2

Q Вр δõ

Matches Query Match

76;

Conservative

0;

Local

Similarity

20.6%;

Score 76; Pred. No. Mismatches

DB 21; 2.5e-29; 0;

Length 359; Indels

0

Gaps

0

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cc anticorvulsant; and antidepressant. The sESTs can be used for gene cc therapy and in vaccines. The sESTs are useful as probes for the cidentification and isolation of full-length cDNAs and genomic DNA cc molecules which correspond to the sESTs. Proteins encoded by the sESTs care useful in assays for determining biological activity and raising cantibodies. They may be useful for treatment of autoimmune disorders cc (multiple sclerosis, insulin dependent diabetes), allergic conditions (casthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, costeoporosis, osteoarthritis, central nervous system disorders (C (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation cdisorders (haemophilia, thrombosis), inflammatory disorders (Crohn's cdisease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA45926 to AAA45931 represent linker variants which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jacobs K,
Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                   chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective; antiasthmatic; vulnerary; antipaction; osteopathic; neuroprotective; notropic; antiparkinsonian; antipsoriatic; cerebroprotective; notropic; antiparkinsonian; antipsoriatic; cerebroprotective;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (sESTs), isolated from human, mouse, chicken and rat tissue sources. The sESTs can have a range of activities depending on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 437-438; 803pp; English.
Sequence 359 BP; 91 A; 66 C; 93 G; 109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the tissues they were isolated from. The activities include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McCoy JM,
Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LaVallie ER,
Bowman MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Evans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a monoclonal antibody (MAb) to lipoteichoic caid of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bid to whole bacteria and enhance phagocycosis and killing of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating cor preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacteria infections. Sequences AAX05579-83 represent gene fragments encoding the heavy chain variable regions of the anti-lipoteichoic antibody 96-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                            neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasia; antibody ID9 heavy chain variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 17; Fig 12;
                                                                                                                                                                                       Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic
                                                                                                                                                                                                                         Murine antibody 1D9 heavy chain variable region encoding DNA
                                                                                                                                                                                                                                                             16-OCT-2001
                                                                                                                                                                                                                                                                                                                               AAD13178 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  w antibodies to lipoteichoic acid of gram positive bacteria - used develop products for the diagnosis, prevention and treatment of fections caused by gram positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.7%; Silarity 100.0%; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP; 14 A;
                                                                                                                                                                                                                                                                                                                                                                                                                    69
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                                                                                                                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 G; 16 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR-2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgE-mediated altergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal lumanised antibodies are also useful for inhibiting narrowing of the
                                                                                                                                                                                                                                                                                                                                                                                                                                 (CCK2), comprising an antigen binding region. The and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting the infection of the invention are useful for inhibiting the interaction of an immunoglobulin of human origin. The interaction of an immunoglobulin of human origin. The interaction of a cell expression of inhibiting the interaction of a cell expression are useful for inhibiting or treating a cell expression are useful for inhibiting the interaction of a cell expression of the invention are useful for inhibiting the interaction of a cell expression are useful for inhibiting or treating the invention are useful for inhibiting the invent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-Chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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                                                                      lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
a vessel in a mammal, preferably associated with vascular intervention.
The present sequence is a DNA encoding murine antibody 1D9 heavy chain
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DB; AAE07033.
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58..411
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412..443
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/note= "CDS does not include start and stop codon"
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Query Match Best Local S Matches 58

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Score 58; 108

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5.4e-20; hes 0; DB 22; T; 0 other;

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                                                                                                                                                                                                                                                                    The invention relates to a monoclonal antibody (MAb) to lipoteichoic cald of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and cantibodies or peptides (encoded by a DNA of the variable region of antibodies or peptides (encoded by a DNA of the variable region of cantilpoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating cor preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacterial infections. Sequences AXX05579-83 represent gene fragments encoding the heavy chain cariable regions of the anti-lipoteichoic antibody 96-100.
                                                                                                                  Query match
Best Local S
Matches 57
                                                                                                                                                                                                                                     Sequence 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Fig 12; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies to lipoteichoic acid of gram positive bacteria - to develop products for the diagnosis, prevention and treatment infections caused by gram positive bacteria
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1999-095329/08.
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                                                                                                                                              Similarity
                                                                                                                                                                                                                                     BP; 13 A; 12 C; 19 G; 13 T; 0 other;
                                                                                                                     Conservative
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                                                                                                                 Sequence 57 BP; 24 A; 8 C; 10 G; 15 T; 0 other;
                                                                                                                                            variable regions of the anti-lipoteichoic antibody
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P-PSDB; AAW94737.
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(JACK-) JACKSON FOUND ADVANCEMENT
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                                                           Conservative
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                                                       15.4%; Score 57; DB
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tive 0; Mismatches
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                                                                          Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
                                                                                                                                                                                                                                                                                                                                                                                             The recombinant DNA is an insert coding for a heavy chain murvariable region, which is specific for human carcinoembryonic and originates from genomic DNA of the cell line CE 25. See and originates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric monoclonal antibody to human carcinoembryonic antigen - consisting of variable regions of mouse origin and human constant regions, for cancer diagnosis and therapy.
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Chimeric -
                                   AIDS;
                                                      multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
                                                                                                                                                                16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                               Sequence 857
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 30; page 37; 53pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JAN-1988;
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                                                                                                                                        Humanised murine antibody heavy chain 1D9RHA DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP323806-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAN90301;
                                           fibrotic disease; angioplasty; acquired immune deficiency syndrome;
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                                                                                                                                                                                                                                                                      804
                                                                                                                                                                                                                                                                                  329 TGGACTACTGGGGTCAAGGAACCTCACTCACCGTCTCCTCA 369
                                                                                                                                                                                                                                                                                                                           Local
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                   inflammatory glometimal hyperplasia;
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                                                                                                                                                                                                             standard; DNA;
Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chimeric monoclonal antibody; light chain; heavhuman carcinoembryonic antigen; cell line CE25
                                glomerulopathy;
                                                                                                                                                                                                                                                                                                                           11.1%;
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Pred. No.
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                      109
                                vascular intervention;
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                                                                                                                                                                                                                                                                                                                                                               236 T;
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AAA40202 ID AAA4

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standard; DNA;

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ВP

RESULT 15

Ъ S

145

Query Match Best Local S Matches

l Similarity 40; Conserv

Conservative

0;

Mismatches

10.8%;

Score 40; Pred. No.

DB 22; 1.2e-10

Length 357 Indels

.2e-10;

0;

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CC leukocyte trafficking, for treating CCR2-mediated disorders such as criminating contributions of the minimum disorders such as rheumatoid contributions and multiple sclerosis, atherogenesis and atherosclerosis. CC and for inhibiting restenosis. They are useful in therapy or diagnosis. CC and in the manufacture of a medicament for treating CCR-2 mediated CC disease. They are also useful for treating allergy, anaphylaxis, CC malignancy, chronic and acute inflammation, histanine and IgE-mediated allergic reaction, shock, stenosis, allograft rejection, CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired CC immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. CC Humanised antibodies are also useful for inhibiting narrowing of the CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of CC a vessel in a mammal, preferably associated with vascular intervention. CC The present sequence is a DNA encoding humanised murine antibody heavy Chain regions, ID9RHA. ID9RHA sequence consist of the complementarity CC chain region, ID9RHA. ID9RHA sequence consist of the complementarity catermining regions (CDRs) of the murine ID9 antibody heavy chain cc variable (VH) region genetically inserted into the framework regions of the murine ID9 antibody heavy chain complementarity consists of the murine ID9 antibody heavy chain regions of the murine ID9 antibody heavy chain complementarity of the complementarity complementar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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DB; AAE07034.
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  BP;
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/note= "CDS does not include start and stop codo
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A; 79 C;
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95 G; 84 T; 0 other;
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(first entry)

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                                                                                                                                                  This invention describes a novel method for the detection of a mammalian CC infection by an acid-resistant microorganism (A) by treating a faecal CC sample with at least two different monoclonal antibodies (MAb) (or their fragments or derivatives) or aptamers (collectively (I)) and detecting CC formation of a complex (C) between (I) and the corresponding antigen of CC (A). The first and second (I) bind to epitopes of different antigens CC (A). The first and second (I) bind to epitopes of different antigens CC (in at least some mammals, and have either: (i) their native structure; CC or (ii) a structure against which an antibody is produced by an animal CC infected or immunized with (A), or its extract, lysate, derived protein CC or fragment, or with a synthetic peptide. Practically all mammals display CC at least one of the specified epitopes. The method is used to detect infection by acid-fast bacteria, particularly of the genera Helicobacter, Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, CC interapeutically. The method is direct and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible degradation of antigens during passage through the intestines. This could be compared to the method of the invention.
                                                                       Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a faecal!sample with two binding reagents for antigens that survive intestinal passage .
                                                                                                                                               Sequence 375 BP; 102 A; 86 C; 89 G; 98 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 4; 84pp; German.
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06-NOV-1998;
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10.3%; Score 38; DB 21; 1 ilarity 100.0%; Pred. No. 1.3e-09; Conservative 0; Mismatches 0;
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Search completed: November 27, 2002, 05:37:40 Job time: 207.697 secs

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DEFINITION
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TITLE
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      Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lnl.gov

plate: LLAM11181 row: i column: 11

High quality sequence stop: 797.

Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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602916745F1 NCI_CGAP_Lu29
mRNA sequence.
BI150936
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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BC967007 602834239
B1455668 603173852
BI102617 602888151
BE309336 601093720
BO21928 AGENCOURT
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BC966355 602832843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M. G.E. Cons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BF135929 9
601781259F1 NCI_CGAP_Lu30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                          Plate: LLAM9245 row: e column: High quality sequence stop: 652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
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Mammalia; Eutheria; Rodentia;
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                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1; Site_1: SalI; transgenic model wNT-1, expression driven by MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies.
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                                                                                                                                /clone_lib="NCI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="DH10B"
                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:4009334"
                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="CZECH II"
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Stem cell origin."
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/clone="IMAGE:5067346"
/clone_lib="NCI_CGAP_Lu29"
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/strain="CZECH II"
Investigator providing samples: Gilbert Smith, NIH"
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RESULT 2 BF135929 LOCUS

DEFINITION

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VERSION KEYWORDS

ACCESSION

SOURCE

ORGANISM

COMMENT

REFERENCE

TITLE

JOURNAL AUTHORS

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BB843560
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                            further details
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                                                                                                                                                                                                                                                                                                                                                                                                      Computer-based methods for the mouse full-length cDNA
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/organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                           Location/Qualifiers
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UI-HF-BKO-abn-h-04-0-UI.rl NIH_MGC_36
IMAGE:3056887 5', mRNA sequence.
                                                                                                                                                                     Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. cDNA Library Preparation: M.B. Soares Lab cDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MCC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 365)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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51; Conservative
                                                                                                                                           /ww-bio.llnl.gov/bbrp/image/image.html
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//dev_stage="6 days neonates"
//dev_stage="6 
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/organism="Homo sapiens"
                                                                     Location/Qualifiers
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RESULT 4 AW403942

KEYWORDS VERSION

TITLE

FEATURES

Query Match 9.8%; Sometimes 9.

Score 36; DB s; Pred. No. 1.1 0; Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLCM1664 row: J column: 20
High quality sequence start: 65
High quality sequence stop: 565.
Location/Qualifiers '
1 cscs
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602637877F1 NIH_MGC_48 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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National Institutes of Health, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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           /tissue_type="primary, B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGAGGG). Site-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
18 a 155 c 169 g 123 t
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/note="Vector: pT773-Pac; Site_1: Not1; Site_2: Eco
/note="Vector: pT773-Pac; Site_1: Not1; Site_2: Eco
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by
M. Staudt, Ph.D. Library preparation by Maria de Fat
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

88 c 108 g . 93 t
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/cell_line="MGC85"
                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4765555"
/clone_lib="NIH_MGC_48"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="lymph
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100.0%; Pr
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2e-10;
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KEYWORDS

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RESULT 7
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                                                                                                                                          TCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATT
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mRNA sequence.
BG963642
BG963642.1 GI
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CH230-119P2.TJ CHORI-230
CH230-119P2, DNA sequence
                                           BG963642
602828443F1 NCI_CGAP_Co24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 119 row: p column: 2
Seq primer: SP6
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jong, P. and Rat BAC End
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Medical Center Dr., Rockville,

301 838 0200

301 838 0208
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ilarity 100.0%;
Conservative 0;
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/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: E
CHORI-330 Rat (BN/SSNHSd/MCW) BAC library produced
Pieter de Jong"
101 c 116 g 161 t
                                                                                                                                                                                                                                                                                                                                                                    /clone="CH230-119P2"
/clone_lib="CHORI-230 Segment
                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
 GI:14351279
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llni.gov
plate: LLAM11001 row: n column: 09

High quality sequence stop: 770.
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The T.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can I

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

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High quality sequence stop: 658.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; I
(bases 1 to 781)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/db_xref="taxon:10090"
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a 186 c 159 g 164 t
Location/Qualifiers
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musculus cDNA clone IMAGE:4988744
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hes 0;
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                                                                    Local
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; M

E 1 (bases 1 to 861)

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: MCC Gene distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM11639 row: 1 column: 16
                                                       Similarity
35; Conser
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llarity 100.0%;
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/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Noti;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 205 c 194 g 182 t
                                                                                                                                                                           /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                  /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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0; Mismatches 0;
                                                                      Score 35;
Pred. No.
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                                                                      DB 13;
4.5e-08;
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IMAGE:5253279 5',
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; Murinae; Mus
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph
                                                   NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 864)
                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                         BE309336.1
                                                                                                                                                                                                                                                          mRNA sequence.
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601093720F1 NCI_CGAP_Mam5
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Location/Qualifiers
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
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National Institutes of Health, Mammalian
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602888151F1 NCI_CGAP_Kid14 Mus
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Plate: LLAM11119 row: e column:
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                                                                                                                                                                                     house mouse
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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(bases 1 to 862)
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/db_xref="taxon:10090"
/clone="IMAGE:5043444"
/clone="ib="NCI_CGAP_Kid14"
/lab_host="DH10B (T] phage resistant)"
/note="organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. | "
a 231 c 209 g 211 t
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/strain="FVB/N"
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   Robin Humphreys
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IMAGE:3488309 5',
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IMAGE:5043444
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                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: The Cepko Laboratory

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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AGENCOURT_8952829 NCI_CGAP_Co24
IMAGE:6475284 5', mRNA sequence
B0921928
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Plate: LLNM8527 row: h column: 06
High quality sequence stop: 645.
Location/Qualifiers
                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM14013 row: m column: 13
High quality sequence stop: 608.
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Similarity 100.0%;
35; Conservative 0;
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Clone distribution: MGC clone distribution information can
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                     /clone_lib="NCI_CGAP_CO24"
/lab_Nost="DH108 (T1 Phage-resistant)"
/note="Organ: colon: Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: coloned unidirectionally. Primer: Oligo d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall
Site_2: NotI; Cloned unidirectionally. Primer: Oligo di
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
  Average insert size 1.6
                                                                                                       /db_xref="taxon:10090"
/clone="IMAGE:6475284"
                                                                                                                                                  /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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/clone="IMAGE:3488309"
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nes 35; Conserv
                                                                           CTATGCTATGGACTACTGGGGTCAAGGAACCTCA 431
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NISC_ff15c05.y1 NCI_CGAP_Mam5
5', mRNA sequence.
                                                                                                                                      34;
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Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen/Robin Humphreys
cDNA Library Preparation: Life Technologies
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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EST.
BG966355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing Center (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicqap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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MGI:1046572
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                                                                                                                                                      Similarity
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Site_2: NotI; Cloned unidirectionally. Primer: Olic
Library constructed by Life Technologies. Investigat
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                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:2865800"
                                                                                                                                                                                                                                            providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                     /clone_11b="NCI_CGAP_Mam5"
/tlssue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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Rodentia;
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Pred. No. 1.4e-0
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Sciurognathi; Muridae;
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3 others
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AUTHORS
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Best Local Similarity
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 963)

1 (bases 1 to 963)

1 (hases 1 to 963)

1 (hases 1 to 963)

1 (hases 1 to 963)

2 (hatp://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
BF578938
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Plate: LLAM10998 row: e column: 12
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone="TMAGE:4987379"
/clone_1b="NCI_CGAP_CO24"
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/note="organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo d'
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/clone=1b="NCI_CGAP_CO24"
//lab_host="DH10B (TI phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo draverage insert size 1.6 kb. Constructed by Life
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2002
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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 US-08-767-128-23
US-08-442-542-1
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US-08-752-844-36
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US-08-96-33-131-49
US-08-96-45-61-33-49
US-08-96-45-61-33-212
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RESULT 1
US-08-767-128-23
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; Patent No.
; GENERAL IN
                                                                                   APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
 INFORMATION FOR SEQ ID NO:
                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
EILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
EILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767.
FILING DATE:
CLASSIFT?...
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 612/371-5278
                                                       NAME: Carter, Charles G. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                  55402
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| 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 |
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| | | | 9.5 | | | | | | | | | | | | | | |
| | | | 732 | | | | | | | | | | | | | 57 | |
| 1 US-07-958-140-1 | 6 5455030-10 | 2 US-08-636-936-1 | 1 US-08-230-843-1 | 6 5455030-8 | 4 US-08-973-518-3 | 4 US-08-943-136-3 | | 3 US-08-603-024-1 | 1 US-08-253-877C-7 | 3 US-08-767-128-37 | 3 US-08-881-037-49 | 2 US-08-672-176A-1 | 1 US-08-447-422-14 | 3 US-08-767-128-5 | 3 US-08-881-037-13 | 2 US-08-591-196-42 | 2 US-08-591-196-30 |
| Sequence 1, Appli | Patent No. 5455030 | Sequence 1, Appli | Sequence 1, Appli | Patent No. 5455030 | Sequence 3, Appli | Sequence 3, Appli | Sequence 7, Appli | Sequence 1, Appli | Sequence 7, Appli | Sequence 37, Appl | Sequence 49, Appl | Sequence 1, Appli | Sequence 14, Appl | Sequence 5, Appli | Sequence 13, Appl | ` | Sequence 30, Appl |

ALIGNMENTS

CORRESPONDENCE ADDRESS: ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt STREET: 3100 No. 6111079west Center, 90 South Seventh St APPLICANT: WYLIE, DWANE E. APPLICANT: LOPEZ, OSVALDO APPLICANT: MURRAY, PETER JOSEPH APPLICANT: GOEBEL, PETER TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE NUMBER OF SEQUENCES: STREET: 3100 No. 6 CITY: Minneapolis STATE: MN COUNTRY: USA INFORMATION: 3, Application US/08767128 6111079 46

PCT/US96/09258

35,093

8648.49USF1

US/08/767,128:

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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 182;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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LENGTH: 330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: MURRAY, PETER JUSEPH
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WYLIE, APPLICANT: LOPEZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE:
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HYPOTHETICAL:
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                                                                                                                                   FILING DATE:
CLASSIFICATION: 424
                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Coding LOCATION: 1...330
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                                                                                                                                                                                                                                                                                       55402
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MN
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                                                                                                                                                                                                                                                                                                     USA
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SYSTEM: DOS
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1079west Center, 90 South Seventh St
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Pred. No. 4.4e-61;
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; LOCATION: 1...345
; OTHER INFORMATION:
US-08-767-128-35
                                                                                                                                                                                                                                                                                                           US-08-442-542-1
                                                                                                                                                                                                                                                                             Sequence 1, Application US/08442542 Patent No. 5686600
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                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: HYPOTHETICAL: NO ANTI-SENSE: NO
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                   APPLICANT: Carozzi, Nadine B.
APPLICANT: Koziel, Michael G.
TITLE OF INVENTION: Antibodies which Bind to
TITLE OF INVENTION: Proteins and their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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ORIGINAL SOURCE:
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                                                                          COUNTRY: UZIP: 10532
                                                                                                                       CITY: Hawthorne
                                                                                                                                      ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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 Version
    #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 345;
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CLASSIFICATION: 530 PRIOR APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 16-MA

16-MAY-1995

US/08/442,542

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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/267,641
FILING DATE: 28-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                          COMPUTER READABLE FORM:
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                            CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: C1ba-Ge19y Corporation
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Carozzi, Nadine B. APPLICANT: Koziel, Michael G.
                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: cDNA
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                              APPLICATION NUMBER: US/08/765,469 FILING DATE:
                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                        STREET: 7 Skylin
CITY: Hawthorne
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                                                                                                                                                                                                                                                                              STATE:
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STRANDEDNESS: sing
                                                  FILING DATE
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region from pCIB4613"
                                                               08/267,641
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Patent No. 5686600
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Best Local
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TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: ...
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                                                                         TELEFAX: 919-54
INFORMATION FOR SEQ
                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/267,641
FILING DATE: 28-JUN-1994
ATTORNEY/ARGENT INFORMATION:
NAME: Spruill, W. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Carozzi, Nadine B. APPLICANT: Koziel, Michael G. TITLE OF INVENTION: Antibodie TITLE OF INVENTION: Proteins NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1797 base pairs
                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Hawthorne
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
                                                                                                                                REFERENCE/DOCKET NUMBER: CGC LECOMMUNICATION
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 16-MAY
                                                                                                                                                                 NAME: Spruill, W. Murray REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 GGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCTCATGTGCAGCCTC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
STRANDEDNESS:
                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Ciba-Geigy Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 TGGATTCACCTTCAATAACT 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  10532
nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antibodies which Bind to Insect Gut
                                                                                                                                                                                                                                                                                                                                                        Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "3B1 heavy chain variable
region from pCIB4613"
                                                                                                                                                                                                                                                                                                                 US/08/442,542
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; Pred. No. 2.4e-33;
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OTHER INFORMATION:
OTHER INFORMATION:
US-08-765-469-17
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 Query Match
Best Local Similarity
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Best Local Similarity
Matches 80; Conserv
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                                                                                                                                                                                                                     TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1797 base pairs
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                 MOLECULE TYPE:
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ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
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OPERATING SYSTEM: PC-DOS/MS-DOS
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OTHER INFORMATION:
OTHER INFORMATION:
142-542-17
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                                                                                                    NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                                                                                                                                 POPOLOGY:
                                                                                                                                                                           nucleic acid
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Koziel, Michael G.
VENTION: Antibodies which Bind to Insect Gut
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                                                                                                                                                 linear
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 21.7%;
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                                                      /note= "3B1 single chain antibody from pCIB4631"
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from pCIB4631"
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 Score 80;
Pred. No.
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. 2.6e-33;
DB 3; Lt
2.6e-33;
             Length 1797;
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US-08-752-844-36
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                                                                      Sequence 36, Application US/08591196 Patent No. 5977316
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                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                            Query Match
                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 494-079
TELEX: 706141
INFORMATION FOR SEQ ID NO:
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                          APPLICANT:
                                                                                                                                                                                                                                                                                     TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 351 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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APPLICANT:
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                                                                                                                                                                         319 GACTATGCTATGGACTACTGGGGTCAAGGAACCTCA 354
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                                                                                                                                                         304 GACTATGCTATGGACTACTGGGGTCAAGGAACCTCA 339
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD
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                                                                                                                                                                                                                 Similarity 100 36; Conservative
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5935821
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                                                                                                                                                                                                                                                                                                                               nucleic acid
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(415) 494-0792
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                          Chatterjee, Mala
Foon, Kenneth A.
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                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                     DNA (genomic)
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                                                                                                                                                                                                                                100.0%;
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                                       Malaya
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Pred. No.
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                                                                                                                                                                                                                                DB 2; L
. 6.9e-10;
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                                                                                                                                                                                                                                             Length 351;
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US-08-591-196-36
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0.
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                CITY: Arlington
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 1.106141
                                  CLASSIFICATION:
                                                                                                                                                                                                                                           STREET:
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                                                                  APPLICATION NUMBER:
                                                                                                                                                                                           COUNTRY:
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1755 S. Jefferson Davis Highway, Suite 400
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                         SHIMAMURA,
                                                                                                                                                                                                                                                                           OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
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                                                                                               Release #1.0, Version #1.25
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   JP 028173/1993
                                                                US/08/197,834
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Pred. No.
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Query Match
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                                                                                                             ENGTH:
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US-07-834-539A-41
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                                                                               TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
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                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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 MOLECULE TYPE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/
FILING DATE: 1992-02-05
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                   TOPOLOGY:
                                STRANDEDNESS:
                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                          CLASSIFICATION:
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California
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DNA (genomic)
                                  single
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Pred. No.
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9.5%;

Score 35;

DB 1;

Length 42;

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RESULT 12
US-08-645-641-49
; Sequence 49, Application US/08645641
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                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0:
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 18-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08
FILING DATE: 26-APR-1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew ADDRESSEE: One Market Plaza, Steuart Tower, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY_AGENT INFORWATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE_FORCET NUMBER: 14637-0-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                     320 ACTATGCTATGGACTACTGGGGTCAAGGAACCTCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/990,860 FILING DATE: 16-DEC-1992
                                                                                                                                                                                                         Local Similarity
les 35; Conserv
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                    1 ACTATGCTATGGACTACTGGGGTCAAGGAACCTCA 35
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100.0%; Pr/
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Pred. No.
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2.1e-09
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US-07-853-408B-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                        SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
                                                                                                                                                                                                                                                                    APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5789650-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
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LENGTH: 42 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN 1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 20-MAY-CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 150
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Transgenic No. 5719032-Human Animals TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 ACTATGCTATGGACTACTGGGGTCAAGGAACCTCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: Two Emparcac
CITY: San Francisco
                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 100.
nes 35; Conservative
                                                                                                                                                                                      CITY: San Francisco
                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/645,641 FILING DATE: 20-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
           APPLICATION NUMBER:
                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ACTATGCTATGGACTACTGGGGTCAAGGAACCTCA 35
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5. 5789650
                                                                                                                                  94105
                                                                                                                                                                     California
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Kay, Robert M.
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00.0%; Pred. No.
         US/07/853,408B
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                                            Version #1.25
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Length 42; Indels

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Gaps

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RESULT 14
US-08-096-762-49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810
FILING DATE: 17-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF THE PROPERTY ADDRESS:

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

ADDRESSEE: Townsend and Townsend Khourie and Crew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5814318-Human Animals
TITLE OF INVENTION: Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
NAME: Smith, William M.
14
                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (primer)
                                                                                                                                                    APPLICATION NUMBER: US 07/904,068 FILING DATE: 23-JUN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/096,762
FILING DATE: 22-JUL-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                       FILING DATE:
                                                                                                                                       APPLICATION NUMBER:
REFERENCE/DOCKET NUMBER:
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18-MAR-1992
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Pred. No.
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320 ACTATGCTATGGACTACTGGGGTCAAGGAACCTCA 354

ACTATGCTATGGACTACTGGGGTCAAGGAACCTCA 35

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RESULT 15
US-08-800-353-41
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                                                                 ; STRANDEDNESS: single
; TOPOLOGY: Linear
; MOLECULE TYPE: DNA (ger
US-08-800-353-41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. GENERAL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 41, Application US/08800353 Patent No. 5874299
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                                   Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                      TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07,
FILING DATE: 1992-02-05
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/800,35:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Transgenic No. 5874299-TITLE OF INVENTION: Producing Heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lonbe APPLICANT: Kay,
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320 ACTATGCTATGGACTACTGGGGTCAAGGAACCTCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                    Local
                                                                                                                                         LENGTH: 42 base pairs
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                    Similarity
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100.0%; Pr
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                    Score 35; pred. No.
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Pred. No.
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      Mismatches
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                                   DB 2;
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Search completed: November 27, 2002, 05:39:23 Job time : 49.3581 secs

Page 8

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Total number of hits satisfying chosen parameters:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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27.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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                     51
417
420
466
414
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414
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                10 US-09-007-093-3

10 US-09-881-823-11

10 US-09-949-559-105

10 US-10-146-305-6

12 US-10-006-773-12

10 US-09-753-436-42

10 US-09-910-059-18

10 US-09-910-059-18

10 US-09-252-150-44
                                                                                                                                                 0 US-09-893-615-86

0 US-09-881-823-15

0 US-09-840-459-99

0 US-09-840-459-97

0 US-09-840-459-97

0 US-09-840-459-103

US-10-040-739-911

US-08-779-784-7
                                                                                                                                                                                                                                                                                                                                               SUMMARIES
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Sequence 97, Appl
Sequence 97, Appl
Sequence 103, App
Sequence 911, Appl
Sequence 13, Appl
Sequence 7, Appli
Sequence 105, Appli
Sequence 105, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 18, Appli
Sequence 17, Appli
                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                       Sequence 86, Appl
Sequence 15, Appl
Sequence 96, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-893-615-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 86, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION:
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
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ALIGNMENTS

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WONG, Hing
Stinson, Jeffrey L.

Stinson, Jeffrey L.

Stinson, Jeffrey L.

CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF
ROSITIVE BACTERIA

NUMBER OF SEQUENCES: 89

CORRESPONDENCE ADDRESS:

ADDRESSE: FINEARA, HENDERSON, FARABOW, GARRETT 6

STATE: DC

STATE: DC

COUNTRY: Washington
STATE: DC

COUNTRY: USA
ZIP: 20005-3315

COUNTRY: USA
ZIP: 20005-3315

COUNTRY: BASHINGTON

MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: DAM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/09/893,615

FILING DATE: 29-10n-2001
ATTOREY/AGENT INFORMATION:
NAME: Elnaudi, Carol P.
REGISTRATION NUMBER: 32-20
REFERENCE/DOCKET NUMBER: 04995.0041-00000

TELECOMMUNICATION INFORMATION:
TELECHONES: 202-408-4000

TELECHONES: 202-408-4000

INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 369 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TOPOLOGY: linear
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NAME/KEY: CDS

LOCATION: 1..365

SEQUENCE DESCRIPTION:
US-09-893-615-86
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                                                                             ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14)..(442)
US-09-881-823-15
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                                                                                                                                                                        PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application UP Patent No. US20020068066A1
                          Matches
                                                     Query Match
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                                                                                                                                                                                                                           APPLICANT: TRINH, RYAN
APPLICANT: WIMS, LETITIA
APPLICANT: CHEN, LI
TITLE OF INVENTION: Method for the Treatment and Prevention
FILE REFERENCE: 22851-032
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR APPLICATION NUMBER: US 07/378,577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 369;
                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SHI, WENYUAN APPLICANT: ANDERSON, MA
                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                               TYPE: DNA
ORGANISM: Murine
                                                                                                                                                            ENGTH: 466
200 AAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATGCTCTATCTGCAAATGAACA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 GTCTCCTCA 369
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                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC
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                       101;
                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTCTCCTCA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09881823
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ilarity 100.0%;
Conservative C
                          Conservative
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                                     27.48;
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                          0;
                                     Score 101; DB 10; Pred. No. 1e-44;
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Pred. No. 1.1e-188;
; Mismatches 0;
                          Mismatches
                          0;
                                               Length 466;
                          Indels
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TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION UMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND TITLE OF INVENTION: METHODS OF USE THEREFOR FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/3121,781
PRIOR FILING DATE: 1998-07-23
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; TYPE: DNA
; ORGANISM: Mus musculus
US-09-840-459-96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: LaRosa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 99, Application US/09840459 Patent No. US20020150576A1
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Best Local Similarity
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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Newman, Walter
Jones, S. Tarran
O'Brien, Siobhan H.
O'Keefe, Theresa
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Jones, S. Tarran
O'Brien, Siobhan H.
O'Keefe, Theresa
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ilarity 100.0%;
Conservative (
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h, Christopher
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; Pred. No. 1.3e-21
0; Mismatches 0
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US-09-840-459-103/c
Sequence 103, Application US/09840459; Patent No. US20020150576A1; GENERAL INFORMATION:
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; ORGANISM: Mus musculus
US-09-840-459-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-840-459-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR APPLICATION NUMBER: 09/121,781
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 99
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ
SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. US20020150576A1
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Best Local :
APPLICANT: LaRosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Slobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-840-459-97
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APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: LaRosa, Gregory J. APPLICANT: Horvath, Christop APPLICANT: Newman, Walter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Humanized heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 357
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                                                                                                                                                                                                                                                                                                     106 TGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG 145
                                                                                                                                                                                                                                                                                                                                             106 TGGGTCCGCCAGGCTCCAGGAAAGGGTTTGGAATGGGTTG 145
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                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     10.8%; Score 40;
100.0%; Pred. No.
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5.8e-12;
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1.3e-21;
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PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1988-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 103
LENGTH: 357
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No. US200201736
GENERAL INFORMATION:
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Best Local Similarity
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CURRENT FILING DATE: 2001-02-02
INFORMATION FOR SEQ ID NO: 911 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                             ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/036,520
ETLING DATE: 03-JUN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1519
CORRESPONDENCE ADDRESS:
                                                                             TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spaulding, Vikki TITLE OF INVENTION: SECRETED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
                                                          TELEPHONE: (617)
                                                                                                                                                                                                                        CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/040,739 FILING DATE: 07-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Cambridge
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                    REGISTRATION NUMBER: 32,724
                                                                                                                        NAME: Brown, Scott A.
                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Genetics Institute, STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/10040739
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Treacy, Maurice
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                                       876-5851
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Pred. No.
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TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-040-739-911
                                                                                                                             ; MOLECULE TYPE: ; HYPOTHETICAL: US-08-779-784-13
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US-08-779-784-13
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                                                                             Query Match
Best Local Similarity
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Best Local
                                                               Matches
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                                                                                                                                                                                                                                                                    TELEFAX: 201-343-1684 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784 FILING DATE: 07-JAN-1997 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rodriguez, Moses
APPLICANT: Miller, David J.
APPLICANT: ASBAURIA, KUnihiko
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOANTIBODIES
NUMBER OF SEQUENCES: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 29-APR-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 00 FILING DATE: 08-AUG-1996 PRIOR APPLICATION DATA:
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               320 ACTATGCTATGGACTACTGGGGTCAAGGAACCTCA 354
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                                                                                                                                                                                                                                                                                                                                    NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                               STRANDEDNESS: double TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                                                                                                                                                                                   ENGTH:
ACTATGCTATGGACTACTGGGGTCAAGGAACCTCA 36
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New Jersey
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                                                                                                                                                                                                                  nucleic acid
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                                                                                                                                                                                                                                   51 base pairs
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                            linear
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1 Hackensack Ave, Continental Plaza, 4th
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29-APR-1994
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100.0%;
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Pred. No.
                                                               Mismatches
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2.5e-09;
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RESULT 10
US-09-007-093-3
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US-08-779-784-7
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                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 417 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/08779784 Patent No. US20020164325A1
Sequence 3, Application US/09007093
Patent No. US20020025315A1
                                                                                                                                                                                           Best Local Similarity Matches 35; Conserva
                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DN
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/779,784
FILING DATE: 07-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 29-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/692,084
FILING DATE: 08-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/236,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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APPLICANT: ASSAURA, KUNIĥIKO
TITLE OF INVENTION: PROMOTION OF CENTRAL NERVOUS SYSTEM
TITLE OF INVENTION: REMYELINATION USING MONOCLONAL AUTOJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                     320 ACTATGCTATGGACTACTGGGGTCAAGGAACCTCA 354
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                                                                                                                  368 ACTATGCTATGGACTACTGGGGTCAAGGAACCTCA 402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1199-1-001 CIPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
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ZIP: 07601
                                                                                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Jersey
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                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                          DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                 double
                                                                                                                                                                                                            9.5%; Score 35;
100.0%; Pred. No.
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                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                              DB 7; L. 2.8e-09;
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                                                                                                                                                                                                                               Length 417;
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GENERAL INFORMATION: ·

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APPLICANT:

APPLICANT:
APPLICANT:

Anand, Naveen N Barber, Brian H Cates, George A

APPLICANT:

Caterini, Judith E

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В
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Best Local Similarity
Matches 35; Conserv
                                                                                                           SOFTWARE: PatentIn version 3.0 SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09881823
                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. US20020068066A1
                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/881,823 CURRENT FILING DATE: 2001-06-15 PRIOR APPLICATION NUMBER: US 07/378,577 PRIOR FILING DATE: 1999-08-20 NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                          TITLE OF INVENTION: method for the Treatment and Prevention of Dental Caries FILE REFERENCE: 22851-032
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: SHI,
APPLICANT: ANDE
                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
                                                      ORGANISM: Murine
NAME/KEY: CDS
LOCATION: (11)..(442)
                                         FEATURE
                                                                                                                                                                                                                                                                                  PPLICANT:
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                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 420 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,576
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 ACTATGCTATGGACTACTGGGGTCAAGGAACCTCA 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                              466
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M5G 1R7
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EDNESS: single
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Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420 base pairs
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100.0%; Pr
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Pred. No.
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TO SELECTED CELLS OF THE II
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. 2.9e-09;
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US-09-949-559-105
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US-10-146-305-6
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; ORGANISM: Escherichia coli
US-10-146-305-6
                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local Similarity
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                                                                 SEQ ID NO 6
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Patent No. US20020151682A1
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FILE REFERENCE: Carp-0095
CURRENT APPLICATION NUMBER: US/09/949,559
CURRENT FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 0013810.7GB
PRIOR FILING DATE: 2000-06-06
                                                                                                                                                 CURRENT FILING DATE: 2002-05-15
                                                                                                                                                                                  TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV TITLE OF INVENTION: S-SURFACE ANTIGEN AND A GENE ENCODING THE SAME FILE REFERENCE: OV17440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/875,221
PRIOR FILING DATE: 2001-06-06
                                                                                 SOFTWARE:
                                                                                                                   CURRENT FILING DATE: 2002-05-15
PRIOR APPLICATION NUMBER: KR 10-2001-26634
PRIOR FILING DATE: 2001-05-16
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                                                                                                   NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                       APPLICANT: YUHAN CORPORATION
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                              LENGTH: 41
TYPE: DNA
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LOCATION: (1)..(354)
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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Weir, Andrew Neil Charles
Popplewell, Andrew George
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Pred. No.
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Pred. No. 2.9e-09;
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US-09-753-436-42
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; LOCATION: (14)..(430)
; OTHER INFORMATION: 4D4 Heavy chain V region, plus leader
US-10-006-773-12
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US-10-006-773-12
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Patent No. US20010029293A1
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION: ICAM-Related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/006,773
CURRENT FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: 60/250,089
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Junghans, Richard P.
TITLE OF INVENTION: Antibodies as Chimeric Effector Cell Receptors Against Tumor AntiFILE REFERENCE: 003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 12, Application US/10006773 Patent No. US20020132983A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Mus sp.
FEATURE:
                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: ICAM-Related Materials and Methods NUMBER OF SEQUENCES: 120
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Born STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                          STREET: 6300 S
CITY: Chicago
STATE: Illinoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 TATGCTATGGACTACTGGGGTCAAGGAACCTCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 CTATGCTATGGACTACTGGGGTCAAGGAACCTCA 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383 TATGCTATGGACTACTGGGGTCAAGGAACCTCA 415
APPLICATION NUMBER: US 08/487,113 FILING DATE: 07-JUN-1995 RIOR APPLICATION DATA:
                                                       FILING DATE:
                                                                      APPLICATION NUMBER:
                                                                                                                            FILING DATE:
                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                      RY: United States of America 60606-6402
                                                                                                                                                                                                                                                                                                          Illinois
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100.0%; Pred. No. 9.8e-09;
                                                                        09/382,289
                                                                                                                                            US/09/753,436
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South Wacker Drive
                                                                                                                                                                               Version #1.25
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. 3.5e-08;
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Gaps

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Search completed: November 27, Job time: 50.3581 secs
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                                                                                                                                             Query Match
Best Local S
Matches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/889,724

FILING DATE: 26-MAY-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,689

FILING DATE: 27-JAN-1992

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    TELEFAX: (312) 474-044
TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 33
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/286,754
FILING DATE: 05-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                         371 ATGCTATGGACTACTGGGGTCAAGGAACCTCA 402
                                                                                                          323 ATGCTATGGACTACTGGGGTCAAGGAACCTCA 354
                                                                                                                                             Local Similarity
nes 32; Conserv
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                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Williams, Joseph A., REGISTRATION NUMBER: 38,659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                           8.7%; Score 32; ilarity 100.0%; Pred. No. Conservative 0; Mismatch
                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JAN-1993
                                                                                                                                                                                                                                                                     single
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                    2002, 07:14:51
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                                                                                                                                               Mismatches
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Result
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to I score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                    Score
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32.5
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2: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT: *
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5: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1984.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
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  AAW01587
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                                                                        Mouse germline hea
Anti-Her2neu singl
Anti-Staph (HAY) 9
Anti-Staph (HAY) 9
3Bl heavy chain va
                                                                                                                                                                                                                                                                                 Description
3B1 single chain a Murine 1D9 antibod Murine mAb 1D9 hea
                                                                                                                                                                                                      Lead binding MAb 6
Lead binding MAb 2
                                                                                                                                                                                                                                                                                                                                                                                                                                     to have
being pr
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|--------------------|------------|----|-----|------|----|
| Human BLyS binding | ABP45806 | 23 | 249 | 13.0 | 16 |
| Human BLyS binding | ABP45871 | 23 | 239 | 13.0 | 16 |
| ACZ885 antibody he | 90 | 23 | 137 | 13.0 | 16 |
| le h | AAR56287 | 15 | 125 | • | 16 |
| , humar | AAR30772 | 14 | 122 | | 16 |
| region | AAR13182 | 12 | 121 | 13.0 | 16 |
| of. | AAR47040 | 15 | 120 | • | 16 |
| cha | 076 | 14 | 120 | • | 16 |
| chain | AAR25412 | 13 | 118 | | 16 |
| chain va | AAR28748 | 13 | 114 | | 16 |
| prote | 69 | 22 | 494 | • | 17 |
| S | ABP45333 | 23 | 250 | ٠ | 17 |
| Humanised murine a | AAE07034 | 22 | 119 | | 17 |
| Humanised murine h | AA014981 | 23 | 117 | | 17 |
| murine | AA014980 | 23 | 117 | 13.8 | 17 |
| Humanised murine 1 | AAE06955 | 22 | 117 | • | 17 |
| Humanised murine 1 | AAE06954 | 22 | 117 | • | 17 |
| Humanised 1D9 heav | AAU09927 | 22 | 117 | | 17 |
| | AAR76969 | 16 | 62 | ٠ | 17 |
| BLyS bindin | ABP45326 | 23 | 253 | 14.6 | 18 |
| 3 | AAR31534 | 14 | 142 | | 18 |
| Staph (HAY) | AAW94737 | 20 | 19 | | 19 |
| ti-Staph (H | AAW94736 | 20 | 19 | • | 19 |
| ri 26 kDa | AAB10022 | 21 | 125 | 17.1 | 21 |
| ed | AAO14983 | 23 | 118 | | 21 |
| ed murine | AAO14982 | 23 | 117 | 17.1 | 21 |
| | AAE06957 | 22 | 117 | • | 21 |
| Humanised murine 1 | AAE06956 | 22 | 117 | ٠ | 21 |
| 109 | AAU09930 | 22 | 117 | | 21 |
| 1D9 | AAU09929 | 22 | 117 | 17.1 | 21 |
| ised 109 hea | AAU09928 | 22 | 117 | | 21 |
| aph (HAY) | | 20 | 23 | • | 23 |
| Murine antib | AAE07033 : | 22 | 148 | | 24 |
| Mouse heavy chain | AAO14978 | 23 | 117 | 19.5 | 24 |
| Murine 1D9 antibod | AAE06947 | 22 | 117 | 19.5 | 24 |

ALIGNMENTS

22-AUG-1997 AAW01587;

(first entry)

Lead binding

MAb 6F5 heavy chain variable region

AAW01587 standard; Protein; 110 AA.

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RESULT 1
AAW01587
ID AAW
XX AAW
XX AAW
XX AAW
XX AAW
DT 22-2
DT 22-2
DX Lead
XX Honc
KW Phal
K
DNA encoding heavy metal binding polypeptide sequences -
                                                                                             WPI; 1997-043140/04
N-PSDB; AAT58261.
                                                                                                                                                                                                                                                                                                                                                                                           10-OCT-1995;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monoclonal antibody; Fd fragment; lead cation; perfume; pharmaceutical; health care; skin treatment; pesticide; heavy metal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9639518-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                          Lopez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-DEC-1996
                                                                                                                                                                                                                                                                                                      (BION-) BIONEBRASKA INC
                                                                                                                                                                                                                  Ó
                                                                                                                                                                                                                  Murray PJ,
                                                                                                                                                                                                                                                                                                                                                                                           95US-0541373
95US-0462798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US09258
                                                                                                                                                                                                                          Wylie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cosmetic;
herbicide;
    used
        for
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RESULT 2
AAW01593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence was derived from RNA isolated from mouse hybridoma cells. The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials for electronic components.
The present sequence represents the heavy chain variable region for monoclonal antibody (MAb) 284, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from mouse hybridoma cells. The protein can be used for binding heavy metals, such as lead cations.
                                                                                                                                                                 DNA encoding heavy metal bir detecting, removing, adding
                                                                                                       Claim 12;
                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                                             10-OCT-1995;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW01593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents the heavy chain variable monoclonal antibody (MAb) 6F5, which immunoreacts with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detecting, removing,
                                                                                                                                                lead
                                                                                                                                                                                                                                                                                            zəqod
                                                                                                                                                                                                                                                                                                                                    (BION-) BIONEBRASKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9639518-AI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heavy metal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lead binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW01593 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRR 101
                                                                                                                                                cations
                                                                                                                                                                                                                                                    1997-043140/04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy metals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page
                                                                                                       Page
                                                                                                                                                                                                                                                                                          Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAb 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                     89; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                          95US-0541373
95US-0462798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,
                                                                                                                                                                                                                                                                                                                                                                                                                                        96WO-US09258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        health care;
                                                                                                                                                                                                                                                                                            , Lq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fd fragment; lead cation; perfume;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.5%;
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                                                                                                                                                                                                                                                                                            Wylie
                                                                                                                                                                 binding polypeptide sequences - i
ing or neutralising heavy metals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for applications involving minute amounts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
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amounts of
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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorders autolimmuno disorders such as channes tid

inflammatory disorder, autoimmune disorders such as arthritis and multiple sclerosis, atherogenesis and

atherosclerosis rheumatoid

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                  Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity CCR2, and a non-human antigen binding region and human immunoglobu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
fibrotic disease; angioplasty; acquired immune deficiency syndrome;
AIDS; inflammatory glomerulopathy; vascular intervention;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE06972 standard;
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                                                                                                                                                                                                                                                                                                                    Disclosure;
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                                                                                                                                                                                                                                                                                                                    152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody; CC-chemokine receptor 2: CCR2; nephrotropic; immunosuppressive; human immunodeficiency virus;
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                            The patent discloses a novel retroviral vector, particularly Spleen Necrosis Virus (SNV) vector, having target cell specificity. The vector has a targetting envelope which is a chimeric protein consisting of an antigen binding site of an antibody (e.g. anti-DNP-scFv) or another peptide that binds to a specific cell surface protein, fused to the carboxy terminal part of the retroviral envelope protein. The presence of the wild type envelope protein serves as a helper molecule to improve or supplement a functional membrane fusion domain. The antigen binding site replaces the natural viral receptor binding site. The retroviral vector is used for cell specific gene transfer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Retroviral vector; cell specific gene transfer; Spleen Necrosis Virus; SNV; antibody-envelope fusion protein; retroviral envelope protein; gene therapy; antigen binding site; single chain antibody; human; Her2neu cell surface marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cell specific gene transfer using antibody-envelope fusion proteins
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8.2e-30;
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RESULT 5
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                       The invention relates to a monoclonal antibody (MAb) to lipoteichoic CC acid of gram positive bacteria, where the MAb is a chimeric cimmunoglobulin comprising at least part of a human immunoglobulin constant region and at least part of a non-human immunoglobulin variable constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and killing of the bacteria and enhance protection from lethal infection. The criming of the bacteria and enhance protection if the variable region of anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating corresponding infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacteria infections.

Sequences AAW94735-39 represent heavy chain variable regions of the anti-lipoteichoic antibody 96-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 36; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          range limitation of retroviral vectors. The present sequence is an anti-Her2neu single chain antibody (sca). The couding sequence of this antibody was used in the construction of plasmid pAJT which contains a tagetting vector comprising the anti-Her2neu scA fused to
                                                                                                                                                                                                                                                                                             Claim 21; Fig
                                                                                                                                                                                                                                                                                                                          New antibodies to lipoteichoic acid of gram positive bacteria - to develop products for the diagnosis, prevention and treatment infections caused by gram positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-095329/08
N-PSDB; AAX05582.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Fischer GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW94738 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mmunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 DSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCV 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96-110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCV
32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HAY) 96-110 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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AA;
                                                                                                                                                                                                                                                                                           12; 150pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phagocytosis; infection; epitope; peptide mimic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Stinson
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₿
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2.2e-27;
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Query Match

26

Score

32;

DB 20;

Length 32;

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RESULT 6
AAW94735
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                                                                                                                          В
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a monoclonal antibody (MAb) to lipoteichoic CC acid of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin variable CC tensuant region and at least part of a non-human immunoglobulin variable CC region having specificity to lipoteichoic acid of gram positive bacteria. CC The antibodies bind to whole bacteria and enhance phagocytosis and CC tiling of the bacteria and enhance protection from lethal infection. The CC antibodies or peptides (encoded by a DNA of the variable region of CC anti-lipoteichoic acid antibody or characterised by amino acids CC corresponding to one or more of the complementarity determining regions CC (CDRs) of the variable region of the antibody can be used for treating CC or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacteria infections. CC Sequences AAW94735-39 represent heavy chain variable regions of the antibody 96-100.
                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antibodies to lipoteichoic acid of gram positive bacteria - used to develop products for the diagnosis, prevention and treatment of infections caused by gram positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 21; Fig 12; 150pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fischer GW,
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MAb 96-110.
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                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                      1 EVMLVESGGGLVQPKGSLKLSCAASGFTFN 30
                                                                                                                          EVMLVESGGGLVQPKGSLKLSCAASGFTFN
                                                                                                                                                                                                                                                                                           30;
                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        30 AA;
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                                                                                                                                                                                                                                                                                                                             Score 30;
Pred. No.
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                                                                                                                                                                                                                                                                                                                             DB 20;
2.4e-22;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                               cells with a tumour cell line; isolating the fused cells, culturing t and cloning positive hybrid cells; and screening the hybrid cells for prodn. of the required MAbs. The MAbs, bind to the gut of a target ins but do not bind to mammalian BBMs. The DNA sequence can be operably linked to a toxin molety, esp. selected from e.g. Bacillus toxins, pseudomonas exotoxin and phytolaccin, etc.. The Abs are useful for control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and
                                                                                                                                                                                                                                                                                                                                                                                                                       using insect guts, partic. insect brush border membranes (BBMs), esp. corn rootworm, as antigen; immunising a donor animal with the antigen; isolating immunocompetent B cells from the immunised animal; fusing B isolating immunocompetent B cells from the immunised animal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              delta endotoxin;
WCRW; maize; pes
                                   3B1 single chain antibody from pCIB4631.
                                                               25-JUN-1996
                                                                                        AAR90837;
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New monoclonal antibodies which bind insect gut proteins - used partic. with toxin moieties for the control of insect pests, partic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAT15725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-077494/08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-1994;
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                                                                                                                 AAR90837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CIBA ) CIBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-JUN-1995;
                                                                                                                                                                                                                                                                                                                      Lepidoptera. The pesticidal compsn. is pref. applied to a plant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in plants
                                                                                                                                                                               \frac{3}{3}
                                                                                                                                                                                            33 AMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                             Local
                                                                                                                                                                               AMNWVRQAPGKGLEWVARIRSKSNNYAT
                                                                                                                                                                                                                               ch 22.8%; l similarity 100.0%; 28; Conservative (
                                                                                                                standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 50-51; 106pp; English.
                                                                                                                                                                                                                                                                                  119 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    are monoclonal antibodies or a binding fragme t guts, partic. insect brush border membranes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pesticide; brush
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                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillus thuringiensis; western corn rootworm;
ticide; brush border membrane vesicle; monoclonal;
                                                                                                                 Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MG
                                                                                                                 599
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                                                                                                                                                                                                                                            Score 28;
Pred. No.
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                                                                                                                                                                               60
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                                                                                                                                                                                                                                            DB 17;
7.4e-20;
                                                                                                                                                                                                                                                        Length 119;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fragments
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 produced
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                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                    for
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them
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delta endotoxin; Bacillus thuringiensis; western corn rootworm; WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;

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RESULT 9
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AND OFFI
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isolating immunocompetent B cells from the immunised animal; fusing B cells with a tumour cell line; isolating the fused cells, culturing them and cloning positive hybrid cells and screening the hybrid cells for prodn. of the required MAbs. The MAbs bind to the gut of a target insect but do not bind to mammalian BBMs. The DNA sequence can be operably linked to a toxin moiety, esp. selected from e.g. Bacillus toxins, Pseudomonas exotoxin and phytolaccin, etc. The Abs are useful for control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g.
                                                            HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; ID9 antibody; neointimal hyperplasia; VH; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR90829-39 are monoclonal antibodies or a binding fragments produced by using insect guts, partic. insect brush border membranes (BBMs), esp. corn rootworm, as antigen; immunising a donor animal with the antigen; isolating immunocompetent B cells from the immunised animal; fusing B cells with a tumour cell line; isolating the fused cells, culturing them
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Page 68-72; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New monoclonal antibodies which bind insect partic. with toxin moieties for the control in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carozzi NB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9600783-A1
                                                                                                                                                                             Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephro neuroprotective; immunosuppressive; human immunodeficiency virus;
                                                                                                                                                                                                                           Murine 1D9 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAT15733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUN-1994;
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                                                                                                                                                                                                                                                             16-OCT-2001
                                                                                                                                                                                                                                                                                                                           AAE06971 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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   WO200157226-A1
                                                                                                                                                                            neuroprotective;
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28; Conservative
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                                                                                                                                                                                                                                                           (first
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                                                                                                                                                                            immunosuppressive; human
                                                                                                                                                                                                                                                                                                                           Protein; 101
                                                                                                                                                                                                                           partial heavy chain variable (VH) region.
                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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of insect pests
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Murine mAb 18-JUN-2002 AAU09919;

(first entry)

1D9 heavy chain variable region protein sequence

graft rejection; allergic disease; antipsoriatic; antiarthritic; nephrotropic; antithyroid; resteno dermatological; anaphylaxis; cell adhesion inhibi

restenosis;

inflammatory bowel disease; ulcerative colitis;

Mouse; mAb 1D9 heavy chain variable region; vasotropic; antiinflammatory; collagen disease; immunosuppressive; antiasthmatic; insulin-dependent diabetes mellitus;

Вb Ş

4

27

4 LVESGGGLVQPKGSLKLSCAASGF 27 LVESGGGLVQPKGSLKLSCAASGF

Matches Best

Local

Similarity

100.0%;

Conservative

0;

Mismatches

.8e-16;

Indels

0

Gaps

0

RESULT 10

AAU09919 standard;

Protein;

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CC (CCR2), comprising an antigen binding region of non-human origin CC and at least a portion of an immunoglobulin of human origin. The chumanised antibodies are useful for inhibiting the interaction of CC a cell expressing CCR2. They are useful for inhibiting or treating CCR introduced in the proteins of the invention are useful for inhibiting controduced in the proteins of the invention are useful for inhibiting controduced in the proteins of the invention are useful for inhibiting controduced in the manufacture of a medicament for treating cCR2 mediated discretes such as the controduced in the manufacture of a medicament for treating cCR2 mediated controduced in the manufacture of a medicament for treating cCR2 mediated controduced in the controduced controduced in the controduced con
                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-2001;
                                                                                  Sequence
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Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
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                             DB 22;
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                          Length 101;
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RESULT 11
AAE06947
ID AAE06
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                                                                                                                                                                                                          В
                                                                                                                                                                                                                              CC The present invention relates to a new method of inhibiting stenosis or CC restenosis of a blood vessel following vascular injury in a subject. The CC new method comprises administering to the subject agents which inhibit CC the adhesion and/or recruitment of neutrophils and mononuclear cells to CC a site of vascular injury by binding CD18 or CCR2. The method of the CC invention inhibits stenosis or restenosis of a blood vessel following CC vascular by-pass or transplantation surgery. The method is also useful CC for treating a subject having an inflammatory disease or condition CC mediated by neutrophil and mononuclear cell activity e.g. asthma and CC graft versus host disease. Chronic inflammatory diseases of the lung, CC collagen diseases, and insulin-dependent diabetes mellitus can also be treated. The method is further useful for treating inflammatory bowel CC diseases, such as ulcerative colitis. Additional diseases or conditions include inflammatory or aliergic diseases and conditions, including CC systemic anaphylaxis of hypersensitivity responses, drug allergies, CC psoriasis and inflammatory dermatoses, autoimmune diseases such as CC the present sequence represents the protein sequence of the mouse mab CC The present sequence represents the protein sequence of the mouse mab CC that can be used to inhibit stenosis or restenosis.
                                                                                                                                                              Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
             AAE06947 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 30; Fig 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-MAR-2001; 2001WO-US08266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complementarity determining region; CDR; CD18; CCR2; atherosclerosis.
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Inhibiting stenosis or restenosis of a blood vessel following vascular injury or angioplasty in a subject by administering agent which inhibits recruitment or adhesion of neutrophils, mononuclear cells to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             injury site
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                                                                                     2001-607511/69
                                                                                                                                                               Similarity
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                                                                                                                                                                                                          117
                                                                                                                                                Conservative
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                                                                                                                                                                                                          AA;
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50..68
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31..35
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101..10
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                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Part of H1 structure
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               117 AA
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                                                                                                                                                               Score 24;
Pred. No.
                                                                                                                                                Mismatches
                                                                                                                                                               6.6e-1
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                                                                                                                                                Gaps
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CC (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The CC humanised antibodies are useful for inhibiting the interaction of CC a cell expressing CCR2. They are useful for inhibiting or treating CC HIV infection. The proteins of the invention are useful for inhibiting CC leukocyte trafficking, for treating CCR2-mediated disorders such as CC inflammatory disorder, autoimmune disorders such as rheumatoid CC arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, CC and for inhibiting restenosis. They are useful in therapy or diagnosis, CC and in the manufacture of a medicament for treating CCR-2 mediated CC disease. They are also useful for treating allergy, anaphylaxis, CC mediated allergic reaction, shock, stenosis, allograft rejection, CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired commune deficiency syndrome (AIDS), restenosis associated with vascular CC intervention, including angioplasty and/or stent placement in a mammal. The communication of a vessel in a mammal, and inhibiting neointimal hyperplasia of the heavy chain variable (VIV) region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity CCR2, and a non-human antigen binding region and human immunoglobu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-488888/53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angloplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibod; neointimal hyperplasia; VH; heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Larosa
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                                                     present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Fig 8; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Horvath C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specificity for immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1D9 antibody;
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RESULT 12
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Matches 24
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Best Local
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                                                                                                            versus host-companies a merinod of inhibiting graft rejection, graft versus host disease or chronic rejection of a transplanted graft. The method involves administering an antagonist of CC chemokine receptor 2 (CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may be an anti-CCR2 antibody (i.e. containing light and heavy chain complementarity determining regions from various non-human origins). CCR2 is known to be involved in the rejection of transplanted grafts. The method of the invention is useful for inhibiting graft rejection particularly allografts such as kidney, liver, lung, heart-lung, pancreas, bowel and heart. The method of the invention is also useful for inhibiting graft versus host disease and for inhibiting chronic rejection of a transplanted graft. The present amino acid sequence represents a mouse antibody heavy chain variable region (mAb 1D9).
                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US2002042370-A1
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                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2;
                                                                                                                                                                                                                                                                                                                                               Inhibiting graft rejection, rejection of a transplanted
                                                                                                                                                                                                                                                                                                                                                                                                                Hancock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chronic graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; graft rejection; CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
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                     4 LVESGGGLVQPKGSLKLSCAASGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;
transplant; heart-lung transplant; pancreas transplant;
transplant; heart transplant; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVESGGGLVQPKGSLKLSCAASGF 27
                                                                                                                                                                                                                                                                                                                                                                                       2002-351265/38
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                                                             Similarity
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                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rejection; antibody
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ج
                                                                                                                                                                                                                                                                                                          16pp; English.
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                                                            19.5%;
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                                                              .08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemokine receptor 2 antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region (mAb 1D9).
                                                                                                                                                                                                                                                                                                                                               graft versus host disease or chronic graft, involves administering a CCR2
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Pred. No.
                                                            Score Pred.
27
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6.6e-16;
                                                            6.E
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RESULT

13

associated with vascular

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malignancy, chronic and acumediated allergic reaction, fibrotic disease, asthma, i
                                            inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR-2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgE-
                                                                                                                                        The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as infection and the content of the invention are useful for inhibiting contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
                                                                                                                                                                                                                                                                                         Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                         CCR2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        neointimal hyperplasia; antibody 1D9 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroprotective; immunosuppressive; human immunoder; clency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine; humanised antibody; CC-chemokine receptor 2: CCR2; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine antibody 1D9 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                        2-mediated
                                                                                                                                                                                                                                                                                                                                                                       Humanized
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibrotic disease; angioplasty; acquired immune deficiency syndrome; NIDS; inflammatory glomerulopathy; vascular intervention;
                                                                                                                                                                                                                                                                                                                                                                                                       2001-488888/53.
DB; AAD13178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GJ,
                                                                                                                                                                                                                                                                                                                                    immunoglobulin for treating a CC-chemokine receptor d disorder in a patient, comprises a binding specificity a non-human antigen binding region and human immunoglob
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Horvath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000US-0497625
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light chain variable region"
20..137
                                                                                                                                                                                                                                                                                         21; 183pp; English.
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                inflammatory glomerulopathies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148
                                 shock, stenosis, allograft rejection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'Brien
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                                                                                                                                                                                                                                                                                                                                        specificity for immunoglobulin
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RESULT 14
AAW94739
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Best Local
                                                         Immunoglobulin comprising at least part of a human immunoglobulin constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteicholic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and killing of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipoteichoic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating or preventing infections caused by gram positive bacteria. They can also be used for the complementarity determining treating the complementarity determining the comple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is murine antibody 1D9 heavy chain variable region
Sequences AAW94735-39 represent heavy chain variable regions anti-lipoteichoic antibody 96-100.
                                      or preventing infections caused by gram positive bacterial infections be used for the diagnosis of gram positive bacterial infections
                                                                                                                                                                                                                                                                                                                                                                     Claim 21;
                                                                                                                                                                                                                                                                                                    acid
                                                                                                                                                                                                                                                                                                                          The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies to lipoteichoic acid of gram positive bacteria - used to develop products for the diagnosis, prevention and treatment of infections caused by gram positive bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fischer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-JUN-1997;
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                                                                                                                                                                                                                                                                                                    gram
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24; Conservative
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                                                                                                                                                                                                                                                                                               positive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RF,
                                                                                                                                                                                                                                                                                               bacteria, where the MAb is a chimeric
                                                                                                                                                                                                                                                                                                                       to a monoclonal antibody (MAb) to lipoteichoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "complementarity determining
                                                                                                                                                                                                                                                                                                                                                                  English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score; Pred.
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8.1e-16;
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RESULT 15
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Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiinflammatory; collagen disease; immunosuppressive; antiasthmatic; insulin-dependent diabetes mellitus; inflammatory bowel disease; ulcerative colitis; ID9RHB
         17-MAR-2000; 2000US-0528267
                              15-MAR-2001; 2001WO-US08266
                                                                           WO200170266-A2
                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiarthritic; nephrotropic; antithyroid; restenosis;
dermatological; anaphylaxis; cell adhesion inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        graft rejection; allergic disease; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUN-2002
                                                                                                                                  Region
                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vascular injury; autoimmune disease; immunogle
complementarity determining region; CDR; CD18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humanised 1D9 heavy chain variable region, 1D9RHB protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU09928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                     27-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                   Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mouse; 4B4'CL heavy chain variable region;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                             28
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 27..30
                                                                                                                       /note=
                                                                                                                                  101..108
                                                                                                                                                                   /note-
                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                                                                                          /note= "Part of H1 structure loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mutant;
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                                                                                                                                                                                                                                    "Substitution of Ser residue normally present in human 484'CL sequence (AAU09926) by Asn residue normally present in mouse mAb 109 heavy chain sequence (AAU09919). Specification states the mutation as N30S but as sequence has Asn at position 30 the mutation is likely to be S30N"
                                                                                               "Complementarity determining grafted from mouse mAb 1D9 sequence (AAU09919)"
                                                                                                                                                                                        "Complementarity determining grafted from mouse mAb 1D9 sequence (AAU09919)"
                                                                                                                                                 "Complementarity determining grafted from mouse mab 1D9 |
                                                                                                                                           sequence
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hes 0;
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                                                                                                           g region 3 (CDR3),
heavy chain
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heavy chain
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PA (MILL-) MILLENNIUM PHARM INC.

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ROT HORVATH CJ, Rao PE;

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Inhibiting stenosis or restenosis of a blood vessel following vascular prinjury or angioplasty in a subject by administering agent which prinhibits recruitment or adhesion of neutrophils, mononuclear cells to prinjury site

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Thip present invention relates to a new method of inhibiting stenosis or crestenosis of a blood vessel following vascular injury in a subject. The crew method comprises administering to the subject agents which inhibit to the adhesion and/or recruitment of neutrophils and mononuclear cells to cascular injury by binding CD18 or CR2. The method of the such as consistent in procedure such as consistent by pass or transplantation surgery. The method is also useful consisted by neutrophil and mononuclear cell stock as treated by neutrophil and mononuclear cell activity e.g. asthma and collagen diseases, and insulin-dependent diabetes mellitus can also be treated. The method is further useful for treating inflammatory bewelf collagen diseases, such as ulcerative collis. Additional diseases or conditions cystemic anaphylaxis of hypersensitivity responses, drug allergies, processed and inflammatory dermatoses, and canthritis, graft rejection and other diseases including allergies, consists and inflammatory dermatoses, and other diseases including conditions of arthritis, graft rejection and other diseases including antheroscierosis. This sequence represents the variable region of one of several humanised confirmance.

CC This sequence represents the variable region of one of several humanised confirmance. In the production of anti-CCR2 antibody or antigen-binding the sequence. In the production of anti-CCR2 antibody or antigen-binding to the invention for the production of anti-CCR2 antibody or antigen-binding.
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638.431 Million cell updates/sec
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Best Local S
Matches 39
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Result

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| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 | 33 | 32 | 31 | 30 |
|--------|--------|----------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|----------|--------|----------|
| 14 | 14 | 14 | 14 | 14 | 14 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | 15 | L |
| 11.4 | 11.4 | 11.4 | 11.4 | 11.4 | 11.4 | 12.2 | 12.2 | 12.2 | 12.2 | 12.2 | 12.2 | 12.2 | 12.2 | 12.2 | 14.4 |
| 96 | 94 | 94 | 83 | 40 | 40 | 145 | 144 | 143 | 141 | 133 | 133 | 127 | 127 | 123 | 123 |
| N | N | N | N | N | N | N | N | N | N | N | Ν | 2 | N | N | |
| РН0873 | S14580 | PL0120 | C25913 | S33410 | S33406 | 147203 | PH1285 | S23624 | S31669 | PH1287 | PH1286 | S19878 | PT0369 | S34009 | 520/94 |
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| , Id | . Ig | Ig | | Ig | Ig | Ig | Įg | Ιġ | Ig | Ig | Ig | Ig | Ig | Ig | ĐΤ |
| | | Ig heavy | Ιġ | | | | | | | | | | Ig gamma | | ig neavy |
| heavy | heavy | heavy | Ιġ | heavy | gamma | | _ |

ALIGNMENTS

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RESULT 1
A27630
Ig heavy chain precursor V-10 region (MRL-DNA4) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 23-Jul-1999
C; Caccession: A27630
R; Kofler, R.
J. Immunol. 140, 4031-4034, 1988
A; Title: A new murine Ig V-H gene family.
A; Reference number: A27630; MUID:88229103; PMID:3131427
A; Accession: A27630
A; Molecule type: DNA
A; Cross-references: GB:M21470; NID:g196220; PIDN:AAA38634.1; PID:g196221; GB:M
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology <IMM>
                                                                                                                                                           Ig heavy chain precursor V region (MRL4) - mouse
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999
C;Accession: I32513
R;Kofler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M. J. Clin. Invest. 82, 852-860, 1988
A,Title: Immunoglobulin kappa 11ght chain variable region gene complex organization A;Reference number: A94689; MUID:88331394; PMID:3138286
A,Accession: I32513
A,Molecule type: DNA
A;Residues: 1-141 <KOF>
A;Cross-references: GB.M20829; NID:g196951; PIDN:AAA38849.1; PID:g196952
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
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100.0%; Pr
                                                                                31.7%; Score 39; DB
100.0%; Pred. No. 4e
Live 0; Mismatches
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s; Pred. No. 3.5
0; Mismatches
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RESULT 3
S26462
Ig heavy
A; Molecule type: mRNA
A; Residues: 1-137 <SHI>
A; Cross-references: EMBL:X78107; NID:g460798; PIDN:CAA54997.1; PID:g460799
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
                                                                                                                           RESULT 5
$42467
$19 heavy chain V region precursor - mouse
I gheavy chain V region precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: $42467
R;Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
submitted to the EMBL Data Library, March 1994
A;Reference number: $42466
A;Accession: $42467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
PH1091
Ig heavy chain V region (clone P17.79) - mouse (fragment)
Ig heavy chain V region (clone P17.79) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_
C:Accession: PH1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Experimental source: B cell, strain [NZB x NZW]F1 C; Superfamily: immunoglobulin V region; immunoglobulin C; Keywords: heterotetramer; immunoglobulin F;15-100/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies at A:Reference number: PH0971; MUID:92381444; PMID A:Accession: PH1091
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C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
C:Accession: S26462
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                                                                                                            A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-100 <KAV>
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100.0%; Pr
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Pred. No.
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Pred. No.
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A; Note: sequence extracted from NCBI backbone (NCBIP:70715)
R; Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A; Title: Variable region primary structures of monoclonal anti-DNA autoantibodies
A; Reference number: PL0198; MUID:90309768; PMID:2114528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A41940; MUID:92086633; PMID:1749770
A;Accession: A41940
A;Ctatus
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A;Title: An autoantibody to single-stranded DNA: comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Accession: PH1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig heavy chain V region (clone P17.80) - C;Species: Mus musculus (house mouse) C;Date: 30-Sep-193 #sequence_revision 3CC;Accession: PH1092
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                                                                                          F;101-110/Region: complementarity-determining
F;101-106/Region: D region
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                                                                  F;107-115/Region: JH region
                                                                                                                                                                                     C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-118 <SMI>
                                                                                                                                                                                                                                                                                                   A; Accession: PL0201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 07-May-1999
C;Accession: A41940; PL0201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region G2b, autoantibody BV04-01 - mouse (fragment) N;Alternate names: anti-DNA autoantibody BV04-01, heavy chain V regi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;34-119/Domain: immunoglobulin homology <IMM>
                                                                                                                                     F;31-35/Region: complementarity-determining 1
F;50-68/Region: complementarity-determining 2
                                                                                                                                                                                                                                   C; Superfamily: immunoglobulin V region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-110 <TIL>
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Query Match
Best Local Similarity
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  22.8%;
100.0%;
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  Score 28;
Pred. No.
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Pred. No. 4.6e-
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5.2e-21
  DB 2; L
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A;Cross-references: GB:S40679; NID:g252098; PIDN:AAB22669.1; PID:g252099
A;Experimental source: BALB/c mice, myeloma cell line NS-1
A;Note: sequence extracted from NCBI backbone (NCBIN:109337, NCBIP:109338)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;7-92/Domain: immunoglobulin homology <IMM>
R;Yamawaki-Kataoka, Y.; Honjo, T.
Nucleic Acids Res. 15, 5888, 1987
A;Title: Nucleotide sequences of variable region segments
                                                        RESULT 10
$00700
$00700
Ig heavy chain V region - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
C;Accession: $00700
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                                                                                                                                                                                                                                                                                                                                                 A:Experimental source: B cell, strain [NZB x NZW]F1 C:Superfamily: immunoglobulin V region; immunoglobu C:Keywords : heterotetramer; immunoglobulin E:15-100/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: PH1093
R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the A;Reference number: PH0971; MUID:92381444; PMID:151254
A;Accession: PH1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region (clone S17.161) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
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A; Residues: 1-101 <GAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R:Garcia, K.C.; Desiderio, S.V.; Ronco, P.M.; Verroust, P.J.; Amzel, L.M. Science 257, 528-531, 1992
A;Title: Recognition of angiotensin II: antibodies at different levels of A;Reference number: A42575; MUID:92342952; PMID:1636087
A;Accession: B42575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region (anti-angiotensin II) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 05-Dec:1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: B42575
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A; Residues: 1-110 <TIL>
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C;Superfamily: immunoglobulin V region; immuno
C:Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                   A;Cross-references: EMBL:223026; NID:g414023; PIDN:CAA6:561.1; PID:g414024 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                       R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigen
                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain - human (fragm
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence
C;Accession: S38488
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A;Title: Recombinant human Fab to 355-359, 1994
D: Reference number: A49590; MUID: 94105188; PMID: 8278393
A;Accession: E49590
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C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994
C;Accession: E49590
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A; Residues: 1-118 <YAM>
A; Cross references: EMBL; Y00380; NID: 964810;
A; Note: the sequence was determined from the
                                                                                                                                                                         A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-105 <MAR>
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A; Accession: S38488
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8.9e-10;
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8.4e-11;
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                       8.4e-09
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Ig heavy chain V region - human C;Species; Homo sapiens (man) C;Decies: Homo sapiens (man) C;Dete: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999 C;Accession: $20777 C;Accession: $20777 Schroeder, H.W. submitted to the EMBL Data Library, April 1992 A;Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire. A;Reference number: $20764 A;Accession: $20777 A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region (DA-5) - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
C;Accession: S46469
R;Cook, G.P.; Tomlinson, I.M.; Walter, G.; Riethman, H.; Carter, N.P.; Buluwela, L.; Win Nature Genet. 7, 162-168, 1994
A;Title: A map of the human immunoglobulin V(H) locus completed by analysis of the telom A;Reference number: S46460; MUID:95004581; PMID:7920635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ig heavy chain V region - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31678
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the A:Reference number: S31585
A:Accession: S31678
A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z29981; NID:g505463; PIDN:CAA82871.1; PID:g1335180 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z14169; NID:g31003; PIDN:CAA78538.1; PID:g31004 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;31-116/Domain: immunoglobulin homology <IMM>
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A;Molecule type: DNA
A;Residues: 1-34 <COO>
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A; Residues: 1-139 <CUI>
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A;Residues: 1-95 <MOR>
A;Cross-references: EMBL:Zl1947; NID:g33886; PIDN:CAA78004.1; PID:g33887 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
В
                        οy
                                                      Query Match
Best Local Similarity
Matches 15; Conserv
                           34 MNWVRQAPGKGLEWV 48
9 MNWVRQAPGKGLEWV
                                                         Conservative
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Search completed: November 27, Job time: 19.5212 secs 2002, 07:31:21

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  HV1A_RABIT
HV36_MOUSE
HV2B_RABIT
HV41_MOUSE
HV42_MOUSE
HV42_MOUSE
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HV47_MOUSE
HV48_MOUSE
HV48_MOUSE
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HV17_MOUSE
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HV01_RAT
HV3S_HUMAN
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HV3B_HUMAN
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429.695 Million cell updates/sec
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Compugen Ltd.
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p1875 homo sapien
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ID HV56_MOUSE
AC P18527;
OT 01-NOV-1990
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Result No.

332344 332344 332344 33234 33234 33234 33234 33234 33234 33234 33234 33234 33234 33234 33234

Minimum Maximum

Searched:

Run on:

Database :

| 45 | 44 | 43 | 42 | 41 | 40 | 39 | 38 | 37 | 36 | 35 | 34 |
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| 8.1 | 8.1 | 8.9 | 8.9 | 8.9 | 8.9 | 8.9 | 8.9 | 8.9 | 8.9 | 8.9 | 8.9 |
| 115 | 114 | 136 | 123 | 123 | 123 | 123 | 123 | 123 | 122 | 122 | 120 |
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| HV3D_HUMAN | HV01_CANFA | HV16_MOUSE | HV25_MOUSE | HV24_MOUSE | HV23_MOUSE | HV22_MOUSE | HV19_MOUSE | HV18_MOUSE | HV21_MOUSE | HV20_MOUSE | HV3E_HUMAN |
| | P01784 canis famil | | | | | | | | Rus | mus | P01766 homo sapien |

ALIGNMENTS

STANDARD;

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| 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) 19 heavy chain V region 6.96. Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. NCBI_TaxID=10090; [1] STRAIN=B9179149; PubMed=2499654; MEDLINE=89279149; PubMed=2499654; | 16 GSLKLSCAASGETE 29 | Query Match 11.4%; Score 14; DB 1; Length 97; Best Local Similarity 100.0%; Pred. No. 1.8e-07; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps | | -i- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY. PIR; JT0504; HVMS91. HSSP; P01810; 2FBJ. Interpro; IPR003006; Ig_MHC. | AIN-BALB/CJ; LINE-89279149; PubMed-2499654 / N.S., Maliphero U.V., Lebec rly onset of somatic mutation primary immune response."; pp. Med. 169-2007-2019(189) | 01-NOV-1990 (Rel. 16, Created) 01-NOV-1990 (Rel. 36, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) 19 heavy chain V region 914. Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID-10090; [1] SEQUENCE FROM N.A. |

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FROM A WALDENSTROM

Hilschmann

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Length 116;

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AN IGG1 MYELOMA

Euteleostomi;

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RESULT 3
HV3B_HUMAN
ID HV3B_HI
AC P01763
AC P01763
AC P01763
DT 21-JUL
DT 21-JUL
DT 21-JUL
DT SEQUEN
OC Mammal
OX NCBLT
RN SEQUEN
RX MEDLIN
RA GON1 F
RT JAMINO
RT GON1 F
RT GABLACT
RL Proc.
CC -1- MI
CC AG
CC AG
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CC TO AG
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CC SEQUEN
CX MART;

RESULT 4
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InterPro: IPR003596; Ig_v.
Pfam; PF00047; Ig; I.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
NON_TER 98 98
  HV3T_HUMAN
P01781;
21-JUL-1986
21-JUL-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Create
21-JUL-1986 (Rel. 01, Last s
15-JUL-1999 (Rel. 38, Last a
To heavy chain V-III region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gon1 F., Frangione B.;

"Amino acid sequence of the Fv region of a human monoclonal IgM
"Amino acid sequence of the Fv region of a human monoclonal IgM
(protein wEA) with antibody activity against 3,4-pyruvylated
galactose in Klebsiella polysaccharides K30 and K33.";
proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

1- MISCELLANEOUS: THIS CELAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
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InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
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J. Exp. Med. 169:2007-2019(1989).
-!- MISCELLANEOUS: THIS SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Early onset of somat
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  (Rel.
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                                                                     STANDARD;
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    01,
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100.08; Pr/
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                                                                     PRT;
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VH genes
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HV30_HUMAN
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SEQUENCE
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InterPro; IPR003596; Ig_v.
pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
NON_TER 116 116
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                                                                                                                                                                                                                        PIR; A02059; G1HUWS.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                               hypervariable regions.";
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                         "Variable region sequences of five human immunoglobulin heavy chains of the VH3 subgroup: definitive identification of four heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=74142702;
Capra J.D., Kehoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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21-JUL-1986 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-2002 (Rel. 41, Last annotation update) Ig heavy chain V-III region GAL. Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1975)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain type), subgroup H III. Architecture of the complete igM-molecule. Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=75059123; Watanabe S., Barn
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                                                                                                              Immunoglobulin V region.
                                                                                                                                                                                                                                                                                           -1- MISCELLANEOUS: THIS CHAIN WAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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Hoppe-Seyler's Z. Physiol. Chem.
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116 AA;
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117 t
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                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=4522793;
J.M.;
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THIS
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Pred. No
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    DB 1; 1
2.1e-07;
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P18524;
P18524;
O1-NOV-1990 (Rel. 16, Created)
O1-NOV-1990 (Rel. 16, Last sequence upda 15-JUL-1999 (Rel. 38, Last annotation up 15 heavy chain v region RF precursor. Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Manmalia; Eutheria; Rodentia; Sciurognat
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01-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig heavy chain V region 5-84 precursor.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                         HV54_MOUSE
P18525;
MEDLINE-89279149; PubMed-2499654;
Levy N.S., Malipiero U.V., Lebecque
"Early onset of somatic mutation in
                                                                  SEQUENCE FROM I
STRAIN-BALB/CJ
                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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14; Conser
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                                                                                   N.A.
                                                                                                                                                                                                                                                                                                              STANDARD;
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BY SIMILARITY.
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                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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S.G., Gearhart immunoglobulin
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P01770;
21-JUL-1986 (Rel. (
21-JUL-1986 (Rel. (
15-JUL-1999 (Rel. )
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SEQUENCE
                     MOD_RES
DISULFID
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"The rule of antibody structure. The primary structure monoclonal IgG1 immunoglobulin (myeloma protein Nie). chymotryptic peptides of the H-chain, alignment of the peptides and discussion of the complete structure."; Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
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DOMAIN
                                                                                                                                                                                                                                              Dreker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal IgGl immunoglobulin (myeloma protein NHe), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

"I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
SEQUENCE
                                                                            Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                    DISULFIDE BOND.
MEDLINE-77070267; PubMed-1002129;
COMMARZ J., Reichel W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the primary immune response.";
J. Exp. Med. 169:2007-2019(1989)
                                                                                                                                      HSSP; P01772; 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                        PIR; A02053; G1HUNI.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
19 heavy chain V-III region NIE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=77070269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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Pred. No.
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COMPLEMENTARITY - DETERMINING - 2
FRAMEWORK - 3.
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RA Capra J.D., Kehoe J.M.;
RI Capra J.
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Best Local :
MEDLINE-75046755; PubMed-4139708;
Capra J.D., Kehoe J.M.;
"Structure of antibodies with shared idiotypy: the complete sequence of the heavy chain variable regions of two immunoglobulin M anti-gamma globulins.";
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P01774;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
IG heavy chain V-III region POM.
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
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15-JUL-1999 (Rel. 38, Last annotation
19 heavy chain V-III region LAY.
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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P01775;
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DURING ISOLATION).
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2.1e-07;
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2.1e-07;
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RESULT 11
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HV3K_HUMAN
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Best Local
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                                                                                                                              HV3K_HUMAN
P01772;
                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
15 heavy chain V-III region KOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Amino acid sequence of the VH rec
cryoinmunoglobulin IGG Hil.";
Biochemistry 18:553-560(1979).
-!- MISCELLANEOUS: THIS CHAIN WAS
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15-JUL-1999 (Rel. 38, Last annott
1g heavy chain V-III region HIL.
Homo sapiens (Human).
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
NON_TER 119 119
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PIR; A02054; G1HUHL.
HSSP; P01772; 2FB4.
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MEDLINE-79124695; PubMed-420800;
MEDLINE-79124695; PubMed-420800;
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  Homo sapiens (Human Eukaryota; Metazoa;
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InterPro; IPR003596;
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121 AA;
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                   (Human)
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                                                                                                                                                    STANDARD;
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13566 MW;
Chordata;
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Pred. No.
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  Craniata;
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  Vertebrata;
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Mammalia;

Eutheria;

Primates; Catarrhini; Hominidae; Homo.

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RESULT
HV01_RA
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Best Local S
Matches 14
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MOD_RES 1
DISULFID 22
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"Three-dimensional structure determination of antibodies.
structure of crystallized monoclonal immunoglobulin IgG1 #
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
[2]
                                                        HV01_RAT
P01805;
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NON_TER
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Interpro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region; 3D-structure.
                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence upon 15-JUL-1999 (Rel. 38, Last annotation upon 15 heavy chain V region IR2 precursor.
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STRAND
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
NCBI_TaxID=10116;
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PIR; A02055; G1HUKL.
                                                                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin molecule Kol and its antigen-binding
and 1.0-A resolution.";
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MEDLINE-81072295; Pubmed-7441755;
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                                                                                                                                                                                                                   HELIX
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                                                                                                                 36 WVRQAPGKGLEWVA
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                                                                                                                                      Similarity
                                                                                                                                                          Conservative
                                                                STANDARD;
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Rođentia;
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                                                                                                                                      Score 14;
Pred. No.
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       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                PRT;
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2.2e-07;
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P01780;
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SEQUENCE
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SMART; SM00406; IGv; 1.
Immunoglobulin V region;
SIGNAL 1 19
                                                                                       Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region.
NON TER 115 115
SEQUENCE 115 AA; 12563 MW;
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                                                                                                                                                                                                                                                                  MEDLINE=74142702; PubMed=4522793; Capra J.D., Kehoe J.M.;
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
Ig heavy chain V-III region JON.
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SEQUENCE FROM N.A.
MEDLINE-83064537; PubMed-6292865;
Hellman L., Pettersson U., Engstro
                                                                                                                                                                                                                      hypervariable regions.";
Proc. Natl. Acad. Sci. U.S.A.
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InterPro; IPR003596; Ig_v.
                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                        "Variable
                                                                                                                                                                                                                                                                                            SEQUENCE
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; P01772; 2FB4.
WVRQAPGKGLEWV
             WVRQAPGKGLEWV
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                                             1 Similarity
13; Conser
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                                                                                                                                               IPR003006; Ig_MHC IPR003596; Ig_v.
                                                                                                                                                                                                                                          region sequences of five human immunoglobulin heavy chains subgroup: definitive identification of four heavy chain
                                          10.6%;
nilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 AA;
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142
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THE MRNA WAS ISOLATED FROM
HAT ARISES SPONTANEOUSLY IN
48
                    48
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Pred. No.
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Pred. No.
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WAS ISOLATED FROM
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                                           Mismatches
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RESULT 15 HV3Q_HUMAN

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Search completed: November 27, Job time: 12.8726 secs
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                                                                                                                                                                        Query Match 10.6%; Score 13; DB 1; Length 116; Best Local Similarity 100.0%; Pred. No. 2.3e-06; Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                         SEQUENCE.

SEQUENCE.

MEDILINE-74142702; PubMed-4522793;

Capra J. D., Kehoe J.M.;

"Variable region sequences of five human immunoglobulin heavy chains of the VH3 subgroup: definitive identification of four heavy chain hypervariable regions.";

Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).

-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGAI MYELOMA
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P01778;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
17 d heavy chain V-III region ZAP.

Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;
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ALIGNMENTS

6 Homo

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RESULT 1
208K68
ID 096K
AC 01-7
DT 01-7
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AN Ishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

AN Mishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

AN Takahashi M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

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                                                        32 YAMNWVRQAPGKGLEWV 48
51
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D0047; 19; 4.

PS00290; IG_MHC; UNKNOWN_1.

A94 AA; 53088 MW; 9AID7AEB5AEE4C0E CEC64;
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Pred. No.
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Q96BB9; O1-DEC-2001 (TrEMBLrel. 19, Cree
01-DEC-2001 (TrEMBLrel. 19, Last
01-MAR-2002 (TrEMBLrel. 20, Last
Hypothetical 65.0 kDa protein.
Homo sapiens (Human)
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Submitted (OCT-2001) to the EM
EMBL; BC015760; AAH15760.1; -.
Interpro; IPR003006; Ig_MHC.
Pfam; PF00047; 1g; 5.
PROSITE; PS00290; IG_MHC; UNKN
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01-MAY-2000 (TrEMBLrel. 13, Created)
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Myosin-reactive immunoglobulin heavy chain variable
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MEDLINE-98277139; PubMed-9614934;
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Mammalia; Eutheria; Primates;
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PROSITE; PS00290; IG_MHC; UNKNOWN_3.
Hypothetical protein.
SEQUENCE 597 AA; 65039 MW; 4FCA3;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                      D0633949F2AC149D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4FCA3AD8ECE263D9 CRC64;
                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kalis N.N.,
                                                                                                                                                                NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 AA
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                                                                                                                                                                                       DB 4;
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RESULT
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AC QS
DT 01
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Q9ULB6
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ID 08TC
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Human VH gene sequence.";
Submitted (NOV-1999) to the EI
EMBL; AB035268; BAAR7067.1; -
HSSP; P01772; 2FB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
Q9UL90;
Q9UL90;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8TC77;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2002 (TrEMBLrel. 21, Cr. 01-JUN-2002 (TrEMBLrel. 21, La: 01-JUN-2002 (TrEMBLrel. 21, La: Hypothetical 51.8 kDa protein. Hymosapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                      36 WVRQAPGKGLEWVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 MNWVRQAPGKGLEWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                           WVRQAPGKGLEWVA
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15; Conserv
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14; Conserv
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                                                                 PRELIMINARY;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                  Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL/GenBank/DDBJ databases
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata:
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90A8C6D16D22574A CRC64;
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                                                                                                                                                                                                                                                                                                                                                        Mismatches
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hes 0;
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5.1e-07;
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(TrEMBLrel.

13,

Created)

01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable

region

Homo sapiens (Human).

(Fragment).

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RESULT
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Best Local :
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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MEDLINE-98277139; PubMed-9614934;

MEDLINE-98277139; PubMed-9614934;

Van der Merwe P.L.,
                                                                                                                                                                                        NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLING-98277139; PubMed-9614934;
Mu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003596; Ig-
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                            Interpro; IPR003596; Ig. Pfam; PF00047; 1g; 1. SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998) EMBL; AF035021; AAD56257.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9UL93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF035024; AAI
HSSP; P01772; 2FB4
                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                 HSSP; P01772; 2FB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Myosin-reactive autoantibodies in rheumatic carditis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                         Young D.C.
                                                                                                                                                                                                                                                                                             InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                 "Myosin-reactive autoantibodies
                                      36
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  35
                       WVRQAPGKGLEWVA 49
WVRQAPGKGLEWVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 11.4%;
1 Similarity 100.0%;
14; Conservative
                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113
113 AA;
                                                                                                                                                                  116
116 AA;
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Primates;
  48
                                                                                                                                                                  12434 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12437 MW;
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                                                                                                 11.4%;
                                                                                                                                                                                                                                                                      Ig_v.
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                                                                                                                                                                                                                                                                                             Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14; DB; Pred. No. 1.7
0; Mismatches
                                                                                  0;
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                                                                                                   Score 14; DB 4;
Pred. No. 1.7e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87:184-192(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; |
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                  0DA0348154DD6061 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                 in rheumatic
                                                                                    Mismatches
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. 1.7e-06;
ches 0;
                                                                                               1.7e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Berney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berney
                                                                                                                       Length 116;
                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            region
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Best Local :
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Best Local
                                                                                                              EMBL; AF035030; AAD56;
HSSP; P01772; 2FB4.
InterPro; IPR003006;
InterPro; IPR003596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q920E7
Q920E7;
Q1-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047;
NON_TER 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Atkin J.D., Tape A., Jennings I.G., Horaitts O., Colon Pefinition of the Idiotope of Pterin-Mimicking Antibodi in Mammalian Cells.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF307937, AAL09421.1;
Interpro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                        NON_TER
                                                              SEQUENCE
                                                                                         Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                            Ol-MAY-2000 (TrEMBLrel. 13, Created)
Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                             Q9UL84;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                  Q9UL84
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                                                                                                                                                                                                  Wu X., Liu B.,
                                                                                                                                                                                                                                                                           Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                     fetus.";
                                                                                                                                                                               "Myosin-reactive autoantibodies in rheumatic carditis and
                                                                                                                                                                                          roung D.C.;
                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-98277139;
                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                   (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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36 WVRQAPGKGLEWVA 49
                                                                                                                                                                                                                                                                                                                                                                                                       GSLKLSCAASGFTF
                                                                                                                                                         Immunol. Immunopathol. 87:184-192(1998)
                   l Similarity 100.
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119 AA;
                                                             122
122 AA;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
cking anti-idiotope heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                AAD56266.1;
                                                                                                                                                                                                  PubMed=9614934;
n der Merwe P.L.,
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                                                              13579 MW;
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                                                                                                               Ig_MHC.
                              100.0%;
                                        11.48;
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                              Score 14;
Pred. No.
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                                                             36054D41366545B8 CKC54;
                    Mismatches
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hes 0;
                                        DB 4;
                              1.8e-06;
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                                       Length 122
                                                                                                                                                                                                   Berney
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                    Indels
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Murinae; Mus
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                                                                                                                                                                               normal
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Best Local S
Matches 14
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Q99KA4;
01-JUN-2001 (TrEMBLrel. 17, Crea
01-JUN-2001 (TrEMBLrel. 17, Last
01-DEC-2001 (TrEMBLrel. 19, Last
Hypothetical 52.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:96446; Igh-4.
Interpro; IPR003600; Ig_like.
Interpro; IPR0033006; Ig_MHC.
Interpro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00410; IG_like; 2.
                                                                 InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003600; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
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"Cloning of cDNAs encoding for anti-white pine blister rust me antibody (Mab 7, its light and heavy chains) and construction single chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF152372; AAD40243.1; -.
HSSP; P01842; TFAB.
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                                                                                                                                                                                                                                                                            Strausberg R.;
Submitted (MAR-2001) to the
EMBL; BC004786; AAH04786.1;
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Gammal heavy chain of Mab7 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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NON_TER 1 1
NON_TER 437 437
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Similarity 100.0%;
14; Conservative
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437 AA;
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   IG; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Rodentia;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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5.2e-06;
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RESULT 13
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ID Q9ULR9
AC Q9ULR9
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DE (Frag
OC Eukar
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RN (E1)
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Q8WUK1
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Best Local Similarity
Matches 14; Conserv
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InterPro; IPR003599; Ig_c1.

InterPro; IPR003597; Ig_c1.

InterPro; IPR003006; Ig_wHC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; Ig; 5.

SMART; SM00409; IG; 2.

SMART; SM00406; IGV; 1.

PROSITE; PS00290; IG_MHC; UNKNOWN_3.
         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE-98277139; PubMed-9614934;

Liu B., Van der Merwe P.L.
                                                                                                                                                                                                                                                                                                                                 PROSITE; PSOO
Hypothetical
SEQUENCE 61
                                                                                                                                                         Q9UL87 PRELIMINARY;
Q9UL87;
Q1-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00406; IGV; 1.
SMART; SM00410; IG_like; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein.
SEQUENCE 487 AA; 52554 MW; 7DC8E
                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                          Myosin-reactive
                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAR-2002 (TrEMBLrel. 20, La
01-JUN-2002 (TrEMBLrel. 21, La
Hypothetical 67.3 kDa protein.
                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (DEC-2001) to the
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                                                                                                             (Fragment)
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EMBLrel. 19, Last annotation update)
immunoglobulin heavy chain variable
                                                                             Chordata;
Primates;
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Primates;
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100.0%;
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Pred. No.
                      P.L.,
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                                                                             Craniata; Vertebrata: Catarrhini; Hominidae;
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Myosin-reactive autoantibodies

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Interpro; IPR003006; I
R Interpro; IPR003596; I
R Interpro; IPR003596; I
R Pfam; PF00047; I; 1
SMART; SM00409; IG; 1
SMART; SM00406; IGV; 1
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Best Local 9
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EMBL; AB049915; BAB16829.1; -. HSSP. P01772; 2FB4.
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NON_TER
SEQUENCE
                                                              09UGP3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Immunoblobulin heavy chain (Fragment).
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Single chain Fv (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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EMBL; AF035027; AA
HSSP; P01810; 2FBJ
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InterPro; IPR003596; Ig_v.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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15 WVRQAPGKGLEWV 27
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les 13; Conserv
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IG_11ke; 1.
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11598 MW;
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EMBL; AJ132560; CAB65
HSSP; P01772; 2FB4.
                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                         Krambovitis E.;
"Induction of somatic mutations in human B cells by in vitro immunization.";
                                                                                                                                                                                                                                                                         Zafiropoulos A., Kandilogiannaki M., Dahlenborg
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                    InterPro; IPR003006; Ig_MHC InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                            19
                                                               36 WVRQAPGKGLEWV 48
                                            WVRQAPGKGLEWV
                                                                                     l Similarity
13; Conserv
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112
112 AA;
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                                                                                  10.6%; 5cc.
100.0%; Pr
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Pred. No.
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hes 0;
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Perfect score:
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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US-08-765-469-1
US-08-31-055-46
PCT-US-31-055-46
PCT-US-31-055-46
US-07-934-373C-48
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US-07-934-373C-48
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US-08-437-6428-45
US-08-437-6428-45
US-08-146-206C-20
US-08-146-206C-20
US-08-146-206C-20
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Result

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| 117 | 116 | 116 | 116 | 116 | 116 | 116 | 116 | 116 | 112 | 111 | 109 | 98 | 98 | 461 | 461 | 461 | 461 |
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| US-08-545-809A-107 | PCT-US93-10555-10 | US-09-234-340A-50 | US-09-121-952A-50 | US-09-026-985-50 | US-08-804-444A-50 | US-09-184-658-48 | US-09-027-449-50 | US-08-428-197-10 | US-08-211-202-133 | US-08-211-202-134 | US-08-379-057-32 | US-08-665-202-31 | US-08-211-202-116 | PCT-US91-09133-27 | US-08-923-854-26 | US-08-463-667A-4 | US-08-463-587A-26 |
| Sequence 107, App | Sequence 10, Appl | | | Sequence 50, Appl | | | 50, | | • | Sequence 134, App | | Sequence 31, Appl | Sequence 116, App | | Sequence 26, Appl | Sequence 4, Appli | Sequence 26, Appl |

ALIGNMENTS

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US-08-767-128-24
                                                                                                                                                                    COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEQ Version 1.5
CURRENT APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-UUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-CCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-UUN-1995
PRIOR APPLICATION NUMBER: 08/462,798
FILING DATE: 05-UUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CAITER, CHAILES G.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3100 NO. 0.1
STREET: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt STREET: 3100 No. 6111079west Center, 90 South Seventh St
                                                                       REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENERAL INFORMATION: WYLIE, DWANE E.
APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
                                                                                                                                                  NAME: Carter, Charles G. REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24, Application US/08767128
5, 6111079
                                               612/332-9081
                                                                                                     35,093
35,093
mmR: 8648.49USF1
  24:
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SEQUENCE CHARACTERISTICS:

LENGTH:

110 amino acids

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FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-767-128-24
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US-08-767-128-36
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: PHYPOTHETICAL: NO ANTI-SENSE: NO
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APPLICANT:
APPLICANT:
                                                              REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION: 612/371-5278
                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                   APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                         FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/767,128 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
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                                                                                                                                                                          APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Merchant, Gould, Smith, Edell, Welter & Schmid 3100 No. 6111079west Center, 90 South Seventh St
                                             612/332-908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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"TER: 35,093
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; ORIGINAL SOURCE:
US-08-767-128-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-442-542-2
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Best Local S
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APPLICANT: CATOZZI, Nadine B.
APPLICANT: KOZIEL, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
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                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/267,641
FILING DATE: 28-JUN-11994
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                               33 AMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Spruill, W. Murray REGISTRATION NUMBER: 32, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 16-MAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Clda ucay, company: 7 Skyline Drive
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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AMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                      Similarity
28; Conserv
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   amino acid

GY: linear
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linear
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                                                                                                                      Conservative
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16-MAY-1995
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                                                                                                                   22.8%; Score 28; DB 100.0%; Pred. No. 3e tive 0; Mismatches
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Pred. No.
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                                                                                                                                                      DB 1;
3e-19;
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22.8%; Score 28; DB 1; Length 599; nilarity 100.0%; Pred. No. 1.2e-18; Conservative 0; Mismatches 0; Indels
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Sequence 18, Application US/08765469
Patent No. 6069301
Sequence 18, Application US/08765469
Patent No. 6069301
APPLICANT: Carcazi, Nadine B.
APPLICANT: Koziel, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCES. 49
ADDRESSEE: Ciba-Geigy Corporation
  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,542 FILING DATE: 16-MAY-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM.TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,469
                                                       FILING DATE: 16-MAY-1995
CLASSIFICATION: 530
PRIOR PAPLICATION DATE: 30
PRIOR PAPLICATION DATE: 08/267,641
FILING DATE: 28-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: SPILII, W MULTAY
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REFERNEX/POCKET NUMBER: CGC 1750
TELEPHONE: 919-541-8615
TELEPHONE: 919-541-8615
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
TENTY: 599 amino acids
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REGIGTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC 1750
TELECOMMUNICATION INFORMATION:
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: 7 Skyline Drive
Hawthorne
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/267,641
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amino acid
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
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Matches 28; Conserve
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TOPOLOGY: linear
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10532
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COUNTRY:
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             Sequence 2, Application US/08765469

Patent No. 6069301

GENERAL INFORMATION:

APPLICANT: Carcal, Michael G.

TITLE OF INVENTION: Antibodies which Bind to Insect Gut

TITLE OF INVENTION: Antibodies which Bind to Insect Gut

TITLE OF INVENTION: Antibodies which Bind to Insect Gut

TITLE OF INVENTION: Antibodies and their Use

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ciba-Geigy Corporation

STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 119; 3e-19;
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Patent No. 5686600
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine B.
APPLICANT: Koziel, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
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STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/765,469
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/267,641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFRENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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US-08-765-469-2
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VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES THEREOF
                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/428,197
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC CompALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17; DB 2; LA
Pred. No. 6.5e-09;
                                                                                           ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
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1880 Century Park East - Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/10555
FILING DATE: 29-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 46, Application PC/TUS9310555 GENERAL INFORMATION:
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: FI
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TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 113 amino acids
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Best Local Similarity 100.
Matches 17; Conservative
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TITLE OF INVENTION: VARI
TITLE OF INVENTION: PHER
TITLE OF INVENTION: THER
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-428-197-46
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STATE: California
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PCT-US93-10555-46
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for Prognosticating Responses to Cancer
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                                                            Length 599;
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Patent No. 5891438
GENERAL PROMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Richard J. Rodrick, Becton, Dickinson ADDRESSEE: Company STREET: Becton Drive CITY: Franklin Lakes STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,113
FILING DATE: 07-OCT-1993
                                                              DB 3; Le
1.2e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17; DB 1; I
Pred. No. 1.5e-09;
                                                          Query Match 22.8%; Score 28; DB Best Local Similarity 100.0%; Pred. No. 1.5 Matches 28; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                    187 AMNWVRQAPGKGLEWVARIRSKSNNYAT 214
                                                                                                                                           33 AMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bacus, Sarah S
APPLICANT: Yarden, Yosef
APPLICANT: Yarden, Yosef
APPLICANT: Sela, Michael
TITLE OF INVENTION: Methods and Con
TITLE OF INVENTION: Therapy and for TITLE OF THE PERSON THERAPY
NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.8%; Sc.
100.0%; Pre
0;
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Patent No. 5514554
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: H49het, David W
REGISTRATION NUMBER: 30.265
REFERENCE/DOCKET NUMBER: P-26:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 847.5317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
; MOLECULE TYPE: protein US-08-765-469-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-428-197-46
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                                                                                                                                                                                                                                                               US-08-050-113-1
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Best Local :
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APPLICANT.

APPLICANT.

APPLICANT.

APPLICANT.

TITLE OF INVENTION: WARTHOD FOR STIMULATING PRODUCTION OF

TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES THROUGH

TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUGATES

TITLE OF INVENTION: THEREOF

CORRESPONDENCES.

ADDRESSEE: Spensley Horn Jubas & Lubitz
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Length 113;
                                                      Indels
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FD-2630

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Length 120;
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US-07-934-373C-44
; Sequence 44, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
    APPLICANT: Paul J. Carter
    TITLE OF INVENTION:
    TITLE OF INVENTION: Immunoglobulin Variants
    TUMBER OF SEQUENCES: 48
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Genentech, Inc.
    STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.0%; Score 16; DB 2; Le
100.0%; Pred. No. 6e-08;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER TEADABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TEM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILLING DATE: 21-Aug-1992
CLASSIFICATION: 530
                                                                                                                           US-07-934-373C-42

Sequence 42, Application US/07934373C

Patent No. 5821337

Patent No. 5821337

CENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 42:
                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                       STREET: 1 DNA way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
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Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              94080
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                                                                                                                                                                                                                                                                                                                       13.8%; Score 17; DB 5; Length 113; 100.0%; Pred. No. 6.5e-09;
                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compactable OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/07934373C
Patent No. 582137
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P0709P2
ATTORNEY/AGENT AND STATE OF THE NOVELLS, SECOTE NAME: NAME: NAME: 34,842
REGISTRATION NUMBER: 56.22
TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 455-5100
TELEPHONE: (619) 455-5100
INFORMATION FOR SEQ ID NO: 46: SEQUENCE CHARACTERISTICS: LENGTH: 113 amino acid
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lee, Wendy M. REGISTRATION NUMBER: 40,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 120 amino acids
TYPE: Amino Acid
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Best Local Similarity 100.0
Matches 16; Conservative
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                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-10555-46
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TELEFAX: 6
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Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
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REFERENCE/DOCKET NUMBER: P0709P2C1
FELECOMMUNICATION INFORMATION:
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFRAX: 650/925-9881
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 120 amino acids
Amino Acid
                                                                                                                       LENGTH: 120 amino acids
                                                                                                                                                                                                    Query Match 13.0
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                           36 WVRQAPGKGLEWVARI 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    650/952-9881
                                                                                                                                   TYPE: Amino Acid;
TOPOLOGY: Linear
US-07-934-373C-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94080
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US-08-437-642B-2
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US-07-934-373C-48
Sequence 48, Application US/07934373C
Patent No. 5821337
GENERAL INFORMATION:
APPLICANT: Leonard G. Presta
TILE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
CONTEX: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USAN COMPUTER: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: Winderin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
                      COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 18M PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/O7/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
RICH APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M:
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECHONE: 650/255-1994
TELECHONE: 650/255-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 16; DB 2;
Pred. No. 6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 13.0
Best Local Similarity 100.
Matches 16; Conservative
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                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA

ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINPALIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,642B
FILING DATE: 09-M84-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
RECISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECHOMNICATION INFORMATION:
TELEPHONE: 650/252-1981
TELEPHONE: 650/252-1981
TELEPHONE: 650/952-9881
TELEFAX: 650/952-1981
TELEFAX: 650/952-1981
TELEFAX: 650/952-1981
                                                                                                                                                              RESULT 15
US-08-437-642B-42
; Sequence 42, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INFORTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.0%; Score 16; DB 3; Best Local Similarity 100.0%; Pred. No. 6e-08; Matches 16; Conservative 0; Mismatches (
Best Local Similarity 100.0%; Pred. No. 6e-08; Matches 16; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Genericch, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 120 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-42
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Sequence 16, Appl
Sequence 34, Appl
Sequence 12, Appl
Sequence 10, Appl
Sequence 100, Appl
Sequence 12, Appl
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                                                                                                                                                             November 27, 2002, 07:28:06; Search time 11.3977 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 87,
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1 EVMLVESGGGLVQPKGSLKL.....SGIDYAMDYWGQGTSLTVSS 123
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/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/USOG_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USOT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/USOT_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/USOT_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-881-823-16
US-09-835-087-8
US-09-807-39-12
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337
347
371
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171
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171
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Maximum DB
                                                                                                          OM protein
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                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                Run on:
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| Sequence 17, Appl | Sequence 18, Appl | Seguence 104, App | Seguence 11, Appl | Sequence 1, Appl1 | Sequence 4, Appl1 | Sequence 47355, A | Sequence 2, Appli | Sequence 108, App | Sequence 112, App | 11 | Seguence 118, App | Sequence 7, Appli | Sequence 14, Appl | Sequence 127, App | 81, | 110, | Sequence 35, Appl | Sequence 33, Appl | Sequence 64, Appl | _ | Sequence 51, Appl | Sequence 48, Appl | Sequence 49, Appl | Sequence 38, Appl | Sequence 39, Appl |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|---------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|-------------------|--------------------|------------------|-------------------|-------------------|-------------------|-------------------|------|-------------------|-------------------|-------------------|-------------------|-------------------|
| US-09-840-459-17 | US-09-840-459-18 | US-09-840-459-104 | US-09-971-543-11 | US-09-971-543-1 | US-10-066-895-4 | US-09-864-761-47355 | US-09-974-449-2 | US-09-056-160B-108 | US-09-056-160B-112 | US-09-056-160B-116 | US-09-056-160B-118 | US-09-056-160B-7 | US-09-056-160B-14 | US-09-056-160B-127 | US-09-850-165-81 | US-09-850-165-110 | US-09-974-449-35 | US-09-253-794-33 | US-09-828-708-64 | 5 | US-09-840-459-51 | US-09-840-459-48 | US-09-840-459-49 | 09-84 | US-09-840-459-39 |
| 10 | 10 | 10 | 10 | 10 | 12 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
| 117 | 117 | 119 | 120 | 252 | 98 | 103 | 115 | 118 | 118 | 118 | 118 | 123 | 123 | 123 | 128 | 128 | 218 | 14 | 14 | 87 | 88 | 68 | 8 | 86 | 96 |
| 13.8 | 13.8 | 13.8 | 13.0 | 13.0 | 12.2 | 12.2 | 12.2 | 12.2 | 12.2 | 12.2 | 12.2 | 12.2 | 12.2 | 12.2 | 12.2 | 12.2 | 12.2 | 11.4 | 11.4 | 11.4 | 11.4 | 11.4 | 11.4 | 11.4 | 11.4 |
| 17 | 17 | 17 | 16 | 16 | 15 | 15 | 15 | 15 | 15 | 1.5 | 1.5 | 15 | 15 | 15 | 15 | 15 | 15 | 14 | 14 | 14 | 14 | 14 | 14 | 14 | 14 |
| 20 | 21 | 22 | 23 | 24 | 25 | 36 | 27 | 28 | 29 | 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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DESCURE 87, APPLICATION US/09893615

SEQUENCE 87, APPLICATION US/09893615

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CONTRY 094

CONTRY 094

COMPUTER TRADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPUTIBLE
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COMPUTER
COMPUTER: IBM PC COMPUTER
COMPUTER
COMPUTER: IBM PC COMPUTER
CO
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Gaps

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Indels

Length 143;

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GENERAL INFORMATION:
APPLICANT: Wayne W. Hancock
TITLE OF INVENTION: Method of Treating Graft Rejection Using
TITLE OF INVENTION: Inhibitors of CCR2 Function
FILE REPERENCE: 1855.2008-003
CURRENT APPLICATION NUMBER: US/09/835,087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL NICORAGIO DE LA GENERAL MINTORNA GENERAL MINTORNATION CAPILICANT: LAROSA, Gregory J. APPLICANT: LAROSA, Gregory J. APPLICANT: Horvath, Christopher APPLICANT: Horvath, Christopher APPLICANT: O'BILEN, Slobhan H. APPLICANT: O'BILEN, Slobhan H. APPLICANT: O'BILEN, SLOBhan H. APPLICANT: O'REFE, Theresa TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND FILE REFERENCE: 1855 1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR PELICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10; L. 7.4e-15;
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9.2e-23;
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                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.0%; Pred. No. 9.3
Matches 33; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                     26.8%; Score 33; 100.0%; Pred. No.
                   CURRENT APPLICATION NUMBER: US/09/881,8:
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 07/378,577
PRIOR FILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/09840459 Patent No. US20020150576A1
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US-09-815-087-8
Sequence 8, Application US/09835087
; Patent No. US20020042370A1
    FILE REFERENCE: 22851-032
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; ORGANISM: Murine
US-09-881-823-16
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US-09-840-459-34
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Pred. No. 2.4e-27;
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APPLICANT: HOTVATION:
APPLICANT: HOTVATH, Christopher
APPLICANT: Newman. Walter
APPLICANT: Newman. Walter
APPLICANT: O'Brien, S. Tarran
APPLICANT: O'Brien, S. Tarran
APPLICANT: O'Reien, S. Tarran
APPLICANT: O'Reien, S. Tarran
APPLICANT: O'Reien, S. Tarran
APPLICANT: O'Reien, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED
TITLE OF INVENTION: HUMBER: U$/09/840,459
CURRENT APPLICATION NUMBER: U$/09/840,459
CURRENT FILING DATE: 2000-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/397,625
PRIOR APPLICATION NUMBER: 09/397,635
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-23
NUMBER OF SED ID NOS: 107
SOFTWARE: FASTSED for Windows Version 3.0
                                                                   100.0%; Score 123; DB 10;
100.0%; Pred. No. 4.5e-103;
Live 0; Mismatches 0;
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100.0%; Pred. No. ...
0; Mismatches
; SEQUENCE DESCRIPTION: SEQ ID NO: 87: US-09-893-615-87
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Patent No. US20020068066A1
GENERAL INFORMATION:
APPLICANT: SHI, WENYUAN
APPLICANT: ANDERSON, MAXWELL
APPLICANT: TRINH, RYAN
APPLICANT: TRINH, RYAN
APPLICANT: WINS, LETITIA
APPLICANT: WINS, LETITIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 35, Application US/09840459
Patent No. US20020150576A1
GENERAL INFORMATION:
                                                                                         Best Local Similarity 100.
Matches 123; Conservative
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Best Local Similarity 100.
Matches 38; Conservative
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US-09-840-459-35
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US-09-881-823-16
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LENGTH: 100
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Query Match
Best Local Similarity 100.0%; Pred. No. 8.3e-15;
Matches 24; Conservative 0; Mismatches 0; Indels
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                  GENERAL INVORMATION

APPLICANT: LARGAS, Gregory J.
APPLICANT: LARGAS, Gregory J.
APPLICANT: Newman, Walter
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Brien, Siobhan H.
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED OF USE THEREFOR
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: DOT/02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-07-22
PRIOR PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1999-07-23
SOFTWARRE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-9840-459-100
Sequence 100, Application US/09840459
Patent No. US20020150576A1
GENERAL INFORMATION:
APPLICANT: LARGESA, Gregory J.
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: O'Brien, Slobhan H.
CHERESE INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED PRICE
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: US/09/840,459
PRIOR FILING DATE: 2001-02-03
PRIOR PRICE TILING DATE: 2000-02-03
PRIOR PRILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEO ID NOS: 107
SEQ ID NOS: 107
SEQ ID NO 100
LENGTH: 148
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; ORGANISM: Mus musculus
US-09-840-459-100
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COCATION: (1)...(117)

COCATION: (1)...(117)

COCATION: (1)...(117)

COCATION: (31)...(35)

COCATION: (31)...(35)

COCATION: (50)...(68)

COCATION: (50)...(68)

COCATION: (50)...(68)

COCATION: (101)...(106)

COCATION: (101)...(106)
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; LOCATION: (1)...(117)
; OTHER INFORMATION: Murine mAb 1D9 heavy chain variable region US-09-035-087-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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Fatent No. US200201063691
GENERAL INFORMATION:
APPLICANT: Horvath, Christopher J.
TITLE OF INVENTION: Method of Inhibiting Stenosis and
TITLE OF INVENTION: Restenosis
FILE REFERENCE: 1855.1069-003
CURRENT ELLING DATE: 2000-01-03-15
PRIOR APPLICATION NUMBER: US/09/809,739
PRIOR PELING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 117
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                                                                                                                                                                                                                                                                                                                                                                                              19.5%; Score 24; DB 10; I 100.0%; Pred. No. 8.3e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 09/549,448
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 117
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; Patent No. US20020150576A1
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Matches 24; Conservative
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ORGANISM: Mus Musculus
FEATURE:
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ORGANISM: Unknown
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US-09-840-459-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lenith 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia E.
JITLE OF INVENTION: Method of Inhibiting Stenosis and
TITLE OF INVENTION: Restenosis
FILE REFERENCE: 1855.1069-003
CURRENT APPLICATION NUMBER: US/09/809,739
CURRENT FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: US 09/528,267
PRIOR PILING DATE: 2000-03-17
NUMBER OF SEC ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEC ID NO 22
LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Horvath, Christopher J.
APPLICANT: Rao, Patricia E.
TITLE OF INVENTION: Method of Inhibiting Stenosis and
TITLE OF INVENTION: Restenosis
FILE REPERBEC: 1855.1069-003
CURRENT APPLICATION NUMBER: US/09/809,739
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: US 09/528,267
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 17.1%; Score 21; DB 10; I
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Humanized sequence US-09-809-739-22
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  GENERAL INFORMATION:
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US-09-809-739-23
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Sequence 12, INPORMATION:

Patent No. US20020042370A1

GENERAL INPORMATION:

APPLICANT: Wayne W. Hancock

TITLE OF INVENTION: Method of Treating Graft Rejection Using

TITLE OF INVENTION: Inhibitors of CCR2 Function

FILE OF INVENTION: Inhibitors of CCR2 Function

CURRENT FILING DATE: 2008-0935,087

CURRENT APPLICATION NUMBER: US/09/835,087

FILE REFERENCE SEQ 10 NATE: 2000-04-14

NUMBER OF SEQ ID NOS: 19

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12

EBNOTH 117
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Fatent No. US/0020042370A1
GENERAL INFORMATION:
APPLICANT: Wayne W. Hancock
TITLE OF INVENTION: Method of Treating Graft Rejection Using
TITLE OF INVENTION: Inhibitors of CCR2 Function
FILE REFERENCE: 185.2006-003
CURRENT APPLICATION NUMBER: US/09/835,087
CURRENT PILING DATE: 2000-043
PRIOR PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-04-14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
LENGTH: 117
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; Patent No. US20020106369A1
                          23 LVESGGGLVQPKGSLKLSCAASGF 46
4 LVESGGGLVQPKGSLKLSCAASGF 27
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Conservative
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US-09-835-087-13
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US-09-809-739-22
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Sequence 12, Application US/09828708

Sequence 12, Application US/09828708

Patent No. US20020146753A1

GENERAL INFORMATION:
APPLICANT: Ditzel, H.
APPLICANT: Burton, D.
APPLICANT: Schaller, M.
TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their part
TITLE OF INVENTION: autoimmune disease
FILE REFERENCE: 1361.005US1
CURRENT APPLICATION NUMBER: US/09/828,708
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 13.8%; Score 17; DB 10; 1
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 17; Conservative 0; Mismatches 0;
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TYPE: PRT
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APPLICANT: Nowman, Walter
APPLICANT: JONES, S. Tarran
APPLICANT: O'BRIEN, Slobhan H.
APPLICANT: O'Reffe, Thereso
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMBRE: 0.02
CURRENT APPLICATION NUMBER: PCT/USO1/03537
PRIOR PILING DATE: 2001-02-02
PRIOR PLILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
PRIOR PLICATION NUMBER: 09/121,781
PRIOR PLICATION NUMBER: 09/121,781
PRIOR PLICATION NUMBER: 09/121,781
PRIOR APPLICATION NUMBER: 09/121,781
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TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND TITLE OF INVENTION: METHODS OF USE THEREFOR
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                        TITLE OF INVENTION: METHODS OF USE THEREFOR FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 1909-07-02
PRIOR PILING DATE: 1999-07-22
PRIOR PILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 117
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Sequence 20, Application US/09840459
Sequence 10, US20020150576A1
GENERAL INFORMATION:
APPLICANT: LAROSA, Gregory J.
APPLICANT: Horvath, Christopher
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Length 116; undels

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; Search time 1253.48 Seconds (without alignments) 7383.171 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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318
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em_htgo_mus:* em_htgo_other:* em_htg_other:* em_v1:* em_htg_hum:* em_htg_inv:* em_htgo_hum:* em_htg_mam:* em_htg_vrt:* em_htg_mus: * em_htg_pln:* em_htg_rod:* gb_ro:* gb_sts:* em_fun:* em_hum:* em_pl:* em_ro:* em_sts:* gb_sy:* gb_un:* gb_vi:* em_pat:* gb_ba:* gb_htg:* gb_in:* gb_ov:* gb_pat:* gb_ph:* em_ba:* еш_оv:* em_in:* em_mu:* gb_pl:* gb_pr:* em_or: em_un: gb_om: * em_om: em_sy:

Pred. No. is the number of results predicted by chance to have a

AF178619 318 bp mRNA linear ROD 22-MAY-2000 Mus musculus 8-3 immunoglobulin light chain variable region mRNA,

partial cds. AF178619 AF178619.1 GI:5853221

DEFINITION

ACCESSION

RESULT 1 AF178619 LOCUS Mus musculus. Mus musculus

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

ALIGNMENTS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 318)
Putterman,C., Deocharan,B. and Diamond,B.
Molecular analysis of the autoantibody response in peptide-induced

AR096196 Sequence
AR210595 Sequence
AR210512 Sequence
AR210595 Sequence
AR096195 Sequence
AR096195 Sequence
AR210594 Sequence
AR210594 Sequence
AR710594 Mus muscu
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A81397 Sequence 17
AR182927 Sequence 27
AR085831 Sequence 57
AR085831 Sequence 57
AR085831 Sequence 57
AR00422 Sequence 52
AR182965 Sequence 62
AX182965 Sequence 14
AX058906 Mus muscu
U37887 Mus muscu AX256247 Sequence AF77092 Synthetic AX057984 Sequence AX057947 Sequence AX057947 Sequence AY049714 Synthetic score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES AR210595 AR096128 AR210527 AR210594 AR210594 AR178620 MMU231219 S48339 MUSIGKAFE MUSIGKAAR 110 AF178620 10 AMU321319 10 AF137625 10 AF137625 10 AF137625 10 AF137625 10 AF137625 10 AMSIGKAFE 10 AF129247 10 AF129237 10 AF26630 10 AF26630 11 AF26630 6 AX56247 6 AX567945 6 AX657945 6 AX657945 MUSIGKAFI AF206030 MUSIGKCNA AF139231 A20585 A83197 AF178619 AR096196 MMIGVKP4 AY049714 AR182927 A51863 A83237 AR085831 AR182961 AX000421 A83232 AR182956 10 765 1239 1280 403 403 Length 293 360 321 318 318 300 Match Query 131 131 131 131 125 126 120 120 120 120 Score Result S. U

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PAT 20-JUN-2002
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                                                                    52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGACCAGCAGC 111
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                          Gaps
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1 (bases 1 to 318)

Blackburn, Meal., Church, W. Robert., Feuerstein, G. Zee Gross, M. Stuart., Nichols, A. John., Padlan, E. Agustin., Patel., A. Haribhai. and Sylvester, D. Robert.

Patel. factor IX/IXa antibodies
Patent: US 6391299-A 104 21-MAY-2002;
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Sequence 104 from patent US 6391299.
AR210595. GI:21513363
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6 from patent US 6005091.
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           99.68;
           Best Local Similarity 99.6
Matches 222; Conservative
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Matches
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ACCESSION
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ORIGIN
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FEATURES
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AR210595
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KEYWORDS
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KEYWORDS
SOURCE
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AR096128
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PWISATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQOWSSNPPTFGGGTK
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                                              (bases 1 to 318)

2 (bases 1 to 318)

Putterman,C., Deocharan,B. and Diamond,B.

Direct Submission

Submitted (17-1999) Rheumatology/Medicine, Albert Einstein

College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 CAGCAGAAGCCAGGATCCTCCCCCAAACCTGGATTTCTGCCACATCCAACCTGGCTTCT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 GGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGC 225
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                                                                                                                                                                                                                                                                                          /product="immunoglobulin light chain variable region"
/protein_id="AAD54372.1"
/db_xref="GI:5853222"
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Blackburn, M.Neal., Church, W.Robert., Feuerstein, G.Zeev., Gross, M.Stuart., Nichols, A.John, Paddlan, E.Agustin., Patel, A. Haribhai. and Sylvester, D.Robert.
Nucleic acids encoding immunoglobulin domains
Patent: US 6005091-A 104 21-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 318;
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                                                                                                                                                                                                                                                                /note="IgM kappa; anti-peptide antibody"
                                                                                                                                                                /organism="Mus musculus"
/strain="AALB/c"
/db_xxef="taxon:10090"
/cell_line="8-3"
/cell_type="hybridoma"
/note="from peptide-immunized mouse"
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 199; DB 10; Pred. No. 1.5e-110;
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100.0%; Pred. No. 1.....
'... 0; Mismatches
                   J. Immunol. 164 (5), 2542-2549 (2000) 20143847
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Sequence 104 from patent US 6005091.
AR096196.1 GI:10024781
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1. .318
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Best Local Simi
Matches 199;
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AR096196
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20-JUN-2002
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Blackburn, M. Neal., Church, W. Robert., Feuerstein, G. Zeev., Gross, M. Stuart., Nichols, A. John., Padlan, E. Agustin., Patel, A. Haribhai. and Sylvester, D. Robert.
Nucleic acids encoding immunoglobulin domains
Patent: US 6005091-A 102 21-DEC-1999;
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Blackburn, M.Neal., Church, W.Robert., Fewerstein, G.Zeev., Gross, M.Stuart., Nichols, A.John., Padlan, E.Agustin., Patel, A. Haribhai. and Sylvester, D.Robert.
Anti-factor IX/IXa antibodies
Patent: US 6391299-A 102 21-MAY-2002;
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Pred. No. 6.2e-94;
0; Mismatches 1;
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Pred. No. 6.2e-94;
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Sequence 102 from patent US 6391299.
AR210594
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                                                                     Sequence 102 from patent US 60 AR096195
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1. .335
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97 c 85 q
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97 c 85 g
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99.6%;
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99.68;
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Blackburn,M.Neal., Church,W.Robert., Feuerstein,G.Zeev.,
Gross,M.Stuart., Nichols,A.John., Padlan,E.Agustin.,
Patel,A.Haribhai. and Sylvester,D.Robert.
Anti-factor IX/Txa antibodies
Patent: US 6331299-A 6 21-MAY-2002;
Location/Qualifiers
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             Feuerstein, G. Zeev.,
          Blackburn, M. Neal., 'Church, W. Robert., Feuerstein, G. Gross, M. Stuart., Nichols, A. John., Padlan, E. Agustin., Patel, A. Haribhai. and Sylvester, D. Robert.
Nuclet, acids encoding immunoglobulin domains
Patent: US 6005091-A 6 21-DEC-1999;
                                                                                                                                                                          Length 321;
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Pred. No. 6.2e-94; (
Mismatches 1; Indels
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Pred. No. 6.2e-94;
0; Mismatches 1;
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Sequence 6 from patent US 6391299.
AR210527
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92 c 79 g
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(bases 1 to 321)
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Best Local Simi
Matches 222;
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                                                        TITLE
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AR210527
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Mus musculus.

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 767)

Schaeble,K.F., Thiebe,R., Bensch,A., Brensing-Kneppers,J., Heim,V.,

Ritschbaum,T., Lamm,R., Ohnrich,M., Pourrajabi,S.,

Roeschenthaler,F., Schwendinger,J., Wichelhaus,D. and Zocher
                                                                                                                  ROD 02-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-DEC-1998) T. Kirschbaum, Adoli-Butenandt-Institut
fuer, Physiologische Chemie, Schillerstr. 44, D-80336 Muenchen, FRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MDFQVQIFSFLLISASVIMSEG01VLSQSPAILSASPGEKVTMT
CRASSSVSYMHWYQQKPGSSPKPWIYATSNLASGVPARFSGSGSGTSYSLTISRVEAE
DAATYYCQQMSSNPP"
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Characteristics of the immunoglobulin Vkappa genes, pseudogenes,
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/protein_id="CAB46133.1"
/db_xref-"G1:5305000"
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IgVk gene; immunoglobulin; kappa light chain; variable region.
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/gene="am4"
/note="heptamer recombination signal"
724. .732
         264 GCAGTGGAGTAACCCACCACCATCGGAGGGGGGACCA 304
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/clone_lib="mouse cosmid library"
68. .732
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Eur. J. Immunol. 29 (7), 2082-2086 (1999)
                                                                                                                  DNA
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/gene="am4"
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    .767
    /organism="Mus musculus"

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/db_xref="taxon:10090"
/chromosome="6"
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Mus musculus IgVk am4 gene.
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/haplotype="c"
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Kirschbaum, T.
Direct Submission
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/gene="am4"
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/gene="am4"
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/protein_id="Aab54373.1"
/db_xxef="c1:5853224"
/translation="GIVLFQSPAILSASPGEKVTMTCRASSSVSYMLWYQQKPGSSPK
PWIYATSNLASGVPARFSGSGSGTSYSLISRVEAEDAATYTCQQWSSNPPTFGGGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 118) and Dlamond, B. Putterman, C., Deocharan, B. and Dlamond, B. Molecular analysis of the autoantibody response in peptide-induced
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                                                                                                                      AAGCCAGGATCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTC 171
                                                                     144 TGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTTCAGTGGCAGTGGGGTCTGGGAC 203
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Pred. No. 3.6e-87;
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/note="IgM kappa; anti-peptide antibody"
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/cell_line="39-9"
/cell_type="hybridoma"
/note="from peptide-immunized mouse"
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Putterman, C., Deocharan, B. and Diamond, B.
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100.0%; Pred. No. 3.c..
0; Mismatches
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Mus musculus
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Retter, M.W. and Nemazee, D.
Receptor editing occurs frequently during normal B cell development J. Exp. Med. (1998) In press
J. (bases 1 to 327)

Retter, M.W. and Nemazee, D.
Direct Submission
Submission
Submitted (26-AuG-1998) Pediatrics K1023, National Jewish Medical and Research Center, 1400 Jackson Street, Denver, CO 80206, USA
Location/Qualifiers
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Mus musculus hybrid 2-2Hll immunoglobulin light chain gene, partial
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                                                                                                                       TTACATGCACTGGTACCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTCTGCCAC 149
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/db_xref-"taxon:10090"
             er recombination signal"
149 g 228 t
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Pred. No. 6.2e-78;
0; Mismatches 1;
                                                                  147; DB 10;
No. 1.4e-78;
                                                                                            0; Mismatches
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/note="hybrid 2-2H11"
                                                                     Score
                                                                                  Pred.
             /note="nonamer
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Best Local Similarity 99.5%;
Matches 196; Conservative
                                                                  Query Match
Best Local Similarity 99.5%;
Matches 197; Conservative
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/gene-"am4"
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Mus musculus
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/product-"anti-fluorescein immunoglobulin light chain"
/protein_id-"AAD34819.1"
/db_xref-"GI:4972855"
/translation-"SPAILSASPGEKVTMTCRASSSVSYMHWYQQKPGSSPKPWIYAT
SNLASGVPARFSGSGTSYSLISRPEAEDAATYYCCQWSSNPWTFGGGTKLEIK"
84 c 77 g 66 t
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Mus musculus clone HV3PH4E2 anti-fluorescein immunoglobulin light
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van der Keyl, H., Gellad, Z.F. and Owen, J.A.
Direct Submission
Submitted (35-MAR-1999) Biology, Haverford
Avenue, Haverford, PA 19041-1392, USA
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/organism="Mus musculus"
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AF137624.1 GI:4972854
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/organism="Mus musculus"
/strain="BALB/c"
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ilarity 99.5%;
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TSNLASGVPARFSGSGSGTSYSLIISRVEAEDAATYYCQQWSSNPWTFGGGTKLEI"
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312 nt].
                                                                                                                                                                            Unpublished
2. (bases 1 to 300)
van der Keyl, H., Gellad, Z.F. and Owen, J.A.
Direct Submission
Submitted (25-MAR-1999) Biology, Haverford College, 370 Lancaster
Avenue, Haverford, PA 19041-1392, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 312)
Kasai,Y., Herlyn,D., Sperlagh,M., Maruyama,H., Matsushita,S. and,
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 300)
van der Keyl, H., Gellad, Z. F. and Owen, J. A. Disparity in the kinetics of onset of hypermutation in immunoglobulin heavy and light chains
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J. Immunol. Methods 155 (1), 77-89 (1992)
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Pred. No. 1.8e-75;
0; Mismatches 1;
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/cell_type="hybridoma"
<1. .>300
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chain mRNA, partial cds
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                           AF137625.1 GI:4972856
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ilarity 99.5%;
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/protein_id="aAB23708.1"
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IXTATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYXCOOMSSNPWTFGGGTKLE
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Mus musculus Mouse Ig active kappa-chain mRNA V-region.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/note="anti-idiotypic Fab; This sequence comes from Fig
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1383347
GenBank staff at the National Library of Medicine created this
entry (NCBI gibbsq 118382) from the original journal article.
This sequence comes from Fig. 5.
Location/Qualifiers
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V-region; immunoglobulin light chain; immunoglobulin-kappa;
processed gene.
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Pred. No. 1.8e-75;
0; Mismatches 1;
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/note="anti-idiotypic Fab"
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/db_xref="taxon:10095"
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PWIYATSNLASQVPARFSGSSGFISYSLTISRVEAEDAATYYCQQWSSNPYTFGGGT"
87 c 69 t
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Location/Qualifiers
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Parslow,T.G., Blair, D.L., Murphy,W.J. and Granner, D.K.
Structure of the 5' ends of immunoglobulin genes: a novel conserve
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84194064
                                                                                                                                                                                                                                                              Ouery Match 44.3%; Score 141; DB 10; Length 302; Best Local Similarity 99.5%; Pred. No. 7.5e-75; Matches 191; Conservative 0; Mismatches 1; Indels
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Mouse Ig kappa active V-region from 702/3 cells.
K01641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K01641.1 GI:196460
C-region; V-region; immunoglobulin light chain;
immunoglobulin-kappa.
Mouse 702/3 cell DNA.
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/codon_start=1
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/note="Ig kappa chain variable region"
                                         /cell_line="H142-3H5"
/cell_type="B-cell hybridoma"
<1. .>302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .1370
/organism="Mus musculus"
/db_xref="taxon:10090"
join(776 . 824,1003 . 1337)
/sub_species="domesticus"
/db_xref="taxon:10090"
                                                                                              /codon_start=1
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DEFINITION
ACCESSION
VERSION
KEYWORDS
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MUSIGKAAR
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Coding sequence for Mouse 247 antibody Mouse 247 antibody Mouse 247 antibody Encodes Variable r Encodes A587 antib Plasmid pNG3/A587 wurine A587 Light Plasmid pEE14/A587 A587 F(ab')2 codin IRES-based A587 ch

IL-2 chimeric anti Anti-ILSR-alpha an Anti-Staph (HAY) 9 DNA encoding a fus VK domain of antibo Monoclonal antibod Monoclonal antibod

Mouse monoclonal a Sequence of the an VK domain of antib Monoclonal antibod Monoclonal antibod MAD BW 2128 light

Mouse antibody MAk

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Anti-CD20 single c DNA encoding a CD-2H7 VL sequence in 2H7 Vh sequence. Mouse antibody 2H7 2H7 light chain va 2H7 light chain va 2H7 light chain va

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Word size :

Database

Result Š

Searched:

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Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody; chimeric antibody; antibody engineering; light chain; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blackburn MN, Church WR, Feuerstein GZ, Gross MS;
Nichols AJ, Padlan EA, Patel AH, Sylvester DR;
                                                                                                                                                                                                                                                                                                                Anti-Factor IX MAb chimeric light chain cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM CORP.
(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
                                                                                                                                                                                                                                             ALIGNMENTS
                                                                               AAQ20983
AAQ27350
AAV72047
AAT42508
AAV72081
AAX24806
AAV72076
                                                AAT70869
AAT51043
AAV03927
AAV18558
AAV18594
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AAQ36613
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96US-0010108.
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                                                                                                                                                                                                                                                                                                                                               Chimeric Mus musculus.
Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                             Chimeric synthetic.
24-OCT-1996;
17-JAN-1996;
                                                                                                                                                                                                                                                                                                    27-DEC-1997
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AAT79900
Mouse-human light
Mouse anti-human F
Murine BC2 light c
Anti-Factor IX MAD
Murine BC2 light c
Mouse Secreted exp
Anti-NKG2D hybrido
DNA encoding a fus
                                                                                                                                                                                                                                                                                                                                                                                                              Anti-Factor IX MAb
                                         November 27, 2002, 03:54:06; Search time 170.803 Seconds (without alignments) 4192.745 Million cell updates/sec
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                                                                  US-09-893-615-88
318
1 CAMATTGTTCTCCCAGTC......GGACCATGCTGGAAATAAGA 318
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                                                                                                                                        4370478
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Compugen Ltd.
                                                                                                                                       fotal number of hits satisfying chosen parameters:
                                                                                                               2185239 segs, 1125999159 residues
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      GenCore version
Copyright (c) 1993 - 2002
                                                                                                                                                                        Post-processing: Listing first 45 summaries
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ABK24005
AAT77377
ABK23937
AAT79899
AAA744004
AAA43472
AAS97128
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Gapop 60.0 , Gapext 60.0
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Similarity
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17-JAN-1996;
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                                            activator
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                                                                                                                                                                                                                                                                                                               231
                                                                                                                                                                                                                                                           52 AAGGTCACAATGACTTGCAGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
                                                                                                                                                                                                                                                                     112 AAGCCAGGATCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTC 171
                                                                                                                                                                                                                                                                                                                                                                  172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGGTG 231
                                                                                                                                                                                                                                        Gaps
                                                                                             This cDNA sequence encodes a mouse-human chimeric antibody light chain (AAW24512) in which the variable region is derived from mouse anti-human factor IX monoclonal antibody BC2 cDNA (see AA779899) and human sequences from the immunoglobulin RF-TS3'CL framework. It was obtained by PCR amplification (see AA779897-98) of BC2 cDNA and insertion of the PCR product into F9HIZHC 1-3 cDNA (see AA77774). Claimed anti-Factor IX chimeric antibodies are useful in the treatment of thrombosis.
                                                                                                                                                                                                                                                                                                                                              CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG
                              Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial inhibition
                                                                                                                                                                                                              ; DB 18; Length 318; 4.7e-75;
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                                                                                                                                                                                                                Score 172; DB
Pred. No. 4.7e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barone FC, Blackburn MN, Feuerstein G2,
                                                                          Example 7; Page 128; 150pp; English.
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99.6%;
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                                                                                                                                                                                                                                       Conservative
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Homo sapiens.
WPI; 1997-385117/35.
P-PSDB; AAW24532.
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Chimeric - Homo
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                                                                                                                                                                                                                            Best Local Sim
Matches 222;
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                                         plasminogen
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Treating post-thromboembolic induced ischaemia in an animal administering anti-factor IX antibody in combination with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse anti-human Factor IX antibody BC2 light chain cDNA.
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(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
                                                                                                                                                              Example 7; Page 154-155; 163pp; English.
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96US-0010108.
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15-MAY-2000; 2000US-0571434.
             05-OCT-2000; 2000WO-US27438
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                                                                                                                                                                        This cDNA sequence encodes the light chain variable region (see ZAWA3520) of mouse anti-human Factor IX monoclonal antibody BC2. Claimed humanised antibodies (see AAWA3504-09) contain CDRs (see AAWA3504-09) of BC2 heavy and light chains inserted into framework regions of selected human antibody sequences. They have self. Infilting neutralising activity, and are useful as anticoagulant agents in treatment of thrombosis associated with myocardial infarction, unstable angina atrial fibrillation, stroke, renal camage, pulmonary embolism, deep vein thrombosis, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulation, sepsis, or artificial organs, shunts or prostheses (claimed). Also claimed are chimeric antibodies (see AAT79900), and Fab and F(ab')2 fragments. The claimed antibodies do not cause uncontrolled bleeding (contrast heparin and warfarin) since they provide only partial inhibition of coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; mouse; BC2; animal post-thromboembolic induced ischaemia; thrombolytic agent; anti-factor IX antibody; plasminogen activator; ss; thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic; vasotropic; cardiant; PCR primer; anti-respiratory syncytial virus; heavy chain variable region; light chain variable region.
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                                                                                          Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial inhibition
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 172; DB 18; Length 321;
Pred. No. 4.7e-75;
0; Mismatches 1; Indels (
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           7, Church WR, Feuerstein GZ, Gross
Padlan EA, Patel AH, Sylvester DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine BC2 light chain variable region cDNA.
                                                                                                                                                 Example 5; Page 64; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK23937 standard; cDNA; 321 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 54.1%;
Best Local Similarity 99.6%;
Matches 222; Conservative
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                                                   WPI; 1997-385117/35
                                                                  P-PSDB; AAW24520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200187339-A1
                        Nichols AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp
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                                                                                                                                                                                                                                       Treating post-thromboembolic induced ischaemia in an animal by administering anti-factor IX antibody in combination with a plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 AAGGICACAAIGACTIGCAGGGCCAGCICAAGIGIAAATIACAIGCACTGGIACCAGCAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 AAGGTCACAATGACTTGCAGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  112 AAGCCAGGATCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 172; DB 24; Length 321;
Pred. No. 4.7e-75;
0; Mismatches 1; Indels
                                                                  Blackburn MN, Feuerstein GZ, Toomey JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 GAGGCTGAAGATGCTGCACTTATTACTGCCAGCAGTGGAGTA 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 321 BP; 78 A; 92 C; 79 G; 72 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-Factor IX MAb BC2 light chain PCR product.
                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Page 94; 163pp; English.
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(SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT79899 standard; cDNA; 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 54.1%;
Best Local Similarity 99.6%;
Matches 222; Conservative
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                                                                                                                                    WPI; 2002-082944/11.
P-PSDB; AAU80976.
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Chimeric synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-1997.
                                                                  Barone FC,
                                                                                                                                                                                                                                                                                                                 activator
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us-09-893-615-88.oli.rng

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22-NOV-2001
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                                                                                  Barone FC,
                                                                                                                                                           activator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAA43472;
                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; mouse; BC2; animal post-thromboembolic induced ischaemia; thrombolytic agent; anti-factor IX antibody; plasminogen activator; ss; thromboembolic stroke: cerebroprotective; anticoagulant; Thrombolytic; vasctropic; cardiant; PCR primer; anti-respiratory syncytial virus; heavy chain variable region; light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This cDNA sequence was obtained by PCR amplification (see AAT79897 and AAT79898) of the light chain variable region (see also AAT7377) of mouse anti-human factor IX monoclonal antibody BCZ cDNA. The amplification resulted in the addition of Scai, NarI ends to the VL region. The PCR product was ligated into Scai, NarI edgested F9H2RC 1-3 (see AAT77374) and digested with Scai, NarI to produce a mouse-human chimeric light chain F9CHLC (see AAT79900, AAW24532). Claimed anti-Factor IX chimeric antibodies are useful in the treatment of thrombosis.
                                                                                                                                                                                                                                                                                                                                                                      52 AAGGTCACAATGACTTGCAGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
                                                                                                                                                                                                                                                                                                                                                                                                              112 AAGCCAGGATCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTC 171
                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                   Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial inhibition
                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                            54.1%; Score 172; DB 18; Length 335; 99.6%; Pred. No. 4.6e-75;
                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine BC2 light chain modified variable region DNA.
                                                                                                                                                                                                                                                                                                       Sequence 335 BP; 80 A; 97 C; 85 G; 73 T; 0 other;
                                                                                  Padlan EA, Patel AH, Sylvester DR,
                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                  (UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE
                                                                        Feuerstein GZ,
                                                                                                                                                                             Example 7; Page 126; 150pp; English.
                                        SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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         96US-0029119
                   96US-0010108
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                                                                        Church WR,
                                                                                                                                                                                                                                                                                                                                                 222; Conservative
                                                                                                      WPI; 1997-385117/35
                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                 P-PSDB; AAW24531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40200187339-A1.
                                                                        Blackburn MN,
         24-OCT-1996;
17-JAN-1996;
                                                                                  Nichols AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-APR-2002
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK24004;
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating post-thromboembolic induced ischaemia in an animal by administering anti-factor IX antibody in combination with a plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGCCAGGATCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 AAGGTCACAATGACTTGCAGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mouse; chicken; rat; secreted expressed sequence tag; sEST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibodies and PCR primers used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 172; DB 24; Length 335;
Pred. No. 4.6e-75;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                            Toomey JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse secreted expressed sequence tag SEQ ID NO:47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 335 BP; 80 A; 97 C; 85 G; 73 T; 0 other;
                                                                                                                                                                                                                                            Feuerstein GZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Page 152-153; 163pp; English.
                                                                                                                                                            (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.1%;
99.6%;
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                                                                            15-MAY-2000; 2000US-0571434.
05-OCT-2000; 2000WO-US27438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                            Blackburn MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 99.6
Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                        WPI; 2002-082944/11.
                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAU81001
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BP

AAS97128 standard; cDNA; 318

(first entry)

26-FEB-2002

AAS97128;

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RESULT 8
AAS97128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                         expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders
                                                                                                                                                                                                                                                                                                                                                                                             AAA43426 to AAA45925 represent specifically claimed secreted expressed
                                                                                                                                                                                                                                                                                                                                                                                                             sequence tags (SESTS), isolated from human, mouse, chicken and rat tissue sources. The SESTS can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90 TTACATGCACTGGTACCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTCTGCCAC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 ATCCAACCTGGCTTCTGGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  239 ATCCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCTCTCACAATCAGCAGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                               proteins, comprising secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
                                                                                                                                                                                                                                           ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
 nervous system disorder; Alzheimer's disease; stroke;
                                                                                                                                                                                                                                           Evans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.3%; Score 141; DB 21; Length 449; 99.5%; Pred. No. 9.4e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                        Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 449 BP; 110 A; 124 C; 107 G; 108 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ï
                                          tumour; infection; depression; psorlasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 9.4e-
0; Mismatches
                                                                                                                                                                                                                                                                                                              Isolated polynucleotides, and encoded
                                                                                                                                                                                                                                        LaVallie ER,
                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 214; 803pp; English.
                                                                                                                                                                                                                                                       Bowman MR;
                                                                                                                                                                                98US-0104436.
                                                                                                                                                       99WO-US24206
                                                                                                                                                                                                            (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.5
Matches 191; Conservative
                                                                                                                                                                                                                                                       Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281
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                                                                                                                                                                                                                                                                                  WPI; 2000-317938/27
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                                                                                                                                                                                                                                          McCoy
                                                                                              WO200021991-A1
                                                                      Mus musculus.
                                                                                                                                                      15-OCT-1999;
                                                                                                                                                                                5-0CT-1998;
                                                                                                                          20-APR-2000.
                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                        Jacobs K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
                                                                                                                                                                                                                                                        Merberg
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The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NKG2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated composition for the treatment of cancer, infections and/or autoimmne conditions. The cancer may be a tumour of the head and neck, stomach, composition for the treatment of cancer, infections and/or autoimmne conditions. The cancer may be a tumour of the head and neck, stomach, comptions, colon, liver, intrahepatic bile ducts, pancress, lung, laynx, breast, ovari, uterus, cervix, prostate, kidney, testis, thyroid, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, crotozoa or helminths. The autoimmune diseases include multiple sclerosis, Grave's disease, ankylosing spondylitis, acute anterior conveils, Goognesture's syndiame, myasthenia gravis, insulin-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                            autoimmune disease; head; neck; stomach; intectious disease; tumour; intrahepatic blie duct; pancreas; lung; larynx; breast; colon; liver; ovary; intrahepatic blie duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytostatic; antimicrobial; immunomodulatory; libiD10; 6H7E7; 8G7C10; 6E5A7; PCR primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     autoimmune hepatitis. The sequences represent the NKG2D receptor DNA, DNA encoding the polypeptides of the invention and PCR primers used to
                                                                                Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Multifunctional polypeptides comprising binding sites that specifically recognise extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 TTACATGCACTGGTACCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTCTGCCAC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 TTACATGCACTGGTACCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTATATGCCAC 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Riethmueller G, Lutterbuese R, Borschert K, Kischel R; Hofmeister R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
Anti-NKG2D hybridoma 6H7E7 variable light chain DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 318 BP; 76 A; 92 C; 80 G; 70 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 131; DB 24;
Pred. No. 8.2e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Fig 16; 114pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancers and infectious diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.2%;
ilarity 99.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2001; 2001WO-EP03414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-MAR-2000; 2000EP-0106467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-055119/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KUFE/) KUFER P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAU72833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200171005-A2
                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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Mayer M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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The present sequence encodes a fusion of an anti-CD20 single chain anti-dody and streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid sequence. Alternatively, the vector construct comprises a nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a.g. adenocarcinomas or hematological malignancies. The vector construct
is useful for expressing of streptavidin fusion proteins. In particular,
these are useful as tools for medical diagnostics and therapeutic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian host.
                                                                     269
                                                                                        110 CTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGGG 269
 ATCCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA 209
                  Reno JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with cancer, e.g. adenocarcinomas -
                                                                   CTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG
                                                                                                                                                                                                                                                                                                                                                                    DNA encoding a fusion of a single chain antibody and streptavidin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanderson JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 765 BP; 169 A; 201 C; 230 G; 165 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                     tumour cell; cancer; adenocarcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schultz JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Page 95; 100pp; English.
                                                                                                                                                                                                                                                               AAC86590 standard; DNA; 765 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                         hematological malignancy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-2000; 2000WO-US15595
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99US-0168976
                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Graves SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces avidinii.
Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200075333-A1.
                                                                                                                                                                                                                                                                                                                                                                                                        Streptavidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1999;
03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                  02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Goshorn SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-DEC-2000
                                                                                                                                       270 GA 271
                                                                                                                                                                        GA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                 AAC86590;
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                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding a fusion of anti-CD20 single chain antibody/streptavidin.
                                                       TTACATGCACTGGTACCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTCTGCCAC 149
                                                                       ATCCAACCTGGCTTCTGGAGTCCCTTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA 209
                                                                                                                             CTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
                                                                                                                                                                                  Reno JM;
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with
                              ö
Length 765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sanderson JA,
                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      tumour cell; cancer; adenocarcinoma;
                             1,
 DB 22;
              Pred. No. 8e-55;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lin Y,
  Score 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schultz JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Fig 11A; 100pp; English.
                                                                                                                                                                                                                                                                                                                          AAC86563 standard; DNA; 1239 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer, e.g. adenocarcinomas -
 41.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      hematological malignancy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-JUN-2000; 2000WO-US15595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0137900.
                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                           Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptomyces avidinii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Graves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-091213/10.
                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NEOR-) NEORX CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptavidin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1999;
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GA 718
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                                                                                                                                                                                                                           GA 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                    AAC86563;
  Query Match
                 Best Local
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Example 2; Fig 11C; 100pp; English.
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GA 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local $
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AAA15019
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functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer, e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian host.
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/product= "anti-CD20 scFv and streptavidin fusion"
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                                                                                                                                                                                                                                                                                                                                                               Sequence 1239 BP; 270 A; 392 C; 356 G; 221 T; 0 other;
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The present sequence encodes a fusion of an anti-CD20 single chain antibody (BBE9) streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector constructs nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding a polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second nucleic acid conding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with concer.
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Pred. No. 7.8e-55;
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                                                                                                                               The present sequence encodes a synthetic CD20-specific chimeric receptor. The specification describes CD-20 specific redirected T cells which express and bear on the cell surface membrane a CD20-chimeric receptor comprising an intracellular signalling domain, a transmembrane domain and an extracellular domain comprising a CD20-specific receptor. The genetically engineered CD20-specific redirected T cells are useful for treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, in a human patient having previously undergone mycoblative chemotherapy and stem cell rescue. The genetically engineered CD20-specific redirected T cells are useful for abrogating an untoward B cell function, such
                                                                                                                                                                                                                                                                                                                                                                  144 TGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGGAC 203
                                                                                                                                                                                                                                                                                                                                        230 TGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGGAC 289
                                                                                                                                                                                                                                                                                                           Gaps
                                                                           Genetically engineered CD20-specific redirected T cells useful for treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, and autoimmune disease -
                                                                                                                                                                                                                                                as autoimmune disease (lupus or rheumatoid arthritis) in a patient.
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                       Length 1925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2H7 VL sequence in which the VK gene contains JK5 sequences.
                                                                                                                                                                                                                                                                   Sequence 1925 BP; 471 A; 554 C; 541 G; 359 T; 0 other;
                                                                                                                                                                                                                                                                                       Score 130; DB 21;
Pred. No. 2.4e-54;
                                                                                                                                                                                                                                                                                            100.0%; Pred. nv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric antibody; Anti-cancer antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/label=leader peptide
67..138
/*tag= b
/label=FRI
                                                                                                                 Example 1; Page 50-53; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                            Wu AM;
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                                                                                                                                                                                                                                                                                       40.9%;
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/label=CDR1
                            Jensen MC,
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(first entry)
                                                                                                                                                                                                                                                                                               Best Local Similarity 100. Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - Homo sapiens.
- Mus sp.
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         (CITY ) CITY OF HOPE.
                                               WPI; 2000-339676/29
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                                                        P-PSDB; AAY84965.
                          Raubitschek A,
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09-APR-1991
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149 CATCCAACCTGGCTTCTGGAGTCCCTGCTTCGGTGGCAGTGGGGTCTGGGGACCTCTT 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chains and 2 heavy chains, each comprising a constant human region and a variable non-human region. Coding sequences for the Ig chains are also claimed. The invention provides consensus sequences of light and heavy chain J regions useful in the design of oligonucleotides (UISs) for use as primers or probes for cloning immunoglobulinlight or heavy chain mRNAs or genes. Depending on the nature of design of a particular UIG, it may be capable of hybridizing to all Ig mRNAs or genes containing a single specific J equence. UIG denotes universal immunoglobulin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The patentors claim a chimeric antibody molecule comprising 2 light
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prodn. of immunoglobulin chains and molecules - is by recombinant DNA procedures, with chimeric antibodies etc. related to cancer specific antigens.
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/label=CDR2
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/label=CDR3
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/*tag= d
/label=FR2
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/label-FR3
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/label=JK5
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/label=FR4
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Matches 125; Conservative
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The present sequence encodes the mouse antibody 2H7 light chain variable region. Antibody 2H7 is specific for human B-cell antigen. The antibody sequence was used to construct a chimeric human-mouse antibody. In the course of the invention. The chimmeric antibody is expressed in a secretion vector comprising a pelB pectate lyses secretion signal peptide. The pelB pectate lyses secretion sequence is useful for producing a protein such as a chimeric antibody in a bacterial host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          209 ACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT 268
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               pelB pectate lyase; secretion signal; chimeric antibody;
light chain; B-cell antigen; antibody 2H7; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 404 BP; 100 A; 113 C; 93 G; 98 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu AY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: November 27, 2002, 05:37:46 Job time: 177.303 secs
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/note= "partial CDS"
                                                                                       Location/Qualifiers
21..404
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88US-0142039.
92US-0987555.
93US-0020671.
94US-0357234.
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85US-0793980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilcox GL;
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01-NOV-1985;
24-JUL-1987;
11-JAN-1988;
08-DEC-1992;
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09-DEC-1994;
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355 GGAGT
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                                                               Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence, derived from M13 subclones of gene fragments, carries the variable region of chimeric immunoglobulin sequence. The antibodies ruseful in passive immunisation avoiding negative reactions. They are also useful in assaying and in vitro imaging.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse antibody 2H7 light chain variable region encoding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.3%; Score 125; DB 10; Length 403; 100.0%; Pred. No. 7.5e-52; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polynucleotide(s) encoding Immunoglobulin molecules - used for efficient prodn. of chimeric human or non-human or class switched antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Better M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 403 BP; 100 A; 112 C; 93 G; 98 T; 0 other;
                                                                                                                            Antibodies; passive immunisation; pH3-6a; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Horwitz AH, Wall R,
                                                                                                                                                                                        Location/Qualifiers
20..403
/*tag= a
320..352
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/note="JK5 region."
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AAN91147 standard; DNA; 403
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                                                              (first entry)
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Best Local Similarity 100.
Matches 125; Conservative
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P-PSDB; AAP94778.
                                                                                          2H7 Vh sequence.
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"Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.; I (bases 1 to 639)

S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
AL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Office Generalist Consortium/LLNL at:
CDNA Library Preparation: Office Consortium/LLNL at:
High quality Sequence stop: 639.
High quality Sequence stop: 639.
I. 639
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BG9911133 ACENCOURT
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BF142976 601791755
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BF138873 601781783
BG149077 uu88f09.y
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602836416F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4991067 5',
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   mRNA sequence.
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BG968852 602836142
BE654609 uu24c05.y
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BG964957 602829274
BF583310 602101781
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3912.201 Million cell updates/sec
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                                                                                                 November 27, 2002, 05:31:20 ; Search time 1316.44 Seconds
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1 CAAATTGTTCTCCCCAGTC......GGACCATGCTGGAAATAAGA 318
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             GenCore version 5.1.3 . Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                                                                                                                              16154066 seqs, 8097743376 residues
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                                            /db_xref="taxon:10090"
/clone="IMAGE:4991067"
/clone=line="NCI_CGAP_CO24"
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S NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

L'unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: gapbs.rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM1006 row: d column: 12

High quality sequence stop: 620.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/db_xeref="taxon:10090"
/db_xeref="taxon:10090"
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/clone=lib="NCI_CGAP_Co24"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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/organism="Mus musculus"
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1. .413
/organism="Mus musculus"
/do_ref="texton:10090"
/clone="lib="Soares_mammary_gland_NMLMC"
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/tissue_type="mammary gland"
/lab_host="DH10B"
/note="Vector: pT7T3D-pac (Pharmacia) with a modified polylinker; lst strand cDNN was prepared from mammary gland tissue from a lactating female, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNN was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the I and cloned into the Not I and Eco RI sites of the
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IMAGE:3372872 5' similar to gb:L09085 IG KAPPA CHAIN V-I REGION
(HUMAN); gb:M63550 Mouse Ig rearranged kappa-chain mRNA V-region,
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1082476
                                                                                                                                                                                                                              259 TGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGGTTCAGTGGCAGTGGGTCTGGGAC 318
                                                                                                                                                                                                   144 TGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGGAC 203
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100.0%; Pred. No. 2.6e-30;
live 0; Mismatches 0;
                                                                                  DB 13;
                                                                               Query Match 28.0%; Score 89; DB Best Local Similarity 100.0%; Pred. No. 2.7 Matches 89; Conservative 0; Mismatches
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High quality sequence stop: 391.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="ImAGE:5036622"
/clone=lib="MCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
/tissue_type="spontaneous tumor, metastatic to mammary.
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/lote="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; SalI;
/lote="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI; SalI;
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                                                                                                                       BI104783 532 bp mRNA linear EST 26-JUN-2001 602891329F1 NCI_CGAP_Lu29 Mus musculus CDNA clone IMAGE:5036622 5',
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Mammalia; Eutherla; Rodentla; Sciurognathl; Muridae; Murinae; Mus.
1 (Bases 1 to 569)
NIH-MGC http://mgc.nci.nlh.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
http://mage.llnl.gov
High quality sequence stop: 532.
Location/Qualifiers
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1 Similarity 100.0%; Pred. No. 2.8e-30;
81; Conservative 0; Mismatches 0;
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/organism="Mus musculus"
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BG964957
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1. 569
/organism="Mus musculus"
/strain="FYB/N"
/db_xeref="texon:10090"
/clone=lib="NCI_CGAP_CO24"
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/lab_host="DH10B (T1 phage-resistant)"
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/note="Organ: colon; Vector: pcmV-sPORT6; Site_1: Not1;
/note="Organ: colon; Vector: phage-resistant"
/note="Organ: colon; Vector: phage-resis
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National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CLONA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10989 row: c column: 20

High quality sequence stop: 569.

Location/Qualifiers

Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CLone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.b column: 21
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA691311 396 bp mRNA linear EST 16-DEC-1997 vol4f01.rl Barstead mouse irradiated colon MPLRRY Mus musculus cDNA clone IMAGE:1138201 5' similar to gb:X67211 M.musculus rearranged immunoglobulin kappa light chain (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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/clone="IMAGE:4224692"
/clone_lib="NGI_GGAP_GG24"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: colon, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musil (bases 1 to 396) November 1 (bases 1 to 396) Novemb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty.free through LLNL ; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
MGI:619473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 CACATCCAACCTGGCTTCTGGAGTCCCTGCTCGGTGGGCAGTGGGGTCTGGGACCTC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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/dev_stage="8 weeks"
/lab_host="DH108"
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Contact: Marra MyMouse Exp Project
WashD-HHMI Mouse ExT Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                      ch 25.5%; Score 81; DB 12; Length 639;
1 Similarity 100.0%; Pred. No. 2.9e-30;
81; Conservative 0; Mismatches 0; Indels
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1. 396
/organism="Mus musculus"
/strain="FVB/N"
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The WashU-HHMI Mouse EST Project
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/clone="IMAGE:1138201"
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AA691311.1 GI:2692247
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VERSION
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

CLONE distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image llnl.gov

Plate: LiAM9802 row: a column: 14

High quality sequence start: 3

High quality sequence start: 3

High quality sequence start: 3

High quality sequence stop: 631.

Location/Qualifiers

/ organism="Mus musculus"

/ clone="InAGE: 4219669"

/ clone="InAGE: 4219669"

/ clone="InAGE: 4219669"

/ clone="InAGE: 4219669"

/ loce="Corgan: colon; Vector: pCWV-SPORT6; Site_I: NotI;

Site_2: Sali; cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI_CGAP Library."

NT 282 a 259 c 221 g 198 t
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 960)

11 (bases 1 to 960)

12 (bases 1 to 960)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                        157 CTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCT 216
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                  constructed by Bob Barstead.
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                                                                                                            DB 9;
3.2e-25;
0;
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                                                                                                                    Query Match 22.3%; Score 71; DB Best Local Similarity 100.0%; Pred. No. 3.2 Matches 71; Conservative 0; Mismatches
vector. Library con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence. BF581607
BF581607 GI:11655319
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217 ACAATCAG 224
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National Institutes of Health, Mammalian Gene Collection (MGC)

Longublished (1999)

Longublished (1999)

Email: cgapba:rémail.inh.gov

Tissue Procurement: The Cepko Laboratory

CONTact: Robert Strausberg, Ph.D.

Email: cgapba:rémail.inh.gov

Tissue Procurement: The Cepko Laboratory

CONA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAMI4012 row: k column: 06

High quality sequence stop: 714.

Location/Qualifiers

roc
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                            BQ946795

AGENCOURT_8949642 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6474845 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:6474845"
/clone="lb="NCI_CGAP_CG24"
/lab-host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies: Note: this is a NCI_CGAP Library."
257 c 193 g 212 t 10 others
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC) (Contact: Robert Strausberg, Ph.D. Email: cgapbs-rémail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 TGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGGTCTGGGACCTCTTACTCTCTCA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239 TGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTA 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.0%; Score 70; DB 14; Length 918; 100.0%; Pred. No. 1.2e-24; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="FVB/N"
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                                                                                                                          BQ946795.1 GI:22362273
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BQ939046.1 GI:22354524
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299 CAATCAGCAG 308
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                                                          DEFINITION
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AUTHORS
TITLE
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RESULT 9
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1. 959
/organism="wus musculus"
/strain="FVBus"
/db_xref="taxon:10090"
/db_xref="IMAGE:6395050"
/clone="IMAGE:6395050"
/clone="IMAGE:6395050"
/clone="IMAGE:6395050"
/clone="IMAGE:6395050"
/clone="IMAGE:6395050"
/clone="IMAGE:6395050"
/lab_host="PHIOB (TI phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI:
/note="Organ: colon; Vector: pCMV-SPO
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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/clone=llb=NrCl_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11004 row: g column: 01
High quality sequence stop: 797.
Tissue Procurement: The Cepko Laboratory cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://mage.llnl.gov b column: 11 High quality sequence stop: 517. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG968518.1 GI:14356142
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Mus musculus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999)
                                                                                                                                                                                 mRNA sequence.
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TITLE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Musmalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.
1 (bases 1 to 755)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs.refmail.nih.gov

Tissue Procurement: Gilbert.Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLONA Library Preparation: MAG.E. Consortium/LLNL at:

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MAG.E. Consortium/LLNL at:

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Clone="Musce Faxon: 10090"

//db.xref="Musce Faxon: 10090"

//db.xref="Musce
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204 c 168 g 165 t
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                       244 CTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAA 303
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                                                                                                                                                   21.1%; Score 67; DB 13; Length 798; 100.0%; Pred. No. 4e-23; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                              67; Conservative
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Best Local Similarity
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                                                                             BASE COUNT
ORIGIN
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AUTHORS
TITLE
JOURNAL
COMMENT
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BI150509
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/organism="Mus musculus"
/strain="CZECH II"
/db_rref="taxon:10090"
/clone="IMAGE:4009755"
/clone_lib="NcI_CGAP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="bullos"
/clote="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: lung; Vector pCMM-SPORT6; Site_1: NotI; Not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by:Incyte Genomics, Inc.

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMB246 row: e column: 22

High quality sequence stop: 650.

Location/Qualifiers

1...950
BF138873 950 bp mRNA linear EST 24-OCT-2000 601781783F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4009725 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 950)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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uu88f09.yl Soares_mouse_NMGB_bcell Mus musculus cDNa clone
IMAGE:3383585 5' similar to SW:KV6F_MOUSE P04940 IG KAPPA CHAIN
V-VI REGION NQ2-17.4.1.;, mRNA sequence.
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19.8%; Score 63; DB 12; 1
Best Local Similarity 100.0%; Pred. No. 4.5e-21;
Matches 63; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                     BF138873.1 GI:10977913
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BG149077.1 GI:12652504
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 918)
NIH-MGC http://mgc.nci.nlh.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Emall: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLAM1890 row: h colunn: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGENCOURT_8920980 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:6395584 5', mRNA sequence. BQ931133 GI:22346164 EST
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               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                  Tumor Gene Index
Uppublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1088581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 280;
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100.0%; Pred. No. 1.2e-19;
Live 0; Mismatches 0; Indels
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/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6395584"
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Location/Qualifiers
                                                                                                                                                                            Seq primer: -40RP from Glbco.
Location/Qualiflers
1. .280
(bases 1 to 280)
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Best Local Similarity 100.
Matches 60; Conservative
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
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BQ931133
LOCUS
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AUTHORS
TITLE
JOURNAL
REFERENCE
                                                                     JOURNAL
                                                                                                                                                                                                 FEATURES
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                                 TITLE
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APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Forest-chin, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Bduardo
APPLICANT: Padlan, Eduardo
APPLICANT: Spivester, Daniel
APPLICANT: Spivester, Daniel
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
             US-08-149-099C-6
US-08-178-967A-6
US-08-190-199A-62
US-08-190-199A-64
US-08-956-047-32
US-08-956-047-32
US-08-956-047-32
US-08-956-047-32
US-08-19-09C-3
US-08-19-09C-3
US-08-19-96-3
US-08-19-866-2
US-08-475-815B-3
US-08-475-815B-3
US-08-475-815B-3
US-08-475-815B-3
US-08-475-815B-3
US-08-343-485A-2
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STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
CLASSIFITEMENTO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster: K1rk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 104, Application US/08783853A Patent No. 6005091 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
 USA
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MOLECULE TYPE:
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 TELEX:
Sequence 17, Appl
Sequence 57, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 12, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 1, Appl
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Sequence 104, App
Sequence 6, Appli
Sequence 6, Appli
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Sequence 102, App
Sequence 1, Appli
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Sequence 15, Appl
Patent No. 5455030
                                                                                                                                            (without alignments)
2736.194 Million cell updates/sec
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                                                                                                                        November 27, 2002, 03:55:59 ; Search time 35.6419 Seconds
                                                                                                                                                                                                            318
1 CAAATTGTTCTCTCCCAGTC......GGACCATGCTGGAAATAAGA 318
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2: /cgn2_6/ptodate/1/lna/5B_COMB.seq:*
3: /cgn2_6/ptodate/1/lna/6A_COMB.seq:*
5: /cgn2_6/ptodate/1/lna/6B_COMB.seq:*
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6: /cgn2_6/ptodate/1/lna/PCTUS_COMB.seq:*
                GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-783-853A-104
US-09-344-050-104
US-09-344-050-104
US-08-783-853A-102
US-08-449-287-102
US-08-449-287-1
US-09-423-439-17
US-09-423-439-17
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US-09-423-439-52
US-08-308-458-110-3
US-08-459-110-3
US-08-457-393-3
US-08-457-393-3
US-08-457-393-3
US-08-836-551-32
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US-08-447-422-15
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US-08-447-422-13
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US-08-619-491-1
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Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_NA:*
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Database :

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112 AAGCCAGGATCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Gross, Mitchell
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbha,
APPLICANT: Patel, Arunbha,
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 318;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.1%; Score 172; DB 4; 99.6%; Pred. No. 2.1e-80; ative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: SmithKline Beecham Corporation 709 Swedeland Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08783853A
Patent No. 6005091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                              104:
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                                               SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 222; Conservative
                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 1...318
; OTHER INFORMATION:
US-09-344-050-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                              ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                              52 AAGGTCACAATGACTTGCAGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 AAGCCAGGATCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTC 171
                                                                                                                                                                                                                                                                                                                               Gaps
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| Sequence 104, Application US/09344050
| Patent No. 6391299
| GENERAL INFORMATION:
| APPLICANT: Blackburn, Milliam
| APPLICANT: Church, William
| APPLICANT: Gross, Mitchell
| APPLICANT: Pederstein, Giora
| APPLICANT: Pederstein, Peder
                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                       Length 318;
                                                                                                                                                                                                                                                                                                                            1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
                                                                                                                                                                                                                                                                    Score 172; DB 3;
Pred. No. 2.1e-80;
0; Mismatches 1.
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24-JUN-1999
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APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELEPHANE: 610-270-5096
TELEPHAN:
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ER: P50438
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APPLICATION NUMBER: US/No // CLACTO
                                                                                                                                                                                                                                                                    54.1%;
                                                                                                                               NAME/KEY: Coding Sequence
LOCATION: 1...318
CTHER INFORMATION:
US-08-783-8534-104
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version
                                                                                                                                                                                                                                                                                                Best Local Similarity 99.6
Matches 222; Conservative
                           ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
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HYPOTHETICAL:
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172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
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APPLICANT: Church, William
APPLICANT: Church, William
APPLICANT: Federstein, Giora
APPLICANT: Pedols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 54.1%; Score 172; DB 4; Length 321; Best Local Similarity 99.6%; Pred. No. 2.1e-80; Matches 222; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 GAGGCTGAAGATGCTGCACTTATTACTGCCAGCAGTGGAGT 274
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                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister: Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 102, Application US/08783853A Patent No. 6005091
                                                                                                                                                             P50438
                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
    24-JUN-1999
                                                                                                                                                                                                                                                                                            LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 709 Swcuc.
                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORIGINAL SOURCE:
US-09-344-050-6
                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-08-783-853A-102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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APPLICANT: Church, William
APPLICANT: Church, William
APPLICANT: Gress, Mitchell
APPLICANT: Feuerstein, Glora
APPLICANT: Peuerstein, Glora
APPLICANT: Paclan, Eduardo
APPLICANT: Paclan, Eduardo
APPLICANT: Paclan, Eduardo
APPLICANT: Paclan, Aunthal
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: AFHROMBOSIS
NUMBER OF SEQUENCES:
ADDRESSEE: SMITHKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
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99.6%; Pred. No. 2.1e-80;
tive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: SmithKline Beecham Corporation 709 Swedeland Road
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SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09344050 Patent No. 6391299
FILING DATE: 24-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P504
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic said
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 99.6
Matches 222; Conservative
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                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-783-853A-6
                                                                                                                                                                                                                                                                             linear
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CITY: K1
                                                                                                                                      TELEFAX:
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172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
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Patent No. 5877293
GENERAL INFORMATION:
APPLICANT: ADALR, John Robert
APPLICANT: MOUNTAIN, Andrew
APPLICANT: OWNENS, Mark William
APPLICANT: CANNENS, BAYONG John
TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
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Best Local Similarity 99.6%; Pred. No. 2.1e-80;
Matches 222; Conservative 0; Mismatches 1.
                                                                                                    COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: TBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: 33,833
REFERENCE/DOCKET NUMBER: 33,833
TELECHONE: 610-270-5096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
      King of Prussia
                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: Coding (
) LOCATION: 1...335
) OTHER INFORMATION:
US-09-344-050-102
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FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
                                                 USA
                                                                     19406
                               ΡA
    CITY: Ki
STATE: P
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 AAGGTCACAATGACTTGCAGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
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Fatent No. 6391299
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Gross, Mitchell
APPLICANT: Remerstein, Glora
APPLICANT: Nichols, Andrew
APPLICANT: Padian, Eduardo
APPLICANT: Patian, Aunbhai
APPLICANT: Patian, Aunbhai
APPLICANT: ANUNCAGULANT AGENTS USEFUL IN TREATMENT:
TITLE OF INVENTION: ANTICOAGULANT
TITLE OF ENQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 54.1%; Score 172; DB 3; Length 335; Best Local Similarity 99.6%; Pred. No. 2.1e-80; Matches 222; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
                                                                                CLASSIFICATION:
PRIOR APPLICATION:
PROOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, KITK
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Coding Sequence: LOCATION: 1...335
CTER INFORMATION:
US-08-783-8534-102
                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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ORIGINAL SOURCE:
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144 TGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGGTTCAGTGGCAGTGGGTCTGGGAC 203
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.7%; Score 120; DB 4; 1
ilarity 100.0%; Pred. No. 2.7e-53;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB9B/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                          SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION: <unknown>
                         STREET: 1100 New York Ave., N.W. CITY: Washington
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: PILLESBURY, MADISON & SUTRO 1100 NEW YORK AVENUE, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: other nucleic acid SEQUENCE DESCRIPTION: SEQ ID NO: 17: US-09-423-439-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAYLORSON, CHRISTOPHER JOHN EGGELTE, HENDRIKUS JOHANNES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHEMICAL COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TARRAGONA-FIOL, ANTONIO
APPLICANT: RABIN, BRIAN ROBERT
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: BOYLE, FRANCIS THOMAS
APPLICANT: BLAKELY, DAVID CHARLES
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: MARSHAM, PETER ROBERT
APPLICANT: HEATON, DAVID HUM
TITLE OF INVENTION: CHEMICAL COMPOUND
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/08860882A Patent No. 5985281 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 705 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
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                                                                                                 COUNTRY: U.S.A.
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Matches 120; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 387;
                                                                                                                                                         ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.7%; Score 120; DB 2; I
llarity 100.0%; Pred. No. 2.6e-53;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/154,389
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB91/01108
FILING DATE: 05-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9014932.9
FILING DATE: 05-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9014932.9
FILING DATE: 05-JUL-1990
ATORNEY/AGENT INFORMATION:
ANAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 28,665
REPERPONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
                                                                  Foley & Lardner
3000 K Street, N.W., Suite 500
TITLE OF INVENTION: Their Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE: A5B7 light chain vl domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                         STREET: 3000 K Street,
CITY: Washington, D.C.
COUNTRY: USA
                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: 1.387
US-08-449-287-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 120; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-423-439-17
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Gaps

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225 TGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTTCAGTGGCAGGGGGTCTGGGAC 284
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                                                                                                                            144 TGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGAC 203
                                                                                     Gaps
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                                          Length 732,
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                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pillsbury Madison & Sutro, LLP STREET: 1100 New York Ave., N.W.
                                          Score 120; DB 4; 1
Pred. No. 2.7e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.7%; Score 120; DB 4;
100.0%; Pred. No. 2.7e-53;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/GB96/01975
FILING DATE: 13-AUG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN-1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
                             37.7%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
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FILING DATE: 13-Feb-1998
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOWELL, Robert I.
TITLE OF INVENTION: Chemical Compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: 1.44 Mb disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 16..720
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-011-769A-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HENNAM, John F.
HENNEQUIN, Laurent F.A.
                                                                                                                                                                                                                                                                                                   RESULT 11
US-09-011-769A-22
; Sequence 22, Application US/09011769A
; Patent No. 6436691
; GENERAL INFORMATION:
 APPLICANT: SLATER, Anthony M.
BLAKEY, David C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 16-AUG-1995 INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                  SLATER, Anthony M. BLAKEY, David C. DAVIES, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MARSHAM, Peter R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 732 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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Best Local Similarity 100.0
Matches 120; Conservative
                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C
                                            Query Match
Best Local Similarity
Matches 120; Conserv
    US-09-423-439-57
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100.0%; Pred. No. 2.7e-53;
11ve 0; Mismatches 0;
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APPLICATION NUMBER: US/09/423.439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION: «UNKNOWN»
PRIOR APPLICATION DATA:
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-423-439-57
Sequence 57, Application US/09423439
Sequence 57, Application US/09423439
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: 16..720
SEQUENCE DESCRIPTION: SEQ ID NO: 57:
                                                                                                                          9901/238653
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      US/08/860,882A
                                                                                                                     REFERENCE/DOCKET NUMBER: 9901
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3027
TELEFAX: (202) 822-0944
TELEX: 6174627 CUSH
INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS:
LENGTH: 732 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 732 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                        25,323
APPLICATION NUMBER: US/08/
FILING DATE: JUNE 23, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                           ATTORNEY/AGENT INFORMATION:
NAME: DONALD J. BIRD
REGISTRATION NUMBER: 25,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
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Best Local Similarity 100.
Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPOLOGY: linear
                                                                                                                                                                                                                                                                                                                  single
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                                                                                                                                                                                                                                                                                                                                       linear
                       FILING DATE: JUI
                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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I Street, N.W., Suite 700
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Sequence 3, Application US/09280028

; Patent No. 6241961

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 292 base pairs
nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                COMPUTER READABLE FORM:
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TOPOLOGY: linear
                    Washington
                                                                             20005-3315
                                                                                                                         MEDIUM TYPE:
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                                       STATE: C
COUNTRY:
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225 TGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGGAC 284
                                     204 CICTIACTCTCACAAICAGCAGAGGGGGGCTGAAGAIGCTGCCACTIATIACTGCCA 263
                                                              144 TGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGAC 203
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APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Tetravalent Bispecific Receptors,
TITLE OF INVENTION: Preparation and Use Thereof
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.7%; Score 120; DB 4; L
100.0%; Pred. No. 2.8e-53;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCI/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                      APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Pillsbury Winthrop, I
STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 52:
US-09-423-439-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08308494A Patent No. 5959083 GENERAL INFORMATION:
                                                                                                                                                                             Sequence 52, Application US/09423439 Patent No. 6339070 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 3217 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 100.0
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dunner
                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-308-494A-12
                                                                                                                                                          US-09-423-439-52
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APPLICANT: BENES, IVAN FRIEDRICH
APPLICANT: BENES, IVAN FRIEDRICH
APPLICANT: BOSSLET, KLAUS
TITLE OF INVENTION: RADIOIMMUNO CONJUGATES FOR USE IN HUMAN THERAPY AND
TITLE OF INVENTION: METHOD FOR THEIR PREPARATION
FILE REFERENCE: BENES
CURRENT APPLICATION NUMBER: US/09/280,028
CURRENT FILING DATE: 1999-03-26
EARLIER APPLICATION NUMBER: 199 11 329.7
EARLIER PILING DATE: 1999-03-15
EARLIER PILING DATE: 1999-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90 TTACATGCACTGGTACCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTCTGCCAC 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150 ATCCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA
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SCFWARE STATES S
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Best Local Similarity 99.0%; Pred. No. 1.1e-37;
Matches 190; Conservative 0; Mismatches 2;
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 ATCCAACCTGGCTTCTGGAGTCCCTGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA 209
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                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                         TYPE: DNA
ORGANISM: Mus musculus
ERATURE:
OTHER INFORMATION: CDNA sequence of codons for amino acids 9-105 of
OTHER INFORMATION: VL exon for k-light chain gene (VK) which codes
OTHER INFORMATION: for the MAb light chain and the amino acid
OTHER INFORMATION: sequence associated therewith
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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APPLICANT: Bosslet, Klaus
APPLICANT: Bosslet, Klaus
TITLE OF INVENTION: Granulocyte-Binding Antibody Constructs,
TITLE OF SEQUENCES: 17
CORRESPONDENCE ADDRESS: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 28.3%; Score 90; DB 4; Length 292; Best Local Similarity 99.0%; Pred. No. 1.1e-37; Matches 190; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURREW APPLICATION DATA:
APPLICATION NUMBER: US/08/459,310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,963
FILING DATE: 03-AUG-1993
APPLICATION UNBER: DE P 422 58 53.7
FILING DATE: 05-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08459310 Patent No. 5645817 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
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EARLIER FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005
COMPUTER READABLE FORM:
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247 GAGTAGTAACCC 258
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COCATION: (2)..(292)
US-09-280-028-3
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150 ATCCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTA 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 CTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTG 269
                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                 Length 315;
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   02481.1317-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: November 27, 2002, 05:39:27
Job time : 39.6419 secs
REFERENCE/DOCKET NUMBER: 0248
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-408-400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 base pairs
                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                   28.3%;
99.0%;
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.08
Matches 190; Conservative
                                                                                                                                                          single
                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 GAGTAGTAACCC 281
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US-08-459-310-3
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Sequence 104, App
Sequence 104, App
Sequence 6, Appli
Sequence 102, App
Sequence 102, App
Sequence 79, App
Sequence 63, Appl
Sequence 63, Appl
Sequence 65, Appl
Sequence 65, Appl
Sequence 73, Appl
Sequence 73, Appl
Sequence 73, Appl
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                                                                                                (without alignments) 3436.030 Million cell updates/sec
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                                                                                 November 27, 2002, 05:34:00; Search time 35.6419 Seconds
                                                                                                                                             318
1 CAAATTGTTCTCTCCCAGTC.......GGACCATGCTGGAAATAAGA 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                                                                                                                                                                                                                                                     1: /cgn2_6/ptodata/1/pupna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubna/USO7_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubna/USO6_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubna/PCTUS_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubna/USO8_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubna/USO8_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubna/USO8_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubna/USO8_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubna/USO8_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubna/USO8_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubna/USO8_PUBCOMB.seq:*
          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-965-099-104
US-09-965-099-104
US-09-965-099-6
US-10-051-852-6
US-10-051-852-6
US-09-965-099-63
US-09-965-099-63
US-10-051-852-63
                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                      341543 seqs, 192557720 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                             Published_Applications_NA:*
                                                                                                                                                                                                                                                                                                                                   Post-processing: Listing first 45 summaries
                                                           nucleic search, using sw model
                                                                                                                                                                                  OLIGO_NUC
Gapop 60.0 , Gapext 60.0
                                                                                                                                                                                                                                                                                               seq length: 0 seq length: 2000000000
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Match 1
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Maximum DB
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                                                                                                                                                                                                                      Searched:
                                                                                                                                                            Sequence:
                                                                                   Run on:
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Schumen.,
Wong, Hing
Wong, Hing
Stinson, Jeffrey L.
TITLE OF INVENTION: OPSONIC AND PROTECTIVE MONOCLONAL AND
CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
POSITIVE BACTERIA
                                                          Sequence 16, Appl
Sequence 16, Appl
Sequence 8, Appl
Sequence 16, Appl
Sequence 31, Appl
Sequence 31, Appl
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Appl
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Appl
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Appl
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332,
34,
43,
61,
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ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATORNATION UNABER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGNT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
                      0.05-0982-107-11

0.05-0982-107-11

0.05-09-910-059-18

0.05-09-910-059-18

0.05-09-910-059-18

0.05-09-976-787-31

0.05-09-976-787-31

0.05-09-976-787-31

0.05-09-965-099-94

0.05-09-965-099-94

0.05-09-965-099-98

0.05-09-965-099-98

0.05-09-965-099-98

0.05-09-965-099-1852-187

0.05-09-965-099-1852-187

0.05-09-965-099-1852-187

0.05-09-965-099-1852-187

0.05-09-965-099-17

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STREET: 1300 I Street, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 88, Application US/09893615
Patent No. US20020082395A1
GENERAL INFORMATION
APPLICANT: Fischer, Gerald W.
Schuman, Richard F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
   100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 
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                                                                                                                                                                                                                                                                                                                                             412
412
165
165
280
321
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3321
3321
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108
US-09-893-615-88
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Sequence 3, Appli Sequence 5, Appli Sequence 11, Appl Sequence 27, Appl

US-09-808-037-5 US-09-897-006-11 US-09-976-787-27

JS-08-940-544-3

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52 AAGGICACAAIGACIIGCAGGGCCAGCICAAGIGIAAAIITACAIGCACIGGIACCAGCAG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                                                                                                Length 318;
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Road
                                                                                                                                                                                                                                                                                                                                                                              Score 172; DB 10;
Pred. No. 8.1e-80;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
RPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: CLASSIFICATION: 
                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 104:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                Coding Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Blackburn, Michael
Church, William
Gross, Mitchell
Feuerstein, Giora
Nichols, Andrew
Padlan, Eduardo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 104, Application US/10051852 Patent No. US20020146411A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patel, Arunbhai
Sylvester, Daniel
                                                         LENGTH: 318 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: SmithKline
STREET: 709 Swedeland
CITY: King of Prussia
                    INFORMATION FOR SEQ ID NO: 104: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                54.18;
99.68;
                                                                                                                                                                                                    <Unknown>
                                                                                                                                                                                                                                                                                 LOCATION: 1...318
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.6
Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SECUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                             ANTI-SENSE: NO
FRAGMENT TYPE: <U
ORIGINAL SOURCE:
FEATURE:
                                                                                                                                                           HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                           US-09-965-099-104
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US-10-051-852-104
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                                                                                                                                                                                                                                                                                                                                                                                  121 TCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGC 180
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                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                            1 CAAATTGTTCTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAAAAGGTCACA 60
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                                                                                                                                          Length 318;
                                                                                                                                                                               Indels
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                 ..
                                                                                                                                      100.0%; Score 318; DB 10; 100.0%; Pred. No. 1.7e-155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TREATMENT OF THROMBOSIS
                                                                                                                                                                                 0; Mismatches
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REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001
CLASSIFICATION: <Unknown>
                                             LOCATION: 1.318

SEQUENCE DESCRIPTION: SEQ ID NO: 88:

US-09-893-615-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 104, Application US/09965099
Patent No. US20020136725A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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Patel, Arunbhai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette
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MEDIUM TYPE: Diske
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                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 318; Conservative
                                     NAME/KEY: CDS
MOLECULE TYPE: CDNA
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US-09-965-099-104
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112 AAGCCAGGATCCTCCCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTC 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SMithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 172; DB 10;
Pred. No. 8.1e-80;
0; Mismatches 1;
              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
FILLING DATE: 26-58P-2001
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/346,487
FILING DATE: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-965-099-6
  SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELERAX: «UNKNOWN»
TELEX: «UNKNOWN»
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Blackburn, Michael
Church, William
Gross, Mitchell
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                                                                                                                                                                                                                                                                                                                                                          LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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Padlan, Eduardo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO FRAGMENT TYPE: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sim
Matches 222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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ADDRESSE: SmithKline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.1%; Score 172; DB 12;
1larity 99.6%; Pred. No. 8.1e-80;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Blackburn, Michael
APPLICANT: Blackburn, Giora
Feuerstein, Giora
Patel, Arubbal
TITLE OF INVENTION: ARTICOAGULANT AGENTS USF
TREATMENT OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE DESCRIPTION: SEQ ID NO: 104:
                                                                                             NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
APPLICATION NUMBER: 09/344,050
              FILING DATE: 25-JUN-1999
APPLICATION UNMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Coding Sequence LOCATION: 1...318
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09965099
Patent No. US20020136725A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                   TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 222; Conserva
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US-09-965-099-6
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Gaps

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172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGGGG 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54.1%; Score 172; DB 10; 99.6%; Pred. No. 8.1e-80; Live 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                   NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: 950438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELERAX: <Unknown>
                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 102:
                                                                                                                                                                                                                                                         APPLICATION WINDER: 09/346,487
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Coding Sequence LOCATION: 1...335 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 102, Application US/10051852
Patent No. US20020146411A1
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
Church, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gross, Mitchell
Feuerstein, Giora
Nichols, Andrew
Padlan, Eduardo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 335 base pairs
TYPE: nucleic acid
                ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 102: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 99.6
Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-965-099-102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 AAGCCAGGATCCTCCCCCAAACCCTGGATTATGCCACATCCAACCTGGCTTCTGGAGTC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 AAGCCAGGATCCTCCCCCAAACCCTGGATTTCTGCCACATCCAACCTGGCTTCTGGAGTC 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172 CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 AAGGTCACAATGACTTGCAGGGCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
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ADDRESSEE: Smithfiline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 172; DB 12;
Pred. No. 8.1e-80;
0; Mismatches 1;
                                                                                                       CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-38n-2002
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY, ACENT.
                                                                                                                                                                                                                                                                                                                                     NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 102, Application US/09965099
Patent No. US20020136725A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Blackburn, Michael
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Patel, Arunbhai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 321 base pairs
TYPE: nucleic acid
                       MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.6%;
Matches 222; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 111
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: <Unknown>
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US-09-965-099-102
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TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGCTCGCTTCAGTGGCAGTGGGTCTGGGACCTCTTACTCTCTCACAATCAGCAGAGTG 231
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                                         Sylvester, Daniel TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGTGGAGTA 274
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                                                                                                                                                                                                                                               Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

54.1%; Score 172; DB 12;
Best Local Similarity 99.6%; Pred. No. 8.1e-80;
Matches 222; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM COMPATILE
COMPUTER: IBM COMPATILE
OPERATING SYSTEM: DOS
SOFTWARE: FRASISCO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION: CURKNOWN>
PRIOR APPLICATION NUMBER: 09/344,050
FILLING DATE: 15-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JUN-1997
ATTONEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REGISTRATION NUMBER: 33,833
REERROKE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEX: <unhanyan;
TELEX: <u
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LOCATION: 1...335
GOTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 102:
US-10-051-852-102
                                                                                                                 OF THROMBOSIS
                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beeck
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
Patel, Arunbhai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: NO
ANTI-SENSE: NO
FRACMENT TYPE: <Unknown>
ORIGINAL SOURCE:
FEATURE:
                                                                                                                                                               NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 CACATCCAACCTGGCTTCTGGAGTCCCTGCTTCGCTTCAGTGGCAGTGGTCTGGG 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
Sequence 79, Application US/09753436

Battent No. US20010029293A1

GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Vazeux, Rosemay
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TIMBER OF SEQUENCES: 120
                                                                                                                                                                                                                                                        CITY: Chicago STATE: Illinois COUNTRY: United States of America ZIP: 6606-6402 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IMM STATEM: APPLICATION DATA: APPLICATION NUMBER: US/09/753,436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.3%; Score 55; DB 10; L
100.0%; Pred. No. 3.6e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,113
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,754
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,852
FILING DATE: 05-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/009,266
FILING DATE: 20-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/894,061
FILING DATE: 20-UN-1992
PRIOR APPLICATION NUMBER: US 07/889,724
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 26-MAY-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
PRIOR APPLICATION NUMBER: US 07/827,689
FILING DATE: 27-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS: ASSOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 09/382,289
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100.08; Pr.
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (312) 474-6300
(312) 474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 390 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 25-3856
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
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Gaps
                     Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
OF THROMBOSIS
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                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
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16.7%; Score 53; DB 12;
Best Local Similarity 100.0%; Pred. No. 3.8e-18;
Matches 53; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                           ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: 17-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: P50438
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CRIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
US-10-051-852-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 65, Application US/09965099
Patent No. US20020136725A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Blackburn, Michael
Feuerstein, Glora
Patel, Arunbhai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                             CITY: King of Prussia
Patel, Arunbhai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 63: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <Unknown>
                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                            COUNTRY: USA
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                                                                                                                                                                                                         STATE: PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                     TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSES: Smithfuline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 16.7%; Score 53; DB 10; I
Best Local Similarity 100.0%; Pred. No. 3.8e-18;
Matches 53; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                            TREATMENT OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 63:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 09/346,487
FILING DATE: «UNKNOWN»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Blackburn, Michael
Church, William
Gross, Micchell
Feuerstein, Glora
Nichols, Andrew
Padlan, Eduardo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 26-Sep-2001 CLASSIFICATION: <Unknown>
                                                             Sequence 63, Application US/09965099
Patent No. US20020136725A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 63, Application US/10051852 Patent No. US20020146411A1 GENERAL INFORMATION:
                                                                                                                                APPLICANT: Blackburn, Michael
                                                                                                                                                          Feuerstein, Giora
Patel, Arunbhai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                    STATE: PA
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                   RESULT 9
US-09-965-099-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-965-099-63
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67 TGCAGGCCCAGCTCAAGTGTAAATTACATGCACTGGTACCAGCAGAAGCCAGG 119
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Patel, Arubbal
TITLE OF INVENTION: TREATMENT OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.7%; Score 53; DB 12; I
100.0%; Pred. No. 3.8e-18;
Live 0; Mismatches 0;
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
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SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Coding Sequence LOCATION: 2...280 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 73, Application US/09965099
Patent No. US20020136725A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Blackburn, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 280 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 65:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: <Unknown>
TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19406
COMPUTER READABLE FORM:
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MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53; Conservative
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Best Local Similarity
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US-09-965-099-73
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.7%; Score 53; DB 10; I
100.0%; Pred. No. 3.8e-18;
tive 0; Mismatches 0;
                                                                                                                                                                APPLICATION DATE:
CORRENT APPLICATION DATE:
ELLING DATE: 26-Sep-2001
CLASSIFICATION: CURROWN>
PRIOR APPLICATION: CURROWN>
PRIOR APPLICATION: CURROWN>
PRIOR APPLICATION OWNER: 09/346,487
FILING DATE: CURROWN>
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: 950438-1
TELEPHONE: 610-270-5096
TELEPHONE: 610-270-5096
TELEPHONE: 610-270-5096
TELEPKX: CURROWN>
TELEPKX: CURROWN>
TELERX: CURROWN>
TELERX: CURROWN>
TELERX: CURROWN>
TELENGTH: 280 base pairs
SEQUENCE CHARACTERISTICS:
LENGTH: 280 base pairs
STRANDEDNESS: single
TOPOLGGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Coding Sequence:
LOCATION: 2...280
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 65:
US-09-965-099-65
                                                           MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASKESO VERSION 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Blackburn, Michael Church, William Gross, Mitchell Feuerstein, Glora Nichols, Andrew Padlan, Eduardo Patel, Arunbhai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 65, Application US/10051852
Patent No. US20020146411A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: «Unknown»
ORIGINAL SOURCE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 111
                ZIP: 19406
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.0
Matches 53; Conservative
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ZIP: 19406
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Gaps

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Length 280; 0; Indels œ

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APPLICANT: SOLOMON, Beka
APPLICANT: HANAN, ELLAL
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
FILE REFERENCE: SOLOMON=20
CURRENT APPLICATION NUMBER: US/19/808,037
CURRENT FILING DATE: 2001-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
16.7%; Score 53; DB 12; L
Best Local Similarity 100.0%; Pred. No. 3.8e-18;
Matches 53; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
16.7%; Score 53; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.9e-18;
Matches 53; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 2001-03-15
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 08/473,653
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-12-29
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 27
LENGH: 357
                     FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERRUCE/DOCKET NUMBER: 950438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Coding Sequence
LOCATION: 1...321
OTHER INDEMATION: F9HZLC 2-0
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/09808037 Patent No. US20020052311A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    LENGTH: 321 base pairs
                                                                                                                                                                                                                                                   TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: synthetic construct
                                                                                                                                                                                                                              TELEFAX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: <Un
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)..(357) US-09-808-037-27
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US-09-808-037-27
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Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.7%; Score 53; DB 10; I 100.0%; Pred. No. 3.8e-18; Iive 0; Mismatches 0;
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APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: VUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                             REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1...321
OTHER INFORMATION: F9HZLC 2-0
SEQUENCE DESCRIPTION: SEQ ID NO: 73:
                                                          APPLICATION NUMBER: 09/346,487
FILING DATE: <URKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF THROMBOSIS
                                                                                                                                NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Coding Sequence
FILING DATE: 26-Sep-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Church, William
Gross, Mitchell
Feuerstein, Giora
Nichols, Andrew
Padlan, Eduardo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 73, Application US/10051852 Patent No. US20020146411A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blackburn, Michael
                                                                                                                                                                                                                                                                                                                                            LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
FEATURE:
                                                                                                                                                                                                                                                     TELEFAX: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 16.7
Best Local Similarity 100.
Matches 53; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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US-10-051-852-73
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Db 196 CTGGCTTCTGGAGTCCCTGCTCCGCTTCAGTGGCAGTGGGTCTGGGACCTCTA 248

Search completed: November 27, 2002, 07:14:52 Job time : 36.6419 secs

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November 27, 2002, 07:19:05; Search time 37.6525 Seconds (without alignments) 375.129 Million cell updates/sec
                                                                                                                                                                                    US-09-893-615-89
106
1 QIVLSQSPAILSASPGEKVT.......CQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                                   908470
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                     908470 seqs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Listing first 45 summaries
                                                                       OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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| A_Geneseq_101002:* | /SIDS2/gcgdata/geneseq/genesegp-emb | /SIDS2/gcgdata/geneseq/genesegp-emb | /SIDS2/acadata/geneseg/genesegp-emb |
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| 1: | /SIDS2/gcgdata/geneseq/genesegp-embl/AA1980.DAT:* |
| .: | /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:* |
| 3: | /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:* |
| 4 | /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:* |
| 5: | /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:* |
| : 9 | /SIDS2/gcgdata/geneseg/genesegp-embl/AA1985.DAT:* |
| 7: | /SIDS2/gcgdata/geneseg/genesegp-embl/AA1986.DAT:* |
| 80 | /SIDS2/gcgdata/geneseq/genesegp-embl/AA1987.DAT:* |
| 6 | /SIDS2/gcgdata/geneseg/genesegp-embl/AA1988.DAT:* |
| 10: | /SIDS2/gcgdata/geneseq/genesegp-embl/AA1989.DAT:* |
| 11: | /SIDS2/gcgdata/geneseq/genesegp-embl/AA1990.DAT:* |
| 12: | /SIDS2/gcgdata/geneseg/genesegp-embl/AA1991.DAT:* |
| 13; | /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:* |
| 14: | /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:* |
| 15: | /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994.DAT:* |
| 16: | /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:* |
| 17: | /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996.DAT:* |
| 18: | /SIDS2/gcgdata/geneseq/genesegp-embl/AA1997.DAT:* |
| 19: | /SIDS2/gcgdata/geneseq/genesegp-embl/AA1998.DAT:* |
| 20: | /SIDS2/gcgdata/geneseq/genesegp-embl/AA1999.DAT:* |
| 21: | /SIDS2/gcgdata/geneseg/genesegp-embl/AA2000.DAT:* |
| 22: | /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:* |
| 23: | /SIDS2/qcqdata/qeneseq/qeneseqp-embl/AA2002.DAT:* |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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| | | Description | Anti-Factor IX MAD | Mouse-human light | Mouse anti-human F | Murine BC2 light c | Anti-Factor IX MAD | Murine BC2 light c | Kappa light chain | Amino acid sequenc | Anti-NKG2D hybrido | Anti-EGFR antibody |
|---|--------|-----------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|
| | | ID | AAW24532 | AAU81002 | AAW24520 | AAU80976 | AAW24531 | AAU81001 | AAW19914 | AAY84965 | AAU72834 | AAR79883 |
| | | BB | 18 | 23 | 18 | 23 | 18 | 23 | 18 | 21 | 23 | 16 |
| | | Match Length DB | 106 | 106 | 107 | 107 | 112 | 112 | 105 | 633 | 106 | 108 |
| ď | Query | Match | 44.3 | 44.3 | 44.3 | 44.3 | 44.3 | 44.3 | 43.4 | 40.6 | 39.6 | 39.6 |
| | | Score | 47 | 47 | 47 | 47 | 47 | 47 | 46 | 43 | 42 | 42 |
| | Result | 0 | - | 7 | m | 4 | ហ | Q | 7 | 80 | o | 10 |

| A fusion of anti-C Sequence encoded b 2 H7 VL gene. 2H7 VL gene. 2H7 Antibody light 2H7 Iight chain variab Mouse 2H7 antibody Mouse 3H7 antibody Murine Abs57 Light Plasmid pNG3/A5B7V Plasmid pNG3/A5B7V Plasmid pEE14/ASB7 IL-2 Chimeric anti Anti-Ti2R-alpha an Anti-Ti2R-alpha an Anti-Tac Iight cha Protein SEO ID NO: Humanised antibody Murine anti-Tac an Murine anti-Tac an Murine anti-Tac an Murine anti-Tac an | Antigen-binding pr Mab32 V-gene heavy Mouse ganglioside Ganglioside GM2 an Murine VL kappa gr Anti-EGFR antibody Anti-CEA antibody |
|---|--|
| | AAU 44 18 AAB 315 9 AAB 315 9 AAB 3167 AAR 79884 AAR 79884 |
| 100 0 100 100 100 100 100 100 100 100 1 | 7400444 |
| 200 200 200 200 200 200 200 200 200 200 | |
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| 112111165111661116611166111661116611166 | 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 |

ALIGNMENTS

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thromboembolic of a thrombolytic

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Gaps

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Length 106; Indels

DB 23; L

Mismatches Score 47; Pred. No.

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fragment, optionally in combination with a plasminogen activator or thrombolytic agent. The method is useful for treating post-thromboembolic-induced ischaemia, for preventing thromboembolic stroke in an animal, and for reducing a required dose of a thromboly agent. Sequences AAU80972-AAU81004 represent antibodies and vector
                                                            polypeptides used in the method of the invention.
                                                                                                  44.3%; Scc.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-385117/35
                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               shunt; prosthesis.
                                                                                     106 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAT77377
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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                                                                                                               Local Sin.
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17-JAN-1996;
                                                                                                                                                                                                                                                                                             26-DEC-1997
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                                                                                     Sequence
                                                                                                                                                                                                                                                                     AAW24520;
                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for treating an animal sost-thromboembolic induced ischemma or reducing a required dose of a thrombolytic agent in treatment of an animal post-thromboembolic induced ischaemla, comprising administering an anti-factor IX antibody or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treating post-thromboembolic induced ischaemia in an animal by administering anti-factor IX antibody in combination with a plasminogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; mouse; BC2; animal post-thromboembolic induced ischaemia; thrombolytic agent; anti-factor IX antibody; plasminogen activator; thrombombolic stroke; cerebroprotective; anticoagulant; Thrombolytic; vasctroptc; cardiant; anti-respiratory synoytial virus; heavy chain variable region; light chain variable region.
                                                                                                                                                                                                                                                                       Gaps
                                                                                                         light chain in which the variable region is derived from mouse anti-human factor IX monoclonal antibody BC2 (see AAW2451) and human sequences from the immunoglobulin RF-TS3'CL framework.

It can be expressed in transfected mammalian cells utilising a CDNA construct (see AAT79900) obtained by PCR amplification (see FAT7987-98) of BC2 CDNA and insertion of the PCR product into antibodies are useful in the treatment of thrombosis.
                       Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial
                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                               Length 106;
                                                                                                This polypeptide comprises a mouse-human chimeric antibody
                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                       QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toomey JR;
                                                                                                                                                                                                                                            DB 18; I
7.3e-35;
                                                                                                                                                                                                                                     44.3%; Scor.
100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feuerstein GZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Page 155-156; 163pp; English.
                                                                       Example 7; Page 128; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse-human light chain polypeptide.
                                                                                                                                                                                                                                                                                                                                                                               Ā
                                                                                                                                                                                                                                                                                                                                                                            AAU81002 standard; Protein; 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-2000; 2000US-0571434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-OCT-2000; 2000WO-US27438
                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blackburn MN,
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - Mus sp.
Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-082944/11.
N-PSDB; ABK24005.
                                                                                                                                                                                                                     106 AA;
N-PSDB; AAT79900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200187339-A1
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                                               inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barone FC,
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activator
                                                                                                                                                                                                                                                                                                                                                                                                   AAU81002;
                                                                                                                                                                                                                                                                                                                                                      RESULT 2
AAU81002
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Mouse anti-human Factor IX antibody BC2 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Thrombosis; therapy; Factor IX; anticoagulant; monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        humanised antibody; antibody engineering; light chain; CDR; complementarity determining region; myocardial infarction; angina; artial fibrillation; stroke; kidney damage; pulmonary embolism; deep vein thrombosis; coronary andioplasty; disseminated intravascular coagulation; artificial organ; sepsis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting thrombosis with self-limiting antibody to coagulation factor – avoids uncontrolled bleeding by providing only partial inhibition
                             1 QIVLSQSPAILSASPGEKVIMTCRASSSVNYMHWYQQKPGSSPKPWI 47
1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKFWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gross MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feuerstein GZ, GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM CORP.
(UYVE-) UNIV VERMONT & STATE AGRIC COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 66-67; 150pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24..33
/label= CDR1
/note= "(Claim 23)"
49..55
/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "(Claim 23)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "(Claim 23)"
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Nichols AJ, Padlan EA, Patel AH,
                                                                                                                                                                                                     AAW24520 standard; Protein; 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88..96
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-US00759
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Gaps

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Indels

DB 23; 1

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stroke in an animal, and for reducing a required dose of a thrombolytic agent. Sequences AAU80972-AAU81004 represent antibodies and vector polypeptides used in the method of the invention.
                                                                                   Query Match
Best Local Similarity 100.0
Matches 47; Conservative
                                                             107 AA;
                                                                                                                                                                                                                                                                                                           27-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-OCT-1996;
17-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nichols AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-1997.
                                                                                                                                                                                                                                                                              AAW24531;
                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                    AAW24531
                                                                                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method for treating an animal post-thromboembolic induced ischaemia or reducing a required dose of a thrombolytic agent in treatment of an animal post-thromboembolic induced ischaemia, comprising administering an anti-factor IX antibody or its fragment, optionally in combination with a plasminogen activator or thrombolytic agent. The method is useful for treating post-thromboembolic-induced ischaemia, for preventing thromboembolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             animal by
with a plasminogen
This sequence comprises the light chain variable region of mouse anti-human Factor IX monoclonal antibody BC2. Claimed humanised antibodies (see AAW24510-18) contain CDRs (see AAW24540-99) of BC2 cantibodies (see AAW24510-18) contain CDRs (see AAW24540-99) of BC2 heavy and light chain variable regions inserted into framework regions of selected human antibody sequences. They have self-limiting neutralising activity, and are useful as anticoagulant agents in treatment of thrombosis associated with mycardial infarction, unstable angina, atrial fibrillation, stroke, renal famence, pulmonary embolism, deep vein thrombosis, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulation, sepsis, or artificial organs, shunts or prostheses (claimed). Also claimed are chimeric antibodies (see AAW24532), and Fab and F(ab')2 fragments. The claimed antibodies do not cause uncontrolled bleeding (contrast heparin and warfarin) since they provide only partial inhibition of coagulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; mouse; BC2; animal post-thromboembolic induced ischaemia; thrombolytic agent; anti-factor IX antibody; plasminogen activator; thromboembolic stroke; cerebroprotective; anticoagulant; Thrombolytic; vasotropic; cardiant; anti-respiratory syncytial virus; heavy chain variable region; light chain variable region.
                                                                                                                                                                and
                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                    1 QIVLSQSPAILSASPGEKVTWTCRASSSVNYMHWYQQKPGSSPKPWI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feuerstein G2, Toomey JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treating post-thromboembolic induced ischaemia in.an administering anti-factor IX antibody in combination
                                                                                                                                                                                                                                                                                                                       1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWI
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                                                                                                                                                                                                                                                                              7.4e-35;
                                                                                                                                                                                                                                                                 DB 18;
                                                                                                                                                                                                                                                                           100.0%; Pred. No. 7.4 :ive 0; Mismatches
                                                                                                                                                                                                                                                               44.38; Score 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murine BC2 light chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 5; Page 97; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAU80976 standard; Protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-OCT-2000; 2000WO-US27438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blackburn MN,
                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-082944/11.
                                                                                                                                                                                                                                 107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activator
                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU80976;
                                                                                                                                                                                                                                                               Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                         AAU80976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This polypeptide sequence comprises a modified light chain variable region (see also AAVA2450) of mouse anti-human factors IX monoclonal antibody BC2. It is encoded by a DNA fragment (see AAV79899) produced by PCR amplification of BC2 cDNA. The modified BC2 VL region is incorporated into novel mouse-human chimeric light chain P9CHLC (see AAVA4532). Claimed anti-Pactor IX chimeric antibodies are useful in the treatment of thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thrombosis; therapy; Factor IX; anticoaqulant; monoclonal antibody; chimeric antibody; antibody engineering; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Inhibiting thrombosis with self-limiting antibody to coagulation factor - avoids uncontrolled bleeding by providing only partial inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWI 47
                                                                                                                                                  1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSSPKPWI
                                                                                                                      1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKFW1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gross
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44.3%; Score 47; DB 18; 100.0%; Pred. No. 7.7e-35
44.3%; Scor.
100.0%; Pred. No. /...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-Factor IX MAb BC2 modified light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNIV VERMONT & STATE AGRIC COLLEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Church WR, Feuerstein GZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 7; Page 126; 150pp; English.
                                                                                                                                                                                                                                                                                                                ¥.
                                                                                                                                                                                                                                                                                                          AAW24531 standard; Protein; 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0029119.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US00759
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-385117/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric Mus muscul
Chimeric synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT79899
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"complementarity determining region 1"

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TrkA receptor; monoclonal antibody; docking site; human p140 TrkA; NGF; hormone-receptor interactive site mapping; artificial receptor agonist; receptor.domain functional correlation; NGF docking site; therapy; neve growth factor; tumour growth inhibitor; neurological disease; neuroma; neoplastic tumour.
                                                                                                                                                /note- "complementarity determining region 2" 88..96 /note- "complementarity determining region 3"
                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                      95GB-0025180.
                                                                                                                                                                                                                                               96WO-CA00815
                                                                                                              24..33
/note=
                                                                                                                                                                                                                                                                                             (UYMC-) UNIV MCGILL.
                                                                                                                                       49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 AA;
                                                                                                                                                                                                W09721732-A1.
                                                                            Homo sapiens
                                                                                                                                                                                                                                               06-DEC-1996;
                                                                                                                                                                                                                                                                      08-DEC-1995;
                                                                                                                                                                                                                                                                                                                     Lesauter L,
                                                                                                                                                                                                                       19-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                               Region
                                                                                                                                      Region
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AAY84965
ID AAY8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a method for treating an animal post-thromboembolic induced ischaemia or reducing a required dose of a thrombolytic agent in treatment of an animal post-thromboembolic induced ischaemia, comprising administering an anti-factor IX antibody or its fragment, optionally in combination with a plasminogen activator or thrombolytic agent. The method is useful for treating post-thromboembolic-induced ischaemia, for preventing thromboembolic stroke in an animal, and for reducing a required dose of a thrombolytic agent. Sequences AAU880972-AAU81004 represent antibodies and vector polypeptides used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                             Treating post-thromboembolic induced ischaemia in an animal by administering anti-factor IX antibody in combination with a plasminogen
                                                                                                                                               thrombolytic agent; anti-factor IX antibody; plasminogen activator; thromboembolic stroke; cerebroprofective; anticoaquiant; Thrombolytic; vasotropic; cardiant; anti-respiratory syncytial virus; heavy chain variable region; light chain variable region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                      Human; mouse; BC2; animal post-thromboembolic induced ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.3%; Score 47; DB 23; Length 11 100.0%; Pred. No. 7.7e-35; rive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QIVLSQSPAILSASPGEKVIMTCRASSSVNYMHWYQQKPGSSPKPWI 47
                                                                                                                                                                                                                                                                                                                                                                    Toomey JR;
                                                                                                             Murine BC2 light chain modified variable region.
                                                                                                                                                                                                                                                                                                                                                                   Feuerstein GZ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 7; Page 153-154; 163pp; English.
                                    AAU81001 standard; Protein; 112 AA.
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                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM CORP.
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                                                                                                                                                                                                                                                                                            05-OCT-2000; 2000WO-US27438
                                                                                                                                                                                                                                                                                                                    15-MAY-2000; 2000US-0571434
                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                   Barone FC, Blackburn MN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-082944/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; ABK24004
                                                                                                                                                                                                                                             WO200187339-A1.
                                                                                    09-APR-2002
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                                                                                                                                                                                                             Mus sp.
Synthetic.
                                                              AAU81001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        activator
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Matches
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                         AAU8100
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             RESULT
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AMM 19914 and AAW19915 represent the kappa light chain and the heavy chain of the monoclonal antibody (MAb) 5C3. MAb 5C3 is an example of an MAb of the invention, optionally having characteristic the invention. The MAb of the invention, optionally having complementarity determining region (CDP)-like domains of hormones, binds che TrkA receptor under physiological conditions. MAb 5C3, directed against human pl40 TrkA, is a structural and functional mimic of NGF and artificial receptor agonist. It binds in the NGF docking site and promotes TrkA internalisation, TrkA and phosphotidylinositol-3 kinase tyrosine phosphorylation and increases transformation of TrkA-expressing fibroblasts. The Ab or a TrkA docking site, are used to screen for agents that inhibit or mimic nerve growth factor (NGF) biological activity. The agents and Ab inhibit tumour growth in situ for treatment or prevention of neurological diseases, neuromas and neophastic tumours expressing TrkA receptor by preventing binding of NGF to TrkA receptor or down-regulating the receptor. The Ab is also used for mapping correlation. The Ab can also induce NGF-like responses, especially differentiation. The Ab can also induce NGF-like responses, especially are the prognosis and diagnosis of human functions, by cells expressing TrkA. The prognosis and diagnosis of human functions, by cells expressing TrkA. The prognosis and diagnosis of human functions is the prognosis and the prognosis of human functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the Ab in biopsies and immunocytochemistry or by labelling the Ab and nuclear imaging. Treatment of these tumours involves coupling the Ab to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TrkA. The prognosis and diagnosis of human tumours can be performed the Ab in biopsies and immunocytochemistry or by labelling the Ab an
                                                                                                                                                       Anti-human TrkA antibody recognising nerve growth factor docking site - useful e.g. for treatment of neurological diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytotoxic agent and administering the complex to the patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 18; Length 105; 5.8e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY84965 standard; Protein; 633 AA.
                                                                                                                                                                                                                                                                                                                                 Example 3; Page 31; 61pp; English.
                                                                                                                                                                                                                                     neuroma(s) or neoplastic tumours
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Best Local Similarity 100.
Matches 46; Conservative
Saragovi HU;
                                                                              WPI: 1997-332727/30.
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ATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS 111

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AAU72834 standard; Peptide; 106

AAU72834;

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The present sequence represents a synthetic CD20-specific chimeric receptor. The specification describes CD-20 specific redirected T cells which express and bear on the cell surface membrane a CD20-chimeric receptor comprising an intracellular signalling domain, a transmembrane domain and an extracellular signalling domain, a transmembrane a CD30-specific receptor. The genetically engineered CD20-specific redirected T cells are useful for treating a CD20+ malignancy, such human patient having previously undergone mycoblative chemotherapy and stem cell rescue. The genetically engineered CD20-specific redirected T cells are also useful for abrogating an untoward B cell function, such as autoimmune disease (lupus or rheumatoid arthritis) in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetically engineered CD20-specific redirected T cells useful for treating a CD20+ malignancy, such as non-Hodgkin's lymphoma or CD20+ acute or chronic leukemia, and autoimmune disease
                                                                                                                                                   CD20-specific receptor; CD-20 specific redirected {\bf T} cell; leukemia; CD20+ malignancy; non-Hodgkin's lymphoma; myeoablative chemotherapy; stem cell rescue; autoimmune disease; lupus; rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                 /note= "signal peptide from murine T86.66 antibody kappa light chain"
                                                                                                       Amino acid sequence of a CD-20 specific chimeric receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   21..126
/note= "anti-CD20 variable regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       521
re- "CD4 transmembrane region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "hinge region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "GS18 linker"
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                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "CH3 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "zeta chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0105014
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                                                  (first entry)
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500..52
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522..63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       633 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAA15019.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200023573-A2
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                                                  21-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-APR-2000
                                                                                                                                                                                                                                                                   Synthetic
AAY84965;
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The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NKG2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated polynciectide are used for the preparation of a pharmaceutical composition for the treatment of cancer, infections and/or autoimmune composition for the treatment of cancer, infections and/or autoimmune composition for the treatment of cancer, infections and/or autoimmune cosophagus, colon, liver, intrahepatic bile ducts, paincras, lung, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid, larynx, breast, ovary, uterus, caused by viruses, bacteria, fungi, the infectious diseases can be caused by viruses, bacteria, fungi, protozoa or helminths. The autoimmune diseases include multiple selections disease, ankylosing spondylitis, acute anterior cuveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and autoimmune papatitis, Goodpasture's Sayndrome, myasthenia gravis, insulin-dependent diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and autoimmune papatitis.
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                                                                                                                                                                                                                                                           autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv; sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytostatic; antimicrobial; immunomodulatory; llB2D10; 6H7E7; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3A-14; p5-15; tetramerisation domain; 3B10xP5-2; 3B10xP4-3; 3B10xP4-14;
                                                                                                                                                                                                                               Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multifunctional polypeptides comprising binding sites that specifically recognise extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating cancers and infectious diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riethmueller G, Lutterbuese R, Borschert K,
                                                                                                                                                 Anti-NKG2D hybridoma 6H7E7 variable light chain CDR1.
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Pred. No. 2.4e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor and the polypeptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 16; 114pp; English.
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100.0%; Pre
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-2000; 2000EP-0106467
                                                                      26-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hofmeister R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-055119/07.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200171005-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kufer P,
Mayer M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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49 ATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQW

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49 ATSNLASGVPARFSGSGSTSYSLTISRVEAEDAATYYCQQWS

Length 633;

DB 21; L

ch 40.6%; Score 43; DB 1 Similarity 100.0%; Pred. No. 1.4 43; Conservative 0; Mismatches

Local Similarity

Query Match

Best Loca Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-epidermal growth factor receptor (EGFR) single chain antibodies and antibodies constructed from anti-EGFR antibody fragments can be used for diagnosis of tumours and assessment of tumour growth in
                                                                                                                                                                                                                                                                                                        Single chain antibody; antibody; epidermal growth factor receptor; EGFR; tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment; phage antibody library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-EGFR antibodies and single chain Fv antibody fragments - obtained from phage-antibody libraries, useful for diagnosis and
                                                                                                                                                                                                                                                           Anti-EGFR antibody light chain variable region (Clone L2 1C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 108;
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49 ATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQW 90
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100.0%; Pred. No. 2.5e-30;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- CDR3.
97..108
/label- Framework region 4.
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/label= Framework region 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Framework region 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Figure 1A; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                   AAR79883 standard; Protein; 108 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label- CDR1.
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/label= CDR2.
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94EP-0104160.
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                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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17-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-1995;
                                                                                                                                                                                                               02-JUL-1996
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                                                                                                                                                                  AAR79883;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Adan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Region
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                                                                  RESULT 10
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8XCCCCCCX8X4415X8X15X5X668X6X6X6451515151515151X6X6X6X6X6X8X8XX

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The present sequence represents a fusion of an anti-CD20 single chain antibody (B9E9) streptavidin. The fusion protein is expressed using vectors of the invention. The specification describes vector constructs for expressing streptavidin fusion proteins. The vector comprises a nucleic acid encoding streptavidin or its functional variant operatively linked to a promoter, and a cloning site for insertion of a second nucleic acid sequence encoding polypeptide to be fused with streptavidin, interposed between the promoter and the first nucleic acid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second concid, operatively linked to a promoter, encoding a polypeptide to be fused with streptavidin, and a cloning site for insertion of a second conciled encoding at least 129 amin acides of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e.g. adenocarcinomás or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reno JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sanderson JA,
                                                                                                                                                                                               A fusion of anti-CD20 single chain antibody/streptavidin.
Streptavidin; tumour cell; cancer; adenocarcinoma:
hematological malignancy; B9E9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "streptavidin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schultz JE,
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Fig 11B; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                   "VL chain"
                                                                                                                                                                                                                                                                                                                                                                                                                     127..248
/note= "VH chain"
249..253
                                                                                               AAB30694 standard; Protein; 412
                                                                                                                                                                                                                                                                                                                                                                                  109..126
/note= "linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "linker"
254..412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer, e.g. adenocarcinomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUN-2000; 2000WO-US15595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0137900.
99US-0168976.
                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Graves SS,
                                                                                                                                                                                                                                                                                                                                                         1..108
/note=
                                                                                                                                                                                                                                                                                      Streptomyces avidinii.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-091213/10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200075333-A1.
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03-DEC-1999;
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                                                                                                                                                               02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-DEC-2000
                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                               AAB30694;
                                                                                                                                                                                                                                                                                                                                                         Protein
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                                                                 RESULT 11
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Best Local Similarity 100. Matches 42; Conservative

Query Match

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Gaps

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0; Indels

Gaps

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Length 423; 0; Indels

DB 22; 8e-30;

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fused with streptavidin, and a cloning site for insertion of a second nucleic acid encoding at least 129 amino acids of streptavidin or its functional variant. The fusion proteins are useful for targeting tumour cells, particularly tumour cells associated with cancer.

e.g. adenocarcinomas or hematological malignancies. The vector construct is useful for expressing of streptavidin fusion proteins. In particular, these are useful as tools for medical diagnostics and therapeutic purposes, e.g. for detecting the presence or absence of, or treating, a target site within a mammalian host.
                                                                                                                                                                                                                                                                                                                                                                 Sequence encoded by the 2H7 VL sequence in which the Vk gene contains \ensuremath{\mathsf{JK5}} sequences.
                                                                                                                                                                                                      Query Match 39.6%; Score 42; DB Best Local Similarity 100.0%; Pred. No. 8e-Matches 42; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric antibody; Anti-cancer antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                    AAP70628 standard; protein; 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/label=leader
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/label=CDR2
79..110
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/label=cDR1
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/label=CDR3
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72..78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= h
/label=JK5
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/label=FR4
                                                                                                                                                                                                                                                                                                                                  (updated)
(first entry)
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/*tag= d
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                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric - Homo sapiens.
Chimeric - Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                     423 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-OCT-1986;
                                                                                                                                                                                                                                                                                                                                  03-OCT-2002
                                                                                                                                                                                                                                                                                                                                            09-APR-1991
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                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reno JM;
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New vector constructs for expressing genomic streptavidin fusion proteins which are useful for targeting tumour cells associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sanderson JA,
                                                     Length 412;
                                                                                                                                                                                                                                                  A fusion of anti-CD20 single chain antibody/streptavidin.
                                                                            Indels
                                                                                                              49 ATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQW 90
                                                                                                   49 ATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQW 90
                                                                                                                                                                                                                                                                       Streptavidin; tumour cell; cancer; adenocarcinoma;
hematological malignancy; B9E9.
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                                                     DB 22; L
7.8e-30;
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                                                     39.6%; Score 42; DB
100.0%; Pred. No. 7.8
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "streptavidin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schultz JE,
         target site within a mammalian host.
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                AAB30695 standard; Protein; 423 AA
                                                                                                                                                                                                                                                                                                                                                                                                       l..259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Fig 11C; 100pp; English
                                                                                                                                                                                                                                                                                                                                                                          "VH chain"
                                                                                                                                                                                                                                                                                                                                                                                                  "linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                              "linker"
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99US-0168976
                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  ...264
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "1
265..423
                                                                 Best Local Similarity 100.
Matches 42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   /note=
151..25
                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
260..26
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                                                                                                                                                                                                                                                                                                                     avidinii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (NEOR-) NEORX CORP
                                412 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAC86564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200075333-A1
                                                                                                                                                                                                                                                                                                                     Streptomyces
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1999;
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                                                                                                                                                                                                                                                                                                           Synthetic.
                                Sequence
                                                                                                                                                                                                      AAB30695;
                                                      Ouery Match
                                                                                                                                                                                                                                                                                                                                                                  Protein
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        SXC
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Better M;

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Sequence carries the variable region of the chimeric immunoglobulin sequence. The antibodies are useful in passive immunisation avoiding negative immune reactions. They are also useful in assaying and in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin G; IgG; light chain; recombinant production; antibody; passive immunisation; serum sickness; anaphylactic shock; immunoassay; imaging; reagent; complement mediated lysis; therapy; variable; region; complementarity determining; CDR; framework.
                                                                                                                                                                                                 Polynucleotide(s) encoding Immunoglobulin molecules - used for efficient prodn. of chimeric human or non-human or class switched antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 SNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                              51 SNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS 91
                                                                                                                                                                                                                                                                                                                                                                                        38.7%; Score 41; DB 10;
100.0%; Pred. No. 2.3e-29;
Live 0; Mismatches 0;
                                                                                                                              Horwitz AH, Wall R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2H7 antibody light chain variable region.
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/label- sig_peptide
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/label- framework_2
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/label= framework_3
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/label= mat_peptide
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'label framework_1
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/label CDR_3
119..128
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/label- CDR_1
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/label- CDR_2
                                        88WO-US02514
                                                                   87US-0077528
                                                                                                (ITGE-) INT GENETIC ENG INC
                                                                                                                                                                                                                                                            Disclosure; ; 7pp; English.
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Best Local Similarity 100.
The 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-OCT-1997 (first entry)
                                                                                                                              Liu AY,
                                                                                                                                                          WPI; 1989-061144/08.
                                                                                                                                                                                                                                                                                                                                                             Sequence 128 AA;
                                                                                                                                                                      N-PSDB; AAN91147.
                                                                                                                              Robinson RR,
                                        25-JUL-1988;
                                                                   24-JUL-1987;
            09-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW10589;
                                                                                                                                                                                                                                                                                                                                  Lmaging.
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Peptide
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                                                                                                                                                                                                                                        The patentors claim a chimeric antibody molecule comprising 2 light chains and 2 heavy chains, each comprising a constant human region and a variable non-human region. Coding sequences for the Ig chains are also claimed. The invention provides consensus sequences of light and heavy chain J regions useful in the design of oligonucleotides (UIGs) for use as primers or probes for cloning immunoglobulinisht or heavy chain mRNAs or genes. Depending on the hypridizing to all Ig mRNAs or genes containing a single specific J sequence. UIG denotes universal immunoglobulin a single specific J (Updated on 03-OCT-2002 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                       Prodn. of immunoglobulin chains and molecules - is by recombinant DNA procedures, with chimeric antibodies etc. related to cancer specific antigens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.7%; Score 41; DB 8; Lv 100.0%; Pred. No. 2.3e-29; Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibodies; passive immunisation; pH3-12a; ss.
                                                                                  ä
                                                                                  Wall
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'label=Leader peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                  Horwitz AH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAP94781 standard; protein; 128 AA
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/label=FR3.
110..118
/label=CDR3.
119..128
/label=FR4.
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/label-CDR1
            85US-0793980
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Tabel-CDR2.
                                       (ITGE-) INT GENETIC ENG INC
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/label-FR2
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/label-FR1.
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                                                                                  Robinson RR, Liu AY,
                                                       ROBINSON R R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                             WPI; 1987-136004/19.
                                                                                                                                                                                                                                                                                                                                                                                                                      128 AA;
                                                                                                                              N-PSDB; AAN70972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 H7 VL gene.
            01-NOV-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP94781;
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Peptide
                                                       (ROBI/)
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AAP94783

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Gaps

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Length 128; Indels

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The present sequence is the light chain variable region of the 2H7 antibody. The 2H7 CDNA was used in the preparation of a novel polynucleotide molecule encoding an Ig fragment. The DNA molecule comprises 2 DNA sequences encoding 2 pectate lyase secretion signal sequences respectively linked to a DNA sequence c single prokaryotic promoter so as to form a dicistronic transcription unit, prowided that the Ig fragment can bind an antigen and is produced and secreted by an E. coli host cell when transcription unit, provided that the Ig fragment can bind an antigen and is produced and secreted by an E. coli host cell when the polynucleotide molecule is expressed in the host cell.

The polynucleotide molecule is used for the production of recombinant antibodies, which can be used for passive immunisation without negative immune reactions (e.g. serum sickness and anaphylactic shock), in labelled forms as immunoassay or imaging reagents, in complement mediated lysis and for therapeutic agent.
                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid encodinding immunoglobulin fragment - comprising discistronic transcription unit with pectate lyase signal sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 128;
                                                                                                                                                                                                                                                                                    Robinson RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.7%; Score 41; DB 18; Best Local Similarity 100.0%; Pred. No. 2.3e-29; Matches 41; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                    Liu AY,
                                                                                                                                                                                                                                                                                  , Horwitz AH, Lei S, Wilcox GL;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Fig 22; 95pp; English.
                                                                                                                             850S-0793980
86WO-0S02269.
87US-0077528.
88US-0142039.
92US-0987555.
                                                                                85US-0793980
                                                                                                               90US-0501092
                                                                                                                                                                                                                                                                                                                                WPI; 1997-107579/10.
N-PSDB; AAT36317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 AA;
                                                                                                                                                                                11-JAN-1988;
08-DEC-1992;
18-AUG-1994;
                                                                              01-NOV-1985;
             US5595898-A.
                                                                                                               29-MAR-1990
                                                                                                                                 01-NOV-1985
27-OCT-1986
                                             21-JAN-1997
                                                                                                                                                                  24-JUL-1987
                                                                                                                                                                                                                                                                                  Better M,
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Search completed: November 27, 2002, 07:28:00 Job time : 38.6525 secs g

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Indels

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 27, 2002, 07:25:20 ; Search time 15.9614 Seconds Run on:

(without alignments) 638.431 Million cell updates/sec

Title: Perfect score:

US-09-893-615-89 106 1 QIVLSQSPAILSASPGEKVT.......CQQWSSNPPTFGGGTMLEIR 106 Sednence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283224 seqs, 96134422 residues Searched:

Word size :

Total number of hits satisfying chosen parameters:

283224

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

summaries Post-processing: Listing first 45

Database :

PIR_73:* 1: pirl:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

| | | Description | | | kappa | | | | Ig heavy chain V r | heavy | kappa | kappa | kappa | | | kappa | light | | light | light | kappa | kappa | kappa | | kappa | kappa chain | kappa chain | kappa chain | kappa cha | kappa chai | |
|-----------|--------|--------------|--------|--------|--------|--------|--------|--------|--------------------|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|-------------|-------------|-------------|-----------|------------|--------|
| SUMMARIES | | QI | PL0082 | PC4405 | PD0011 | S17630 | S17641 | D38601 | S20649 · | | S26339 | S17623 | S17640 | S17642 | S26340 | C33730 | PH1085 | PH1061 | PH1058 | PH1059 | S26338 | PL0276 | PL0277 | PL0278 | KVMS7B | A32513 | 57 | 22 | 22 | S17631 | S17633 |
| | | : BB | 7 | | | | | | 7 | | | | | | | | | | | | | | N | ~ | - | 7 | ~ | N | ~ | ~ | ~ |
| | | Match Length | 106 | 107 | 107 | 91 | 93 | 66 | 86 | 86 | 90 | 93 | 93 | 93 | 94 | 96 | 97 | 98 | 66 | 66 | 105 | 108 | 108 | 108 | 129 | 130 | 130 | 93 | 93 | 93 | 93 |
| | Query | Match | 7 | 35.8 | 7 | ς. | ď. | ď. | 24.5 | 4. | 4 | 4 | 4. | ÷. | ₹. | 4 | ₹. | 4. | 4. | 4. | 4. | ₹. | 4 | ₹. | ÷ | 4 | ₹. | <u>.</u> | m. | ë. | س |
| | 1 | Score | 40 | 38 | 29 | 27 | 27 | 27 | 26 | 26 | 56 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 26 | 56 | 56 | 26 | 26 | 25 | 25 | 52 | 25 |
| | Result | S. | - | 7 | е | 4 | 2 | 9 | 7 | æ | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 59 |

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| S17634 | S17635 | S17636 | S13696 | S13697 | S29582 | S29588 | S13695 | S13698 | 529583 | PS0069 | S13699 | PT0405 | 866536 | S05269 . | 10000 |
| ~ | 7 | 7 | 7 | 7 | ~ | 7 | ~ | ~ | ~ | 7 | ~ | 7 | ~ | 7 | • |
| 93 | 93 | 93 | 101 | 102 | 102 | 102 | 103 | 103 | 106 | 108 | 109 | 109 | 120 | 123 | |
| | | | Q | 9 | 9. | 9. | 9. | 9. | 9. | 9. | 9. | 9. | 9. | 9.6 | , |
| 23.6 | 23.6 | 23.6 | 23. | 23. | 23 | 23 | 23 | 23 | 23 | 23 | 23 | 23 | 23 | 7 | ć |
| 25 23.6 | 25 23.6 | ر د | S | G | s | 25 23 | ິ | S | ວ | S | ر. دى | ر. در | S | S | |

ALIGNMENTS

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C;Accession: PL0082
R;Meek, K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slaoul, M.; Urbain, J.;
J. Exp. Med. 169, 519-533, 1989
A;Title: Structural characterization of antidiotypic antibodies; evidence that Ab2s A;Reference number: PL0080; MUID:89094248; PMID:2492056
A;Accession: PL0082
                                                                                                                                                                                                                                                                                                         A, Morecule Cype: manna
A, Experimental source: strain BALB/c
A, Experimental source: strain BALB/c
A, Note: the sequence shown here is from the V kappa region of an antiidiotypic monocl
C, Superfamily: immunoglobulin V region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin
F;16-69/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                        Ig kappa chain V region (2D3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 37.7%; Score 40; DB 2; Le Best Local Similarity 100.0%; Pred. No. 7.3e-33; Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 SATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYC 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA A; Residues: 1-106 < MEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
PC4405
PL0082
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Ig Kappa chain V region (F3, anti-AFP) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Daceis: Mus musculus (house mouse)
C;Accession: PC4405
R;Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
Chinese Blochem. J. 12, 648-653, 1996
A;Title: Generation of a phage display library of the immunoglobulin repertoire from A;Reference number: PC4405

A;Accession: PC4405
A;Molecule type: mRNA
A;Residues: 1-107 <DEN>
A;Experimental source: spleen cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-89/Domain: immunoglobulin homology <IMM>

Length 107; Score 38; DB 2; L Pred. No. 7.6e-31; 35.8%; Score 38; DB illarity 100.0%; Pred. No. 7.6 Conservative 0; Mismatches Best Local Similarity Matches 38; Conserv Query Match

53 LASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCOOW 90 ò

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53 LASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQW 90 g

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Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
Cispecies: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
Cispecies: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
Cispecies: A: Fasy, T.M.; Novick, K.E.; Monestier, M.
Submitted to the EMBL Data Library, February 1992
A: Description: Relationships among antinuclear antibodics from autoimmune MRL mice re A: Reference number: $20639
A: Reference number: $20639
A: Status: preliminary
A: Status: preliminary
A: Status: Dreliminary
A: Status: Dreliminary
A: Coss-references: EMBL: X65005; NID: 952643; PIDN: CAAA6138.1; PID: 952644
C: Superfamily: immunoglobulin V region; immunoglobulin homoology
C: Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ig heavy chain V region - mouse
C;Specias: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: $20651; $20647
F;Losana, M.; Fasy, T. M.; Novick, K.E.; Monestier, M.
S;Losana, M.; Fasy, T. Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice re
                                                                                                                                                                                                                                                                                                                   Ig Kappa chain V region (6A7) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 21-Jan-2000
C; Accession: D38601
R; Goshorn, S.C.; Retzel, E.; Jemmerson, R.
J. Biol. Chem. 266, J3134-2142, 1991
A; Reference number: A38601; MUID:91115823; PMID:1703527
A; Accession: D38601
A; Reference number: A38601; MUID:91115823; PMID:1703527
A; Accession: D38601
A; Residues: 1-99 <GOS>
A; Residues: 1-99 <GOS>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:M57981; NID:g196408; PIDN:AAA63362.1; PID:g196409 CS: Superfeamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin P:8-81/Domain: immunoglobulin homology  F:8-81/Domain: immunoglobulin homology 
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Length 93;
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                                                            Indels
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   DB 2; L∈
8.1e-20;
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                  100.0%; Preu. ...
100.0%; Preu. ...
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      25.5%; Score 27;
                                                                                                                                                     44 TSNLASGVPARFSGSGTSYSLTISR 70
                                                                                                                      50 TSNLASGVPARFSGSGSGTSYSLTISR 76
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Matches 27; Conservative
                                                         27; Conservative
   Query Match
Best Local Similarity
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D38601
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                                                                                                                                               C'Species: Mus musculus (house mouse)
C'Date: 10-Unl-1998 #sequence_revision 10-Jul-1998 #text_change 21-Jan-2000
C;Accession: pp0011
R;Deng, J.B.; Han, H.; Su, C.Z.; Chen, C.Q.
Chinese Blochem. J. 12, 648-653, 1996
A;Title: Generation of a phage display library of the immunoglobulin repertoire from hum A;Reference number: PC4405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S17630
Ig kappa chain V region - mouse
Ig kappa chain V region - mouse
Signediss Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Caccession: S17630
R; Clackson, T: Hoogenboon, H.R.; Griffiths, A.D.; Winter, G.
R; Clackson, T: Hoogenboon, H.R.; Griffiths, A.D.; Winter, G.
R; Title: Making antibody fragments using phage display libraries.
A; Treference number: S17230; MUID:91326098; PMID:1907718
A; Accession: S17630
A; Status: preliminary
A; Molecule type: nucleic acid
A; Residues: 1-91 <CLA>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotecramer; immunoglobulin
F; 8-81/Domain: immunoglobulin homology <CMM>
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Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: Si7641
R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A;Title: Making antibody fragments using phage display libraries.
A;Reference number: S17230; MUID:91326098; PMID:1907718
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                                                                                                                                                                                                                                                                                                                                                                          A;Accession: PD0011
A;Molecule type: mRNA
A;Residues: 1-107 <DEN>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A Residues: 1-93 <CLA>
C Superfanily: Immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;8-83/Domain: immunoglobulin homology <IMM>
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8.8e:22;
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                                                                                                                      Ig kappa chain V region (VLB10, anti-AFP) - mouse (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 27.4%; Score 29; DB Best Local Similarity 100.0%; Pred. No. 8.6 Matches 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 SGSGSGTSYSLTISRVEAEDAATYYCQQW 90
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A, Status: preliminary
A, Molecule type: nucleic acid
A, Residues: 1-93 <CLA>
                                                                                                                                                                                                                                                                                                                                                           A;Contents: Spleen
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C;Accession: S26340
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a proteil A;Reference number: S26349; MUID:91341421; PMID:1908510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tily kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: S17642
R;Clackson, T.: Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A;Title: Making antibody fragments using phage display libraries.
A;Reference number: S17230; MUID:91326098; PMID:1907718
                                                         Ig kappa chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
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C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 20-Jun-2000
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A; Residues: 1-94 <STA>
A; Cross-references: EMBL:XS9205; NID:g52333; PIDN:CAA41:-15.1; PID:g1334072
C; Superfamily: immunoglobulin V region; immunoglobulin Nomology
C; Keywords: heterotetramer; immunoglobulin
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                                                                                                                                  C;Accession: S17640
R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A;Title: Making antibody fragments using phage display libraries.
A;Reference number: S17230; MUID:91326098; PMID:1907718
A;Accession: S17640
                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;8-83/Domain: immunoglobulin homology <IMM>
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8.2e-1
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A:Molecule type: nucleic acid
A:Residues: 1-93 <CLA>
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A;Molecule type: nucleic acid
A;Residues: 1-93 <CLA>
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R. Stark, S. E.; Caton, A.J.
C. Accession: $26349
R. Stark, S. E.; Caton, A.J.
J. Exp. Wad: 174, 613-624, 1991
A.Title: Antibodies that are specific for a single amino acid interchange in a protein A; Reference number: $26309; MUID:91341421; PMID:1908510
A; Accession: $26339
A; Acc
                            A; Accession: S20651
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-86 <LOS>
A; Residues: 1-86 <LOS>
A; Residues: 1-86 <LOS>
C; Superfemens: EMBL: X65007; NID: 952647; PIDN: CAA46140.1; PID: 952648; EMBL: X65010; C; Superfemily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer: immunoglobulin homology
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: 517623
R;Clackson, T.; Hoogenboom, H.R.; Griffiths, A.D.; Winter, G.
Nature 352, 624-628, 1991
A;Title: Making antibody fragments using phage display libraries.
A;Reference number: 517230; MUID:91326098; PMID:1907718
A;Accession: 517623
A;Accession: 517623
A;Accession: 517623
A;Molecule type: nucleic acid
A;Residues: 1-93 CCLA
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;8-83/Domain: immunoglobulin homology <IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
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7.7e-19;
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Pred. No. 8e-19;
; Mismatches 0:
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Local Similarity 100.0%; P:
les 26; Conservative 0;
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A; Reference number: S20639
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Best Local Similarity
Matches 26; Conserv
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RESULT 14

C33730

Ig kappe chain V region (4.68) - mouse
C; Species: Mus musculus (house mouse)
C; Species: Was musculus (house mouse)
C; Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C; Date: 09-Mar-1990 #sequence_revision 18-Sep-1992 #text_change 21-Jan-2000
C; Accession: C33730
R; Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Scl. U.S.A. 86, 6744-6747, 1989
A; Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, unli
A; Reterence number: A33730; MUID:89367325; PMID:2505260
A; Sccession: C33730
A; Molecule type: DNA
A; Residues: 1-96 <LAMA
A; Residues: 1-96 <LAMA
A; Residues: 1-96 <LAMA
A; Coss-references: GB:M25999; NID:9197117; PIDN:AAA38915.1; PID:9197118
A; Note: the authors translated the codon Trg for residue 34 as Phe
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 16-91/Domain: immunoglobulin homology <IMM>
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19 149ft chain V region (clone 163.42) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

S;Tatlian 1065

N;Tillian Did N; 761-779, 1992

A;Tillian Both 1997 and 196 anti-DNA antibodies are the products of clonally selective B A;Reference number: PH0971; MUID:92381444; PMID:1512540
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A;Molecule type: mRNA
A;Residues: 1-97 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]Fl
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;16-89/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 24.5%; Score 26; DB 2; Length 96; Local Similarity 100.0%; Pred. No. 8.5e-19; nes 26; Conservative 0; Mismatches 0; Indels
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                                               Indels
Best Local Similarity 100.0%; Pred. No. 8.3e-19;
Matches 26; Conservative 0; Mismatches 0;
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Copyright (c) 1993 - 2002 Compugen Ltd.
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SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | ; | musculu | nnsculu | musculu | musculu | musculu | musculu | nnscnln | musculu | sapien | musculu | musculu | musculu | musculu | musculu | musculu | sapien |
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| SOMMANTES | | | KV4A_MOUSE | KV6A_MOUSE | KV6B_MOUSE | KV6C_MOUSE | KV6D_MOUSE | KV6E_MOUSE | KV6F_MOUSE | KV6G_MOUSE | KV6H_MOUSE | KV61_MOUSE | KV6J_MOUSE | KV3V_MOUSE | KV6K_MOUSE | KV3A_MOUSE | KV3C_MOUSE | KV3D_MOUSE | KV3E_MOUSE | KV3R_MOUSE | KV3S_MOUSE | KV3T_MOUSE | KV3U_MOUSE | KV3B_MOUSE | KV3J_MOUSE | KV3K_MOUSE | KV3I_MOUSE | KV3F_HUMAN | KV3P_MOUSE | KV3L_MOUSE | KV3M_MOUSE | KV3N_MOUSE | KV30_MOUSE | KV3Q_MOUSE | KV3I_HUMAN |
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-i - MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
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-I- MISCELLANEOUS: THE TWO SEQUENCES ARE IDENTICAL.
-I- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA PROTEINS THAT BIND GALACTAN.
PIR: A01941; KVWSX4.
HSSP; P01679; 2FBJ.
InterPro; IPR0033006; Ig_MHC.
InterPro; IPR003596; Ig_W.
Ffam; PF00047; Ig_1.
Immunoglobulin V region.
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MEDILINE-81054/57; PubMed-6776525;
Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.:
"Kappa Chain joining segments and structural diversity of antibody combining sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmmalia: Eutheria; Rodentia; Sciurognathi; Muridae; Musinse; Mus.
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MEDLINE-79082830; PubMed-103573;
Rao D.N., Rudikoff S., Potter M.;
"k Chain variable regions from three galactan binding myeloma
proteins.";
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COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
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BY SIMILARITY.
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COMPLEMENTARITY-DETERMINING-1.
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              BIND GALACTAN.
PIR: A01941; KVMSX4.
HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 1g; 1.
SMART; SM0406; IGV; 1.
Immunoglobulin V region.
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Matches 23; Conservative
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PIR, A01941: KYMSX4.

HSSP, P01679; 2FBJ.

InterPro; IPR003006; Ig_WHC.

InterPro; IPR00356; Ig_V.

Pfam; PF00047; 1g; 1.

SMART: SM00406; IGv.

Imminoglobulin V region.

I 23 FRAMEWORK-1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Wusaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Rao D.N., Rudikoff S., Potter M.;
"K Chain variable regions from three galactan binding myeloma
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Rao D.N., Rudikoff S., Potter M.;
"k Chain variable regions from three galactan binding myeloma
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COMPLEMENTARITY-DETERMINING-2.
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COMPLEMENTARITY-DETERMINING-3.
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                                                                                                                                                                                                                       21-701-1986 (Rel. 01, Created)
21-701-1986 (Rel. 01, Last sequence update)
15-701-1999 (Rel. 38, Last annotation update)
18 Aappa chain V-VI region XRPC 44.
Mus musculus (Mouse)
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-VI region XRPC 24.
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X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
MEDLINE-88217852; PubMed-3449853;
Sub S.W., Bhat T.N., Navia M.A., Cohen G.H., Rao D.N., Rudikoff S.,
Davies D.R.;
SEQUENCE.
MEDLINE-81054757; Pubmed-6776525;
Rudikoff S., Rao D.N., Glaudemans C.P.J., Potte: M.:
Rappa Chain joining segments and structural diversity of antibody combining sites.";
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Proc. Natl. Acad. Sci. U.S.A. 77:4270-4274(1980).
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Rudikoff S., Rao D.N., Glaudemans C.P.J., Potter M.;
"Kappa Chain joining segments and structural diversity of antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus NCBI_TaxID=10090;
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COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                                                                                                                                                                       FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.7%; Score 23; DB 1; Length 107; 100.0%; Pred. No. 2.6e-16; Ive 0; Mismatches 0; Indels
                           21.7%; Score 23; DB 1; Length 107; ilarity 100.0%; Pred. No. 2.6e-16; Conservative 0; Mismatches 0; Indels
         11568 MW; 203CD752A5EC34D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11554 MW; 27A2D022A5EC34D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-VI region J539.
                                                                                                                                                  1-101-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-VI region SAPC 10.
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                                                                                                                                   107 AA
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                                                                  53 LASGVPARFSGSGSGTSYSLTIS 75
                                                                           53 LASGVPARFSGSGSGTSYSLTIS 75
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PIR: A01941; KVMSX4.
HSSP; P01679; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Ffan; PF0007; Ig' I.
SMART; SM00406; IGV: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                   STANDARD;
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33
48
87
87
106
                                                                                                                                                                                           Mus musculus (Mouse).
 107 1
107 AA;
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107
107 AA;
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Best Local Similarity
Matches 23; Conserv
                                   Local Similarity
es 23; Conserv
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ID KV6E_MOUSE
AC P01679;
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                                                                                                                                 KV6D_MOUSE
P01678;
NON_TER
SEQUENCE
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                            Query Match
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                                               Matches
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13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-AUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V.1 region NQ2-17.4.1,
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridue; Musinae; Mus.
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                                                                                                                                                                                       COMPLEMENTARITY; DETERMINING-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22; DB 1; Length 107; 
Pred. No. 2.7e-15; 
0; Mismatches 0; Indels
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100.08; Prv
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107
107 AA;
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ID KV6F_MC
AC P04940;
DT 13-AUG
DT 15-JUL
DE IG KAPI
OC EUKARY;
OC MARMANI
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EMBL; K00737; AAA38682.1; -.
HSSP; P01679; 2FBJ.
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Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                 79 AEDAATYYCQQWSSNP 94
                                                                                                                                                                                                                                                                       79 AEDAATYYCQQWSSNP 94
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87
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                                                                                                                                                                                                 107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                   KV6H_MOUSE
P04942;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                          2
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SEQUENCE FROM N.A.
MEDLINE-83271467; PubMed-6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
"mRNA sequences define an unusually restricted IgG response to ;
phenyloxazolone and its early diversification.";
Nature 304:320-334(1983).
-1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
                               MEDLINE-83271467; PubMed-6877353; Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.; mRNA sequences define an unusually restricted IgG response to phenyloxazolone and its early diversification."; Nature 304:320-324(1983).
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16; DB 1; Length 107; Pred. No. 3.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                        -!- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
                                                                                                                                                                                                                                                                                                                                                                                                 6F694284ECFA68E6 CRC64;
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13-AUG-1987 (Rel. 05, Last sequence update)
12-UUL-1999 (Rel. 38, Last annotation update)
1g kappa chain V-VI region NQ2-48.2.2.
                                                                                                                                                                                                                                                                                                                                                                                                                15.1%; Scor.
100.0%; Pred. No. ...
'... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 11561 MW;
                                                                                                                                                                                                             EMBL; K00735; AAA38680.1; -. HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                   InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
es 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 AEDAATYYCQQWSSNP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 AEDAATYYCQQWSSNP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                            49
56
88
97
23
107 AA;
                      SEQUENCE FROM N.A.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-10090;
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P04941;
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SEQUENCE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
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Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
"mRNA sequences define an unusually restricted 1gG response to phenyloxazolone and its early diversification.";
Nature 304:320-324(1983).
-I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 107;
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3.4e-09;
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13-AUG-1987 (Rel. 05, Last sequence update)
13-UUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-VI region NQ5-61.1.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 AA.
                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No. 3.4 ive 0; Mismatches
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR0047; ig; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Hybridoma.
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SMART; SM00406; IGV; 1.
Immunoglobulin V region; Hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                               11556 MW;
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InterPro; IPR003596; Ig_v.
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15-JUL-1999 (Rel. 38, Last annotation update) Ig kappa chain V-VI region NO5-78.2.6. Mus musculus (Mouse).
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SMART; SM00406; IGv; 1.
Immunoglobulin V region; Hybridoma.
                                                                                                                                                                                                                                                                                                                              EMBL; K00744; AAA38689.1; -.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Best Local Similarity 100.
Matches 16; Conservative
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PIR; A01940; KVMS54.
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                                                                       NCBI_TaxID=10090;
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P01674;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-83271467; PubMed-6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
MRNA sequences define an unusually restricted IgG response to 2-phenyloxazolone and its early diversification.";
Nature 304:320-324(1983).
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FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENTARITY - DETERMINING - 2.
                         Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.1%; Score 16; DB 1; Length 107; 100.0%; Pred. No. 3.4e-09; tive 0; Mismatches 0; Indels
                          15.1%; Score 16; DB 1; Length 107
Llarity 100.0%; Pred. No. 3.4e-09;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               -1- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11572 MW; 6F694824ECF0C8E6 CRC64;
 CA6C4284ECFCB550 CRC64;
                                                                                                                                                                                                                             13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 kappa chain V-VI region NOG-8.3.1.
                                                                                                                                                                                     107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAMEWORK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig. 1.
IMMUNG910bulin V region; Hybridoma.
                                                                                                                                                                                                                13-AUG-1987 (Rel. 05, Created)
 11605 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; K00740; AAA38685.1; -. HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 AEDAATYYCQQWSSNP 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                   79 AEDAATYYCQOWSSNP 94
                                                                                                            79 AEDAATYYCOOWSSNP 94
                                                                                                                                                                                     STANDARD;
107 AA;
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                                         Local Similarity
es 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                  KV6I_MOUSE
P04943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KV6J_MOUSE
P04944;
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NON_TER
SEQUENCE
 SEQUENCE
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                             Query Match
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KV6J_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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Matches
                                                                                                                                                                        KV61_MOUSE
                                                       Matches
                                                                                                                                                         RESULT 10
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                           [1]

SEQUENCE FROM N.A.

MEDLINE-83371467; PubWed-6877353;

Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;

MRA sequences define an unusually restricted 1gG response to 2-
phenyloxazolone and its early diversification.";

Nature 304:320-324(1983).

-I- FUNCTION: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBL_TaxID=10090;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-79073152; PubMed-103003; Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPLEMENTARITY - DETERMINING - 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 16; DB 1; Length 107;
Pred. No. 3.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11611 MW; A38290781F3C30D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
11g Kappa chain V-III region PC 2154.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15.1%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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STANDARD;
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79 AEDAATYYCQQWSS 92
            60 SGVPARFSGSGSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kappa chains.";
                                                                        KV3A_MOUSE
P01654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KV3C_MOUSE
P01656;
                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                          SEQUENCE.
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KV3C_MOUSE
                                                    RESULT 14
KV3A_MOUSE
                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-83271467; Pubmed-6877353;
Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
ManNa sequences define an unusually restricted IgG response to 2-phenyloxazolone and its early diversification.";
Nature 304:320-324(1983).
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FRAMEWORK - 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENTARITY - DETERMINING - 2.
                                           COMPLEMENTARITY - DETERMINING - 1.
                                                                COMPLEMENTARITY - DETERMINING - 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.2%; Score 14; DB 1; Length 108; 100.0%; Pred. No. 3.7e-07; ve. 0; Mismatches 0; Indels
                                                                                     COMPLEMENTARITY - DETERMINING - 3
                                                                                                                                                ch 13.2%; Score 14; DB 1; Length 108; 1 Similarity 100.0%; Pred. No. 3.7e-07; 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108
11713 MW; DABF235CD9680AC6 CRC64;
                                                                                                                             11699 MW; D40921D18DAC4B9E CRC64;
                                                                                                                                                                                                                                                                                       13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Augha chain V-VI region NQ2-6.1.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                    108 AA
                                                                                                          SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAMEWORK-1.
                                                      FRAMEWORK-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAMEWORK-3
                                 FRAMEWORK-1
                                                                                              FRAMEWORK-4
                                                                           FRAMEWORK - 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_V.
Pfam: PF00047; ig; 1.
SMART: SW00406; IGv; 1.
Immunoglobulin V region; Hybridoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; K00746; AAA38691.1; -. HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.2%;
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nes 14; Conservative
                                                                                                                                                                                                                                                                     STANDARD;
            SMART; SM00406; IGv; 1.
Immunoglobulin V region
                                  23
38
53
53
101
92
92
                                                                                                                                                                                             55 SGVPARFSGSGSGT 68
                                                                                                                                                                                                        60 SGVPARFSGSGSGT 73
  Pfam; PF00047; 1g; 1.
                                                                                                                              108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108 AA;
                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                     KV6K_MOUSE
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SEQUENCE
                                                                                                         DISULFID
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                               SEQUENCE
                                                                                                                                                   Query Match
                                          DOMAIN
DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                             P04945;
                                                                                     DOMAIN
                                                                                                 DOMAIN
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                                                                                                                                                                                                                                               RESULT 13
KV6K_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                      Matches
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Gaps
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Nature 276:785-790(1978).

1- MISCELLABOUS: THE PC 2880 AND PC 1229 SEQUENCES ARE IDENTICAL.

PIR, A01330; KVMS80.

HSSP; P80362; 1WTL.

INCEPTO; 1PR003066; 1g_MHC.

INCEPTO; 1PR003596; 1g_V.

Pfam; PF00047; ig; 1.

SMART; SM00406; IGv; 1.

Inmunoglobulin V region.

FRAMEWORK-1.
                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gray W.R., Dreyer W.J., Hood L.E.; "Mechanism of antibody synthesis: size differences between mouse
                                                                                                                                                                                                                                                                                                                                                        Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.; "Rearrangement of genetic information may produce immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENTARITY - DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.2%; Score 14; DB 1; Length 111; 100.0%; Pred. No. 3.8e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11980 MW; AFEAC6A9D26FC12D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 155:465-467(1967).
-1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN
PIR; A01930; KVMS80.
                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
18 Kappa chain V-III region PC 2880/PC 1229.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 AA.
111 AA
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PRT;
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                                                                                                                                                                                                                                                                                                                              MEDLINE-79073152; PubMed-103003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Conservative
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                                                                                                           FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.
HSSP; P01679; 2FBJ.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; Ig; 1.

Immunoglobulin V region; Bence-Jones protein.

DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.

DOMAIN 39 53 FRAMEWORK-1.

DOMAIN 39 54 60 COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                           Query Match
13.2%; Score 14; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. No. 3.8e-07;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                11904 MW; 4FE7ABC9DF0FC125 CRC64;
                                                                                                                                                                                                                                                                                 55 SGVPARFSGSGSGT 68
                                                                                                                                                                                                                                                                                               60 SGVPARFSGSGSGT 73
                                                                                                                                                                                                      111 AA;
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SEQUENCE
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Search completed: November 27, 2002, 07:28:47 Job time : 10.2317 secs

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Ogul80 homo septen

Ogweg mus musculu

Oglwg mus musculu

Oglwfez mus musculu

Oglon37 mus musculu

Oglon37 mus musculu

Oglon37 mus musculu

Oglon38 musculu

Oglyfe mus musculu

Oglyfe mus musculu

Oglyfe mus musculu

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Oglama drosophila
                         O9et13 mus musculu
O920e6 mus musculu
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Q9nhu5 drosophila
Q9n666 drosophila
Q81812 drosophila
Q81810 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ognhu8 drosophila
Ognhu7 drosophila
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09JL76 PRELIMINARY; PRT; 97 AA.
09JL76;
01-OCT-2000 (TrEMBLrel. 15, Created):
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
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                         Q9ET13
Q920E6
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Q8TCD0
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Q9QYF0
Q9JL84
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091WF8
08R062
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Q921A6
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Q9NHV3
Q9NHV2
Q9NHV1
Q9NHV0
Q9NHU9
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Mus musculus (Mouse).
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731.044 Million cell updates/sec
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                                                                                                                                                                                          November 27, 2002, 07:24:25; Search time. 29.8764 Seconds
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Copyright (c) 1993 - 2002 Compug
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Q8VDD0
Q9U410
Q91W12
Q9JL78
Q9JL80
Q9UL83
Q9UL83
Q9UL85
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sp_invertebrate:*
sp_mammal:*
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sp_fungi:*
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sp_rodent: *
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AND TITE OF THE PROPERTY OF TH ö Gaps ö Length 97; 0; Indels Score 44; DB 11; 1 Pred. No. 1.5e-37; 41.5%; Scordio 0. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.00%; Pred. No Conservative Similarity Query Match Local 39 Matches Dp

> Q96SA9 Q9UL79 Q9UL77 Q9UL70 Q9UL78

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106 AA; 11478 MW; F20F544426BAE63E CRC64;
                  Ouery Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Q9JL78;
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091W12
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Q9JL78
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SEQUENCE FROM N.A.

A SONG X.T., Feng Z.O., Qiu Z.N., Li Y.O., Huang H.L., Guan X.H.;

A Song X.T., Feng Z.O., Qiu Z.N., Li Y.O., Huang H.L., Guan X.H.;

A maplification, clonding and sequence analysis of the light chain

to variable region gene of monoclonal anti-idiotypic antibody NP30 of

Schistosoma japonicum.';

Schistosoma japonicum.';

R Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.

B RBL; AF207620; AAF19434.1; -.

DR RSP; PO16/9; ZFBJ.

InterPro; IPR003506; Ig_MHC.

DR InterPro; IPR003596; Ig_V.

DR Ffam; PF00047; ig; 1.

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Schistosoma japonicum (Blood fluke).
Bukaryota, Mctazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
Schistosomatoidea; Schistosomatidae; Schistosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Monoclonal anti-idiotypic antibody NP30 immunoglobulin light chain
                                                                                                                           Mus musculus (Mouse).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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o
                                                                                                                                                                                                                                                                                                                                                                                                                           21.7%; Score 23; DB 11; Length 134; 100.0%; Pred. No. 9.4e-16; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              "Targeting T cells to the CNS.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ418331; CAC94866.1;
InterPro; IPR003599; 19.
InterPro; IPR003599; 19_v.
InterPro; IPR003596; 19_v.
Ffam; PF00049; 19_1.
SWART; SM00406; 1Gv; 1.
NON_TER 134 134
                                                                                                                                                                                               STRAIN-BALB/C; Chernajovsky Y .; Chernajovsky Y .; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                        NON_TER 134 134
SEQUENCE 134 AA; 14525 MW; CFDF8E2236E2DOCF CRC64;
                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ANTI-MOG 212 variable light chain (Fragment).
ANTI MOG KAPPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 106 AA.
                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Conservative
                                            PRELIMINARY;
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                                                                                                                                                                                     SEQUENCE FROM N.A.
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RX MEDLINE—20448942; PubMed=10992488;

RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;

RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;

"T-Cell-dependent antibody response to the dominant epitope of

RT "T-Cell-dependent antibody response to the action is cross-reactive.

RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive.

RT with cardiac myosin..;

Infect. Immun. 68:5803-5808(2000).

BEMBL, AF206028; AFF69326.1;

DR HSSP; PO1679; 2FBJ.

InterPro; IPR003096; Ig_MC.

DR InterPro; IPR003096; Ig_W.

DR SMART; SM00406; IGv; 1.

FT NON_TER 101 101
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
Unknown (protein for MGC:6582).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Fragment).
Mus musculus (Mouse).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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             Score 17; DB 5; Length 106;
Pred. No. 1.2e-09;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-BREAST TUMOR;
Strausberg R.;
Submitted (PRR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC006643; AAH06643.1; -.
InterPro; IFR033006; Ig_MHC.
Pfam; PF00047; ig; 2.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SEQUENCE 235 AA; 26021 MW; 5FC73BDBBD5EBFEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
16.0%; Scor.
100.0%; Pred. No. ...
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                                                                                                                                                   60 RFSGSGSGTSYSLTISR 76
                                                                                                                     60 RFSGSGSGTSYSLTISR 76
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Matches 16; Conservative
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Length 111;

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(Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin kappa chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TIEMBLrel. 13, Created)
01-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-DEC-2001 (TIEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.4%; Score 11; DB 4; Length 108; 100.0%; Pred. No. 0.0015; Live 0; Mismatches 0; Indels
                                                                                    111 AA; 12046 MW; 1E46988AA6858526 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC54;
                                                                                                                                  DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL. 18735031; AAD56267.1; -.
INTERPROSSOS, 1WTL.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_V.
SMART; SMO0406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                           108 AA.
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                                                                                                                                                        100.0%; Preu. ...
                                                                                                                                Score 14;
Pred. No.
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MEDLINE-98277139; PubMed-9614934;
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                                                                                                                                        13.2%;
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                                                                                                                                                                                                                                                                        60 SGVPARFSGSGSGT 73
                                                           111
Pfam; PF00047; ig; 1.
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                                                                                                                                                                Local Similarity
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1D 090118
AC 090110
DT 01-M
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Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
"Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                      Length 101;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Pterin-mimicking anti-idiotope kappa chain variable region
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                                                                                                          Indels
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EMBL; AF307935; AAL09419.1; -
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                             01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2001 (TrEMBLrel. 19, Last annotation update)
Ant1-myosin immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 103
103 AA; 11224 MW; EC87D653DB3AAB21 CRC64;
     101 AA; 10778 MW; 0A7F65E6A7E6F14D CRC64;
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                                                      14.2%; Score 15; DB 11; I ilarity 100.0%; Pred. No. 1.3e-07; Conservative 0; Mismatches 0;
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SMART: SM0406; 1Gv; 1.
NON_TER 1 13
NON_TER 103 A3: 11224
                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                      54 RFSGSGSGTSYSLTI 68
                                                                                                                                                              60 RFSGSGSGTSYSLTI 74
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les 14; Conserv
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les 15; Conserv
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Q9UL79;
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Q9UL79
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XX MEDLINE-20448942; PubMed-10992488;

MAIXIES., Liao.L., Cunningham M.W., Diamond B.;

RT ALCALI-dependent antibody response to the dominant epitope of

RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive

RT with cardiac myosin.";

RI infect. Immun. 68:5803-5808(2000).

BR EMBL; AF20604; AAF69322.1; -

DR HSSP; POIGO7; IRE.

BR InterPro; IPR003596; Ig_WIC.

DR InterPro; IPR003596; Ig_V.

DR SMART; SM00406; IG, 1

NOT THE SMART; SM00406; IG, 1
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                           10.4%; Score 11; DB 4; Length 109; 100.0%; Pred. No. 0.0019; 1ve 0; Mismatches 0; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                               01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2001 (TrEMBLrel. 19, Last annotation update)
Anti-myosin immunoglobulin light chain variable region
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                                                                                                                    109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;
fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
RF035029; AAD56265.1; --.
HSSP; P80362; IWTL.
InterPro; IPR003006; Ig_MHC.
Pfam; PP00047; Ag; 1.
SMART; SM00406; IGV; 1.
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Best Local Similarity 100...
9, Conservative
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                                                                                                                                                                                          58 PARFSGSGSGT 68
                                                                                                                                                                                                      1111111111
59 PARFSGSGSGT 69
                                                                                                                                                    Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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58 RFSGSGSGT 66
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Q9UL81;
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Q9JL82;
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09UL81
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AC 09UL8
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-DE
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Anti-streptococcal/anti-myosin immunoglobulin kappa light chain
variable region (Fragment).
Enkarpota: Metazoa: Chordata; Craniata; Vertebrata; Enteleostoml;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                    Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.; "Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98375893; PubMed-9712075;
MEDLINE-98375893; PubMed-9712075;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis human anti-N-acetylglucosamine/anti-myosin antibody V region genes.";
J. Immunol. 161:2020-2031(1998).
EMBL; U96396; AAB68785.1;
EMBL; U96396; AAB68785.1;
Pfam; PF00047; 19; 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidue; Homo.
NCBI_TaxID=9606;
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107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                            Cilc. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035033; AAD56269.1; -.
HSSP; P01607; INEI.
InterPro; IPR003006; Ig_MC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IG; 1.
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100.0%; Pred. No. 0.22;
ative 0; Mismatches
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100.0%; Pred. No. 0.22;
Live 0; Mismatches
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                                                                     SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.5
Best Local Similarity 100.
Matches 9; Conservative
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Thes 9; Conserve
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SEQUENCE FROM N.A.
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                                  Homo sapions (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-98277139; Pubmed-9614934;
Mu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

BEDLINE-98277139; Pubmed-9614934;
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
Young D.C.;
Myosin-reactive immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.5%; Score 9; DB 4; Length 108; Best Local Similarity 100.0%; Pred. No. 0.22; Matches 9; Conservative 0; Mismatches 0; Indels
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8.5%; Score 9; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF03507; AAD56273.1;
HASSP; PO1607; IREI.
InterPro; IPR00306; Ig_MHC.
InterPro; IPR003596; Ig_v.
Ffam; PF00047; Ig; 1.
                                                                                                                                                                                                                         EMBL; AF035035, AAD56271.1; -. HSR4-192(1998).
EMBL; AF035035, AAD56271.1; -. HSSP; P01607; 1REI.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 19; 1.
SMART; SM00406; IGV; 1.
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61 RFSGSGSGT 69
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                                                                                     NCBI_TaxID=9606;
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Gaps
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Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebratu: Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
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MEDINECE FROM N.A.
MEDINE-9827139; PubMed-9614934;
MU X., Liu B., Van der Merwe P.L., Kalis N.N., Rerney S.M.,
Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
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09UL70 PRELIMINARY, PRT, 108 AA. 09UL70. 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Myosin-reactive immunoglobulin light chain variable region
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Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL: AF035044; AMD56280.1;
HXSP: P01607; IREI.
InterPro; IPR003906; Ig_MHC.
InterPro; IPR003966; Ig_V.
Ffam: PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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Matches 9; Conservative 0; Mismatches
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TOPOLOGY: linear
MOLECULE TYPE: protein
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58, Appl
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16, Appl
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Sequence 105, App
Sequence 11, Appl
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-344-050-103
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US-08-484-537-1
US-08-411-202-3
US-09-171-202-3
US-09-111-202-3
US-09-111-202-3
US-09-111-202-3
US-09-111-78E-2
US-08-116-778E-2
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GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Church, Witchell
APPLICANT: Feuerstein, Giora
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
ALIGNMENTS
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
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APPLICATION NUMBER: 60/029,119
FILLING DATE: 24-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                Sequence 105, Application US/08783853A Patent No. 6005091
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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STRANDEDNESS: single
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APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Patel, Aduardo
APPLICANT: Patel, Arunbhal
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: OF THROMBOSIS
CORRESPONDENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkii--
STREFT:
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                                       1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWI 47
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CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
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CLASSIFICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 37,833
REFERENCE/DOCKET NUMBER: 950438
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
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                                                                                                                                              RESULT 3
US-08-783-853A-11
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47;
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  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 4
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                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Church, William
APPLICANT: Church, William
APPLICANT: Feucatein, Giora
APPLICANT: Feucatein, Giora
APPLICANT: Padlan, Eduardo
APPLICANT: ALUbhai
APPLICANT: ALUbhai
APPLICANT: ALUBHAI
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
                                                                                                                                                                    ;
0
                                                                                                                        44.3%; Score 47; DB 3; Length 106; 100.0%; Pred. No. 1.8e-34; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.3%; Score 47; DB 4; Length 106; 100.0%; Pred. No. 1.8e-34;
                                                                                                                                                                                                                               1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWI 47
                                                                                                                                                                                                           1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999
                                                                                                                                                                                                                                                                                                                                                          Sequence 105, Application US/09344050
Patent No. 6391299
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P50438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P5(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
                                                                                                                          Query Match
Best Local Similarity 100.
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                         internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIRGOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                 ANTI-SENSE: NO FRAGMENT TYPE: in ORIGINAL SOURCE: US-08-783-853A-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19406
                                                                                                                                                                                                                                                                                                                                      US-09-344-050-105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: P
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                                                                                                                                                                                                                                                                                                                  RESULT 2
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APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhal
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS.
CORRESPONDENCE 3.11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Feuerstein, Giora
APPLICANT: Nichols, Andrew
APPLICANT: Padlan, Eduardo
APPLICANT: Patel, Arunbhai
APPLICANT: Patel, Arunbhai
APPLICANT: Patel, Arunbhai
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
CORRESPONDENCE: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 3; Length 112;
Pred. No. 1.9e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPW1 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44.3%; Scor.
100.0%; Pred. No. 1...
0; Mismatches
                                                                                                                                                      E: SmithKline Beecham Corporation 709 Swedeland Road
                                                                                                                                                                                                                                                     ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/783,853A
FILING DATE: 16-JAN-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/029,119
FILING DATE: 24-0CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Balmeister Kitz
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 103, Application US/09344050 Patent No. 6391299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blackburn, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Church, William
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gross, Mitchell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 100.
Matches 47; Conservative
                                                                                                                                                                       CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Blackbur
APPLICANT: Church,
APPLICANT: Gross, APPLICANT: Feuerste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
ANTI-SENSE: N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-783-853A-103
                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-09-344-050-103
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                                                         APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Cross, Mitchell
APPLICANT: Gross, Mitchell
APPLICANT: Gross, Mitchell
APPLICANT: Fucurstein, Glora
APPLICANT: Padlan, Eduardo
APPLICANT: Padlan, Eduardo
APPLICANT: Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
TITLE OF INVENTION: OF THROMBOSIS
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-UN-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/783,853
FFILIG DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
TELECOMMUNICATION INFORMATION:
TELECHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 103, Application US/08783853A Patent No. 6005091 GENERAL INFORMATION:
Sequence 11, Application US/09344050 Patent No. 6391299 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Blackburn, Michael
APPLICANT: Church, William
APPLICANT: Gross, Mitchell
APPLICANT: Feuerstein, Giora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 107 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
US-09-344-050-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                             19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-783-853A-103
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 ATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQ 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 37.7%; Score 40; DB 2; Le Best Local Similarity 100.0%; Pred. No. 3.2e-28; Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 ATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION: <un>
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                         PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT GB91/01108
FILING DATE: 05-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9014932.9
FILING DATE: 05-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT GB90/02017
FILING DATE: 21-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 40283/110 CA
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SECTION OF 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 New York Ave., CITY: Washington
                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/154,389
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-423-439-18
Sequence 18, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 235 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 129 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS LENGTH: 129 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein US-08-449-287-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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Patent No. 5877293

GENERAL INFORMATION:
APPLICANT: ADDIR, John Robert
APPLICANT: BODMER, Mark William
APPLICANT: BODMER, Mark William
APPLICANT: OWENS, Raymond John
TITLE OF INVENTION: CDR Grafted Anti-CEA Antibodies and
TITLE OF INVENTION: Their Production
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.3%; Score 47; DB 4; Length 112; 100.0%; Pred. No. 1.9e-34; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWI 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPRPWI 47
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                              SOFTWARE: FASTSEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/344,050
FILING DATE: 24-JUN-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/449,287
                                                                                                                                                                                                                                                                                                                                                             PULGATION DATA:
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baumelster, Kirk
REGISTRATION NUMBER: 33,833
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P50438
                                                                                                                              ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein uvPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE: 1
; ORIGINAL SOURCE:
US-09-344-050-103
                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                    STATE: P
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-449-287-2
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APPLICANT: Hand, Nabil
APPLICANT: Hand, Nabil
APPLICANT: Leonard, John E.
APPLICANT: Reff, Mitchell E.
APPLICANT: Reff, Mitchell E.
APPLICANT: Rastetter, William H.
TITLE OF INVENTION: Therapeutic Application of Chimeric and
TITLE OF INVENTION: Radiolabeled Antibodies to Human B Lymphocyte Restricted
TITLE OF INVENTION: Differentiation Antigen for the Treatment of B-Cell
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Madison & Sutro, LLP
STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 ATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQ 110
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Best Local Similarity 100.0%; Pred. No. 5.3e-28;
Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 ATSNLASGVPARFSGSGGGGTSYSLTISRVEAEDAATYYCQ 88
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:

APPLICATION NAMBER: PCT/GB96/01975
FILING DATE: 13-AuG-1996
APPLICATION NUMBER: GB 9612295.7
FILING DATE: 12-JUN 1996
APPLICATION NUMBER: GB 9611019.2
FILING DATE: 25-MAY-1996
APPLICATION NUMBER: GB 9516810.0
FILING DATE: 16-AuG-1995
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERSTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: BURNS, DOANE, SWECKER & MATHIS 699 Prince St.
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,769A
FILING DATE: 13-Feb-1998
CLASSIFICATION: <UNKNOWN>
  MARSHAM, Peter R.
DOWELL, ROBERT I.
TITLE OF INVENTION: Chemical Compounds
NUMBER OF SEQUENCES: 87
                                                                                                                                                                                            COUNTRY: U.S.A.

211: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb disk
COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 235 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08476275 Patent No. 5776456
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Anderson, Darrell
                                                                                                                                                      CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 699 Princ
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-011-769A-23
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                                                                                                                                Length 235,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                          Indels
                                                                                                                                                                                                              APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 ATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQ 88
                                                                                                                                DB 4; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
37.7%; Score 40; DB 4; L
Best Local Similarity 100.0%; Pred. No. 5.3e-28;
Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE PORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WOLD
CURRENT APPLICATION UNMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: CB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION POR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
                                                                                                                           Query Match 37.7%; Score 40; DB Best Local Similarity 100.0%; Pred. No. 5.3 Matches 40; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
                             , mulecule TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-423-439-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HENNEQUIN, Laurent F.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/09011769A Patent No. 6436691 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   Sequence 58, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SLATER, Anthony M. BLAKEY, David C. DAVIES, David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 235 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  John F.
STRANDEDNESS: single
                    TOPOLOGY: linear MOLECULE TYPE: proteil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HENNAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-011-769A-23
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Gaps

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US-08-434-000A-12; Sequence 12, Application US/08434000A; Patent No. 6046037; GENERAL INFORMATION:
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TELEFAX: (619) 552-0159
TELEX: 67-3510
TELEX: SEQUENCE LISTING
INPORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 105 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-475-815B-7
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Patent No. 6399061
GENERAL INCORMATION:
APPLICANT: ANDERSON, DARRELL R.
APPLICANT: LEONARD, JOHN E.
APPLICANT: REFF, MITCHELL E.
APPLICANT: RASTETER, MILLIAM E.
APPLICANT: RASTETER, MILLIAM E.
APPLICANT: RASTETER, MILLIAM E.
APPLICANT: NEWMAN, ROLAND E.
APPLICANT: REFF, MITCHELL E.
APPLICANT: REFF, MITCHELL E.
APPLICANT: BASTETER, MILLIAM E.
APPLICANT: REFF, MITCHELL E.
APPLICANT: BASTETER, MILLIAM E.
APPLICANT: REFF, MITCHELL E.
APPLICANT: REFF, MITCHELL E.
APPLICANT: REFF, MITCHELL E.
APPLICANT: REFF MITCHELL E.
APPLICANT: MINENTION: TYPHOMA
MUMBER OF SEQUENCES: 11
CORRESPONDESSE: 11
CORRESPONDESSE: 11
CORRESPONDESSE: 11
CORRESPONDESSE: 11
CORRESPONDESSE: MITCHELL E.
APPLICANT: MINTHROP
STREET: 1100 New YORK Avenue, N.W., Ninth FL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.2%; Score 31; DB 1; Length 128; 100.0%; Pred. No. 2.7e-20; 1ve 0; Mismatches 0; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLOATION NUMBER: US/08/475, 815B FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 New York Avenue, N.W., Ninth FL. CITY: Washington
                                                                      APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-UNN-1995
CLASSIFICATION: 424
PRIOR APPLICATION: 424
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03.NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTONNEY,AGENT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-155
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 RFSGSGSGTSYSLTISRVEAEDAATYYCQQW 90
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APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/978,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 128 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.C
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20002
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US-08-475-815B-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-476-275-4
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APPLICANT: K.-C. MA, THOMAS LENBER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
TITLE OF INVENTION: PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/367,395
FILING DATE: 12/30/94
ATTORNEY/AGENT INFORMATION:
NAME: Gulse, Jeffrey W.
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 212/127
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 29.2%; Score 31; DB 4; Lo Best Local Similarity 100.0%; Pred. No. 2.7e-20; Matches 31; Conservative 0; Mismatches 0;
ATTORNEY AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 23522-0157
FELECOMMUNICATION INFORMATION:
FELEFAX: 202-861-3000
TELEFAX: 202-861-3000
TELEFAX: 202-861-3000
TELEFAX: 202-861-3000
TELEFAX: 202-861-3000
TELEFAX: 202-861-3000
TELEFAX: 202-804-4
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 mmino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 RFSGSGSGTSYSLTISRVEAEDAATYYCQQW 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,000A
FILING DATE:
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1, Application US/07634278
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                                                                                                                                                                                                                                                                                                                         ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: 1.106
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-634-278-1
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                                                                                                                                                                                                                                                                                                                       APPLICANT: ANDREW C. HIATT, JULIAN
K.-C. MA, THOMAS LEHNER
TITLE OF INVENTION: IMMUNOGLOBULINS CONTAINING PROTECTION
PROTEINS IN PLANTS AND THEIR USES
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 25.5%; Score 27; DB 4; Length 105; Best Local Similarity 100.0%; Pred. No. 7.5e-17; Matches 27; Conservative 0; Mismatches 0; Indels
                                                       Length 105;
                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UESCRIPTION: Guy's 13 Kappa ; SEQUENCE DESCRIPTION: SEQ ID NO: 12: US-09-312-157-12
                                                       DB 3; Le
7.5e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM COMPAILLLE
COMPUTER: IBM COMPAILLE
COPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/312,157
FILING DATE: 14-May-1999
CLASSIFICATION NUMBER: 08/434,000
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: 08/434,000
FILING DATE: CUNKNOWN>
APPLICATION NUMBER: 34,613
REGISTRATION NUMBER: 34,613
REFERENCE/DOCKET NUMBER: 31,2127
TELECOMMUNICATION INFORMATION:
TELEFRAM: (619) 552-8400
TELEFAX: (619) 552-0159
TELEFX: 67-351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTAL. .
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
storage
   Guy's 13 Kappa
                                                     Query Match 25.5%; Score 27; DB Best Local Similarity 100.0%; Pred. No. 7.5 Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Sulte 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 TSNLASGVPARFSGSGSGTSYSLTISR 76
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                                                                                                                                 50 TSNLASGVPARFSGSGSGTSYSLTISR 76
                                                                                                                                                     50 TSNLASGVPARFSGSGSGTSYSLTISR 76
                                                                                                                                                                                                                 RESULT 14
US-09-312-157-12
; Sequence 12, Application US/09312157
; Patent No. 6303341
; FREENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE LISTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 105 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 12: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
 DESCRIPTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
; TOPOLOGY:
US-08-434-000A-12
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Gaps
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anti-Tac antibody light chain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 25.5%; Score 27; DB 1; Length 106; Best Local Similarity 100.0%; Pred. No. 7.5e-17; Matches 27; Conservative 0; Mismatches 0; Indels
APPLICANT: QUEEN, Cary L.
APPLICANT: CO. Man Sung
APPLICANT: CO. Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BATELICATION
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: SMITCH, WILLIAM M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION NUMBER: 11823-002600
TELECOMMUNICATION NUMBER: 11823-002600
                                                                                                                                                                                                                                                                  E: Townsend and Townsend Khourie and Crew
379 Lytton Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: November 27, 2002, 07:32:11 Job time : 15.7336 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 TSNLASGVPARFSGSGSGTSYSLTISR 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS: single
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RESULT 15 US-07-634-278-1

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us-09-893-615-89.oli.rapb

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(without alignments)
171.849 Million cell updates/sec
                                                                             November 27, 2002, 07:28:06 ; Search time 9.82239 Seconds
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1 QIVLSQSPAILSASPGEKVT.......CQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                  102317
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                 102317 seqs, 15924203 residues
                                                                                                                                                                                                                                                                                                                                                           Post-processing: Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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length: 2000000000
                                                                                                                                     US-09-893-615-89
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Maximum DB seq
                                                                                                                                                  score:
                                                                                                                                                                                          Scoring table:
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Perfect sc
Sequence:
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                                                                              Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

SUMMARIES

| | Description | Sequence 89, Appl | Sequence 105, App | Sequence 105, App | Sequence 11, Appl | Sequence 11, Appl | 103 | • | Ă | | Sequence 23, Appl | ~ | - | Sequence 8, Appli | Sequence 9, Appli | Sequence 89, Appl | Sequence 17, Appl | Sequence 29, Appl | Sequence 28, Appl | Sequence 28, Appl |
|--------------|--------------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------------|------------------|-------------------|------------------|-----------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
| | ID | US-09-893-615-89 | US-09-965-099-105 | US-10-051-852-105 | US-09-965-099-11 | US-10-051-852-11 | US-09-965-099-103 | US-10-051-852-103 | US-09-982-107-12 | US-09-976-787-24 | US-09-865-198-23 | US-09-144-886-88 | US-09-976-787-8 | US-09-865-198-8 | US-09-910-059-9 | US-09-144-886-89 | US-09-910-059-17 | US-09-976-787-29 | US-09-865-198-28 | US-09-976-787-28 |
| | DB | 10 | 10 | 12 | 10 | 12 | 10 | 12 | σ | 10 | 10 | σ | 10 | 10 | 10 | σ | 10 | 10 | 10 | 10 |
| | Query Match Length DB | 106 | 106 | 106 | 107 | 107 | 112 | 112 | 105 | 106 | 106 | 107 | 108 | 108 | 108 | 112 | 235 | 238 | 238 | 240 |
| s o (| Query | 100.0 | 44.3 | 44.3 | 44.3 | 44.3 | 44.3 | 44.3 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 | 25.5 |
| | Score | 106 | 47 | 47 | 47 | 47 | 47 | 47 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 | 27 |
| 1 | No. | 1 | 7 | m | 4 | 2 | 9 | 7 | 80 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 |

| Sequence 27, Appl Sequence 27, Appl Sequence 76, Appl Sequence 76, Appl Sequence 98, Appl Sequence 81, Appl Sequence 81, Appl Sequence 28, Appl Sequence 62, Appl Sequence 62, Appl Sequence 77, Appl Sequence 78, Appl Sequence 66, Appl Sequence 78, Appl Sequence 66, Appl Sequence 67, Appl Sequence 67, Appl Sequence 97, Appl Sequence 95, Appl Sequence 95, Appl Sequence 95, Appl Sequence 95, Appl Sequence 99, Appl | Sequence 6, Appli Sequence 91, Appl Sequence 80, Appl |
|--|---|
| 10 US-09-865-198-27 9 US-09-807-721-2 9 US-09-144-886-76 9 US-09-144-886-98 9 US-09-144-886-98 9 US-09-144-886-82 9 US-09-144-886-82 10 US-09-144-886-82 10 US-09-144-886-82 10 US-09-168-037-6 10 US-09-965-099-62 12 US-10-051-852-57 12 US-10-051-852-66 13 US-09-965-099-78 14 US-09-965-099-78 15 US-10-051-852-66 16 US-09-965-099-74 17 US-09-965-099-74 18 US-09-965-099-74 10 US-09-965-099-74 11 US-09-965-099-74 12 US-10-051-852-95 13 US-10-051-852-95 14 US-09-965-099-95 15 US-10-051-852-95 16 US-09-965-099-95 17 US-09-965-099-95 18 US-09-965-099-95 18 US-09-965-099-95 18 US-09-965-099-95 | 10 US-09-881-823-6 9 US-09-144-886-91 10 US-09-753-436-80 |
| 00000000000000000000000000000000000000 | 131 109 127 |
| 22222222222222222222222222222222222222 | 17.9 17.0 17.0 |
| 77900000000000000000000000000000000000 | 19 18 18 |
| | 4 4 4 4 5 5 |

ALIGNMENTS

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1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWI 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL
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US-10-051-852-105
                                                                                                                                                                                                                US-10-051-852-105
                                                                                                                                                                       RESULT 3
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                                                                                                                                                                                                                                                                                                                                       1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
                                                                                                                                                                                                                                                                                          1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWISATSNLASGVPAR 60
                                                                                                                                                                                                                ö
                                                                                                                                   Length 106;
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Best Local Similarity 100.0%; Pred. No. 1e-34;
Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 FSGSGSGTSYSLTISRVEAEDAATYYCQOWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 FSGSGSGTSYSLTISRVEAEDAATYYCQQWSSNPPTFGGGTMLEIR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Feuerstein, Giora
Patel, Arunbhai
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
TREATMENT OF THROMBOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                          Score 106; DB 10;
Pred. No. 1.8e-86;
: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
APPLICATION: 26-Sep-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: internal ORIGINAL SOURCE: SEQUENCE DESCRIPTION: SEQ ID NO: 105:
; SEQUENCE DESCRIPTION: SEQ ID NO: 89: US-09-893-615-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

**APPLICATION UNBER: 09/346,487

FILING DATE: <ur>
ATTORNEY/AGENT INFORMATION:
**ARTORNEY/AGENT INFORMATION:
**ARTORNEY/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 105, Application US/09965099
Patent No. US20020136725A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Blackburn, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 106 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 105: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                      vuciy match
Best Local Similarity 100.0%;
Matches 106; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
US-09-965-099-105
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Gaps
                                                                                                                                                                                                                    Sylvester, Daniel Sylvester, Daniel TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT OF THROMBOSIS
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44.3%; Score 47; DB 12; Length 106;
Best Local Similarity 100.0%; Pred. No. 1e-34;
Matches 47; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-38n-2002
CLASSIFICATION: «UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
FILING DATE: 16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE:
DESCRIPTION: SEQ ID NO: 105:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM COMPATIBLE OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5
                                                                 APPLICANT: Blackburn, Michael
Church, William
Gross, Micchell
Feuerstein, Giora
Nichols, Andrew
Padlan, Eduardo
Sequence 105, Application US/10051852 Patent No. US20020146411A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 610-270-5096
TELEFAX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION
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INFORMATION FOR SEQ ID NO: 105:
                                                                                                                                                                                                                                                                                                                                                                                      CITY: King of Prussia
                                                                                                                                                                                                           Patel, Arunbha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                               SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                        STATE: PA
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  TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                    ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 44.3%; Score 47; DB 12; Best Local Similarity 100.0%; Pred. No. 1e-34; Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
FILING DATE: 17-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
FILING DATE: 16-JAN-1997
ATTORNEY/AGENT INFORMATION:
RAME: Baumeister, KIFK
REGISTRATION NUMBER: 33,833
TELECHONE, DOCKET NUMBER: P50438
TELECHONE: 610-270-5096
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                        OF THROMBOSIS
                                                                                                      STREET: 709 Swedeland Road CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 103, Application US/09965099 Patent No. US20020136725A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Blackburn, Michael
Feuerstein, Giora
Patel, Arunbhai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 107 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 11:
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                          NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS
                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 19406
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                                                                                                                                                                         COUNTRY:
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                                                                                                                                                                                                                                   ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 44.3%; Score 47; DB 10; Best Local Similarity 100.0%; Pred. No. 1e-34; Matches 47; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                       ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
FILING DATE: 26-Sep-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/346,487
FILING DATE: - CUNROWN:

ATTORNEY/AGENT INFORMATION:

NAME: Baumeister, Kirk

REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE: internal ORIGINAL SOURCE: SCOUENCE DESCRIPTION: SEQ ID NO: 11: US-09-965-099-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Blackburn, Michael Church, William Gross, Mitchell Feuerstein, Glora Nichols, Andrew Padlan, Eduardo Patel, Arunbhai Sylvester, Daniel
                 Sequence 11, Application US/09965099
Patent No. US20020136725A1
GENERAL INFORMATION:
APPLICANT: Blackburn, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 11, Application US/10051852 Patent No. US20020146411A1 GENERAL INFORMATION:
                                                                                                        Feuerstein, Giora
Patel, Arunbhai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 107 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: Single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: CUNKNOWN>
TELEX: CUNKNOWN>
INFORMATION FOR SEQ ID NO: 11:
    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           NUMBER OF SEQUENCES: 111
                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                       USA
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US-09-965-099-11
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Gaps
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Sequence 12, Application US/09902107
Sequence 12, Application US/09902107
Sequence 12, Application US/09902107
Sequence 12, Application Sequence 12, Application:
Sequence 12, Application:
Title OF INVENTION:
TITLE OF INVENTION: METHODS FOR PRODUCING IMMUNOGLOBULINS CONTAINING
TITLE OF INVENTION: PROTECTION PROTEINS IN PLANTS AND THEIR USE
STILE REFERENCE: EP13002E
CURRENT APPLICATION NUMBER: US/09/982,107
CURRENT APPLICATION NUMBER: US/09/982,107
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Unknown Organism: Guy's 13 Kappa
US-09-982-107-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.3%; Score 47; DB 12; Interity 100.0%; Pred. No. 1.1e-34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.5%; Score 27; DB 9; L. 100.0%; Pred. No. 3.6e-17;
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                                                                                                                                                                              NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/344,050
FILING DATE: 25-JUN-1999
APPLICATION NUMBER: 08/783,853
FILING DATE: 16-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 TSNLASGVPARFSGSGSGTSYSLTISR 76
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                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
FILING DATE: 17-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 24, Application US/09976787
; Patent No. US20020064528A1
                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                 TELEFAX: <Unknown>
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Best Local Similarity 100.C
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                       TELEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 47; Conserv
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US-09-976-787-24
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LENGTH: 105
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Nichols, Andrew
Padlan, Eduardo
Patel, Arunbhai
Sylvester, Daniel
TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN TREATMENT
OF THROMBOSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 44.3%; Score 47; DB 10; Length 112; Best Local Similarity 100.0%; Pred. No. 1.1e-34; Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QIVLSQSPAILSASPGEKVTMTCRASSSVNYMHWYQQKPGSSPKPWI,47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                 PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/346,487
FILING DATE: CUNKNOWN:
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: P50438-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/051,852
                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/965,099
FILING DATE: 26-Sep-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 103:
US-09-965-099-103
                                           COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 103, Application US/10051852 Patent No. US20020146411A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Blackburn, Michael
Church, William
Gross, Mitchell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 112 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 103:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: internal
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
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GENERAL INFORMATION:

APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Me
TITLE OF INVENTION: Production
FILE REFERENCE: 11245/47102
CURRENT APPLICATION NUMBER: US/09/865,198
PRIOR APPLICATION NUMBER: US 60/206,749
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 2000-05-24
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                                                                                            Description of Artificial Sequence: BoNT/a clone 265 region VL epitope 2
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-09-976-787-8

Sequence 8, Application US/09976787

Sequence 8, Application US/09976787

Sequence 8, Application US/09976787

GENERAL INFORMATION:
APPLICANT: Zhu, Zhenping

APPLICANT: Air, Lary

TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof

FILE REFERENCE: 11245/46505

CURRENT APLICATION NUMBER: US/09/976,787

CURRENT FILING DATE: 2001-10-12

PRIOR APPLICATION NUMBER: US 69/493,539

PRIOR FILING DATE: 2000-1-28

PRIOR APPLICATION NUMBER: US 60/117,726

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 40

SOFTWARE: WordPerfect 8.0 for Windows
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                                                                                                                                                                                                DB 9; Length 107;
                                                                                                                                                                                             ch 25.5%; Score 27; DB 1 Similarity 100.0%; Pred. No. 3.7 27; Conservative 0; Mismatches
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SOFTWARE: WordPerfect 8.0 for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09865198 Patent No. US20020103345A1
LENGTH: 107
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : ORGANISM: Mus musculus US-09-976-787-8
                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                       FEATURE:
OTHER INFORMATION:
OTHER INFORMATION:
US-09-144-886-88
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APPLICANT: Zhu, Zhenping
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methoractic Fine Production
TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methoractic File Reference: 11245/47102
CURRENT APPLICATION WHBER: US/09/865,198
CURRENT FILING DATE: 2001-05-24
RIOR APPLICATION NUMBER: US 60/206,749
PRIOR APPLICATION NUMBER: US 60/206,749
RIOR FILING DATE: 2000-05-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 23
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Patent No. US20020155114A1
GENERAL INFORMATION:
APPLICANT: Marks, James D
APPLICANT: Amersdorfer, Peter
TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: 1996-1110 Monoclonal Antibodies That Neutralize
FILE REFERENCE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SCOTWARR: PatentIn Ver. 2.0
SEQ ID NO 88
               APPLICANT: Zhu, Zhenping
APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT APPLICATION NUMBER: US/09/976,787
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-10-28
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 40
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 24
LENTH: 106
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3.6e-17;
hes 0;
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Best Local Similarity 100.0%; Pred. No. 3.6e-17;
Matches 27; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.5%; Score 27; DB Best Local Similarity 100.0%; Pred. No. 3.6 Matches 27; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 TSNLASGVPARFSGSGSGTSYSLTISR 76
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Mouse US-09-976-787-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Mouse
US-09-865-198-23
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US-09-865-198-23
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Search completed: November 27, 2002, 07:32:53 Job time : 9.82239 secs
55 TSNLASGVPARFSGSGSGTSYSLTISR 81
                                                                                                                                                                                      Sequence 9, Application US/09910059

Sequence 9, Application US/09910059

Patent No. US20020142359A1

GENERAL INFORMATION:

APPLICANT: Copley, Clive G

APPLICANT: Edge, Michael Derek

TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,

TITLE OF INVENTION: Their Therepeutic use in an Adept System

FILE REFERENCE: 1991-209

CURRENT APPLICATION NUMBER: US/09/910,059

CURRENT FILING DATE: 1090-23

PRIOR APPLICATION NUMBER: CB 9703103.3

PRIOR FILING DATE: 1997-04-29

PRIOR FILING DATE: 1997-02-14

PRIOR FILING DATE: 1997-02-14

PRIOR FILING DATE: 1997-02-14

PRIOR FILING DATE: 1997-02-14

SPIOR FILING DATE: 1996-05-04

NUMBER: OF SEQ ID NOS: 131

SOFTWARE: Patentin version 3.1
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Patent No. US20030155114A1
GENERAL INFORMATION:
GENERAL INFORMATION:
THEORY INVENTION: Therespectic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Therespectic Monoclonal Antibodies That Neutralize
TITLE OF INVENTION: Detailinum Neurotoxins
FILE REFERENCE: 2500.117USO
CURRENT APPLICATION NUMBER: US/09/144,886
CURRENT PILING DATE: 1998-08-31
NUMBER OF SEQ ID NOS: 98
SEQ ID NOS: 98
SEQ ID NO 89
LENGTH: 112
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US-09-144-886-89
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                       50 TSNLASGVPARFSGSGSGTSYSLTISR 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Mus musculus US-09-910-059-9
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US-09-144-886-89
                                                                                                                                                RESULT 14
US-09-910-059-9
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 27, 2002, 05:38:32 ; Search time 8.28185 Seconds Run on:

(without alignments)
241.342 Million cell updates/sec

US-09-893-615-1 91 1 WRMYFSHRHAHLRSP 15 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 seqs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/SIDS2/gcgdata/geneseg/genesegp-emb1/AA1990.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:* /SIDS2/gggdata/geneseq/geneseqp-emb1/AA1980.DAT:*/SIDS2/gggdata/geneseq/geneseqp-emb1/AA1981.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1981.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1981.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1983.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1983.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1983.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1986.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1986.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1987.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1987.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1987.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SIDS2/gggdata/geneseqgg-emb1/AA1988.DAT:*/SI A_Geneseq_101002:

.DAT:* /SIDS2/gcgdata/geneseg/geneseqp-embl/AA1994.DAT:*/SIDS2/gcgdata/geneseg/geneseqp-embl/AA1995.DAT:*/SIDS2/gcgdata/geneseg/geneseqp-embl/AA1996.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1992.DAT:* /SIDS2/gcgdata/geneseg/genesegp-embl/AA1993.DAT:*

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:* /gcgdata/geneseg/genesegp-embl/AA2001.DAT /SIDS2/gcgdata/geneseq/genesegp-embl/AA1997. /SIDS2/gcgdata/geneseq/genesegp-embl/AA1998.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

SUMMARIES

| | Description | Lipoteichoic acid | Sequence 15mer 2nd | Sequence 15mer2-12 | Sequence 15mer2-13 | Sequence 15mer2-10 | Sequence 15mer2-16 | Sequence 15mer2-17 | Sequence 15mer2-14 | Porphorymonas ging | Porphorymonas ging |
|---|-----------------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| | ID | AAW94701 | AAW94733 | AAW94714 | AAW94715 | AAW94717 | AAW94718 | AAW94719 | AAW94716 | AAY34472 | AAY34348 |
| | Query Match Length DB ID | 15 20 | 19 20 | 19 20 | 19 20 | 19 20 | 19 20 | 19 20 | 19 20 | 757 20 | 763 20 |
| æ | Query Match L | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 72.5 | 51.6 | 51.6 |
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ALIGNMENTS

AAW94701 standard; peptide; 15 AA. (first entry) 22-APR-1999 AAW94701; RESULT 1 AAW94701

Lipoteichoic acid epitope peptide mimic for Mab 96-11.0.

Monoclonal antibody; MAD; lipoteichoic acid; gram positive; bacteria; immunoglobulin; phagocytosis; infection; epitope; peptide mimic; MAD 96-110.

Staphylococcus sp.

WO9857994 - A2.

23-DEC-1998

98WO-US12402 16-JUN-1998; 97US-0049871. 16-JUN-1997; Wong

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(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED

Stinson JL, Fischer GW, Schuman RF,

WPI; 1999-095329/08.

New antibodies to lipoteichoic acid of gram positive bacteria - used to develop products for the diagnosis, prevention and treatment of infections caused by gram positive bacteria

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                                                                           The invention relates to a monoclonal antibody (MAb) to lipoteichoic acid of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The artibodies bind to whole bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipoteichoic or peptides (encoded by a DNA of the variable region of anti-lipoteichoic corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody can be used for treating or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacterial. They can also be used for the diagnosis of gram positive bacterial infections. The present sequence represents a specifically claimed lipoteichoic acid epitope peptide minic that can be bound by the antibody of the invention (Mab 96-110).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria; immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
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                               Claim 16; Page 120; 150pp; English.
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N-PSDB; AAX05559.
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Mab 96-110; panning
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killing of the bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipotacicolic acid antibody or characterised by amino acids corresponding to one or more of the complementarity determining regions (CDRs) of the variable region of the antibody) can be used for treating or preventing infections caused by gram positive bacterial. They can also be used for the diagnosis of gram positive bacterial infections. Sequences AAW94726-34 represent common peptide sequences resulting from all library panning experiments. Three series of panning experiments were conducted to identify peptide sequences to which antibody of the invention (Mab 96-110) bound strongly. The translated sequences provide lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
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acid of gram positive bacteria, where the MAb is a chimeric immunoglobulin comprising at least part of a human immunoglobulin constant region and at least part of a non-human immunoglobulin variable region having specificity to lipoteichoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance phagocytosis and

The invention relates to a monoclonal antibody (MAb) to lipoteichoic

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be used for the diagnosis of gram positive bacterial infections. Sequences AAW94705-22 represent sequences resulting from a 15mer library panning second experiment. Three series of panning experiments were conducted to identify peptide sequences to which antibody of the Invention (Mab 96-110) bound strongly. The translated sequences provide lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
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immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
Mab 96-110; panning.
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Best Local Similarity
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acid of gram positive bacteria, where the MAD is a chimeric constant region and at least part of a non-human immunoglobulin constant region and at least part of a non-human immunoglobulin constant region and at least part of a non-human immunoglobulin variable region having specificity to lipotechnoic acid of gram positive bacteria. The antibodies bind to whole bacteria and enhance protection from lethal infection. The antibodies or peptides (encoded by a DNA of the variable region of anti-lipotechnoic acid antibody or characterised by amino acids anti-lipotechnoic acid antibody or characterised by amino acids (CDRS) of the variable region of the antibody) can be used for treating or preventing infections caused by gram positive bacteria. They can also be used for the diagnosis of gram positive bacteria. Infections.

Sequences AAM4705-22 represent sequences resulting from a 15mer library panning second experiment. Three sequences resulting from a 15mer library conducted to identify peptide sequences to which antibody of the
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lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
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100.0%; Pred. No. 8.4e-09;
11ve 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fischer GW, Schuman RF, Stinson JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Fig 6A-B; 150pp; English.
                                                                                                                                                                                                        AAW94717 standard; Protein; 19 AA.
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Best Local Similarity 100.
Matches 15; Conservative
                         17
3 WRMYFSHRHAHLRSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-095329/08.
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                                                                                                                                                                                                                                                                             AAW94717;
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                                                                                                                                   RESULT 5
AAW94717
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RESULT 6 AAW94718

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Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria; immunoglobulin; phagocytosis; infection; epitope; peptide mimic; Mab 96-110; panning.
                                                                                                                                                                                                                                                                        Sequence 15mer2-17/0 resulting from 15mer library punning experiment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibodies to lipoteichoic acid of gram positive bacteria - used to develop products for the diagnosis, prevention and treatment of infections caused by gram positive bacteria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Fig 6A-B; 150pp; English.
                                                                   AAW94719 standard; Protein; 19
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                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-095329/08.
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus sp.
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                                                                                                                                AAW94719;
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RESULT 7
AAW94719
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                                                                                                                                                                                                                                        NAMES OF THE PROOF THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monoclonal antibody; MAb; lipoteichoic acid; gram positive; bacteria; immunoglobulin; phagocytosis; infection; epitope; peptide mimic; Mab 96-110; panning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15mer2-16/0 resulting from 15mer library panning experiment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a monoclonal antibody (MAb) to lipoteichoic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibodies to lipoteichoic acid of gram positive bacteria to develop products for the diagnosis, prevention and treatment infections caused by gram positive bacteria
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100.0%; Pred. No. 8.4e-09;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stinson JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Fig 6A-B; 150pp; English.
                                                                                                                                                                                                                                                                            AAW94718 standard; Protein; 19 AA.
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Matches 15; Conservative
                                   WRMYFSHRHAHLRSP 15
                                                                           3 WRMYFSHRHAHLRSP 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WRMYFSHRHAHLRSP 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus sp.
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Stinson JL, Wong H;

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The invention relates to a monoclonal antibody (MAb) to lipoteichoic
acid of gram positive bacteria, where the MAb is a chimeric
immunoglobulin comprising at least part of a human immunoglobulin
constant region and at least part of a non-human immunoglobulin
constant region and at least part of a non-human immunoglobulin variable
credion having specificity to lipoteichoic acid of gram positive bacteria.
The antibodies bind to whole bacteria and enhance phagocytosis and
contained by a proceed of the variable region of
anti-lipoteichoic acid antibody or characterised by amino acids
corresponding to one or more of the complementarity determining regions
corresponding to one or more of the antibody can be used for treating
creating infections caused by gram positive bacteria. They can also
be used for the diagnosis of gram positive bacterial infections.
Sequences AAM44705-22 represent sequences resulting from a library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                panning second experiment. Three series of panning experiments were conducted to identify peptide sequences to which antibody of the invention (Mab 96-110) bound strongly. The translated sequences provide lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
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100.0%; Pred. No. 8.4e-09;
ive 0; Mismatches 0;
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3 WRMYFSHRHAHLRSP 17

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Porphorymonas gingivalis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a monoclonal antibody (MAb) to lipoteichoic
acid of gram positive bacteria, where the MAb is a chimeric
immunoglobulin comprising at least part of a human immunoglobulin
constant region and at least part of a non-human immunoglobulin variable
region having specificity to lipoteichoic acid of gram positive bacteria.

CC The antibodies bind to whole bacteria and enhance phagocytosis and
c xilling of the bacteria and enhance protection from lethal infection. The
antibodies or peptides (encoded by a DNA of the variable region of
anti-lipoteichoic acid antibody or characterised by amino acids
ccresponding to one or more of the antibody) can be used for treating
cc preventing infections caused by gram positive bacteria. They can also
be used for the diagnosis of gram positive bacteria. They can also
cs be used for the diagnosis of gram positive bacteria. Infections
conducted experiment. Three series of panning experiments were
cc panning second experiment. Three series of panning experiments were
cc conducted to identify peptide sequences to which antibody of the
invention (Mab 96-110) bound strongly. The translated sequences provide
cc lipoteichoic acid epitope peptide mimics to which Mab96-110 bound.
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                                              positive; bacteria; peptide mimic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                    New antibodies to lipoteichoic acid of gram positive bacteria · used to develop products for the diagnosis, prevention and treatment of infections caused by gram positive bacteria
                      Sequence 15mer2-14/0 resulting from 15mer library.panning experiment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66; DB 20; Length 19;
Pred. No. 0.00015;
!; Mismatches 3; Indels
                                            Monoclonal antibody; MAb; lipoteichoic acid; gram
immunoglobulin; phagocytosis; infection; epitope;
Mab 96-110; panning.
                                                                                                                                                                                                                   (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED
                                                                                                                                                                                                                                           Wong H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porphorymonas gingivalis protein PG13.
                                                                                                                                                                                                                                             Stinson JL,
                                                                                                                                                                                                                                                                                                                                                      Example 5; Fig 6A-B; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY34472 standard; Protein; 757 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.5%;
73.3%;
                                                                                                                                                                    98WO-US12402
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 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 73.3
Matches 11; Conservative
                                                                                                                                                                                                                                           Schuman RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WRMYFSHRHAHLRSP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 WRKYFSYHHAHLCSP 17
                                                                                                                                                                                                                                                                  WPI; 1999-095329/08.
                                                                                             Staphylococcus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 AA;
                                                                                                                                                                                                                                                                               N-PSDB; AAX05542
                                                                                                                     W09857994-A2.
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                                                                                                                                                                    6-JUN-1998;
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22-APR-1999
                                                                                                                                                                                                                                           Fischer GW,
                                                                                                                                             23-DEC-1998
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Porphorymonas gingivalis (PC) polypeptide sequences given in AAY34318 to AAY34583. AAX91802 to AAX41989 represent PCR primers used in the isolation of the PC polypeptides. The PC polypeptides have antibacterial activity with a vaccine mechanism of action. The PC polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX91536 to AAX91801 encode two hundred and sixty six antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Porphorymonas gingivalis; PG; periodontal disease; gingivitis;
                                                                                                                                                                                                                                                                                                                                                                                                                Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Length 757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antigenic Porphorymonas gingivalis peptides for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Margetts MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 47; DB
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 450-451; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphorymonas gingivalis protein PG13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY34348 standard; Protein; 763 AA.
                                                                                                                                                                                                                                                                                                                                                                                                            Hocking DM,
Webb EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.6%;
61.5%;
                                                                                                                                                                                         98AU-0001546.
98AU-0002264.
98AU-0002911.
                                                                                   98WO-AU01023
                                                                                                                                                   97AU-0000839
97AU-0001182
                                                                                                                                                                                                                                                                               98AU-0003338
98AU-0003654
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                                                                                                                                                                                                                                                                                                                                                                                                              Agius CT, Barr IG,
Ross BC, Rothel LJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-385613/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     757 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAX91690
                                                                                                                                                                                                                                                                                                                                                                     (CSLC-) CSL LTD.
WO9929870-A1
                                                                                   10-DEC-1998;
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09-APR-1998
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                                           17-JUN-1999
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                                                                                                                                                                         31-DEC-1997
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Agius

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The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activinhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                             Claim 20; SEQ ID NO 24604; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 22; Length 117;
Pred. No. 4.5;
0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 14865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB62691 standard; Protein; 684 AA.
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                                       Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.5%;
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11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
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                                                                           2001-514838/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-656860/75.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HYSE-) HYSEQ INC.
                                       Liu C,
                                                                           WPI; 2001-514838,
N-PSDB; AAI90643
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                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation.
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                                                                                                                                                                         disorders
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                                       Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porphorymonas gingivalis (PG) polypeptide sequences given in AAY34318 to AAY34381. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX91536 to AAX91801 encode two hundred and sixty six antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                            Margetts MB, Patterson MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.6%; Score 47; DB 20; Length 763; 61.5%; Pred. No. 17; 1.ve 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Antigenic Porphorymonas gingivalis peptides for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 308-309; 588pp; English.
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                                                                                                                                                                                                                                                                                        Hocking DM,
Webb EA;
                                                                                                                                    98AU-0002911
98WO-AU01023
                                                                                              98AU-0001546
                                                                                                                                                      98AU-0003128
                                                                                                                                                                       98AU-0003338
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2000US-0577409
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                                                                           97AU-0001182
                                                                                                                98AU-0002264
                                                                                                                                                                                           98AU-0003654
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                                                                                                                                                                                                                                                                                        Barr IG,
Rothel LJ,
                                                                                                                                                                                                                                                                                                                                               WPI; 1999-385613/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           763 AA;
                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAX91566
                                                                                                                                                                                                                                                     (CSLC-) CSL LTD.
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18-MAY-2000;
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10-DEC-1998;
                                                                         31-DEC-1997
30-JAN-1998
                                                                                                              10-MAR-1998
09-APR-1998
                                                                                                                                                      23-APR-1998
05-MAY-1998
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                                                                                                                                                                                           22-MAY-1998
                                                         10-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                           gingivitis
                                                                                                                                                                                                                                                                                      CT,
                                                                                                                                                                                                                                                                                                            Ross BC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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27 - FEB - 2002
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                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention describes the a polypeptide comprising one or more consensus regions of proteins of LIV-1 family or its functional homologue. The polypeptide is useful in the preparation of a medicament for the treating a disease e.g. those involving disorders of zinc homeostasis, in gene therapy and for modifying apoptosis in vitro or in vivo on contact with cells. Diseases involving defects in zinc homeostasis include cancer, neurodegenerative disorders and apoptotic disorders. Recombinant proteins of the LIV-1 family (an
                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIV-1; oestrogen; cytostatic; neuroprotective; zinc homeostasis; gene therapy; apoptosis modulator; cancer; neurodegenerative disorder; apoptotic disorder; zinc-homeostasis related disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of a polypeptide comprising one or more consensus regions of proteins of LIV-1 family for treating disorders of zinc homeostasis such as breast cancer, neurodegenerative disorders, and for modifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                       Disclosure; SEQ ID NO 14865; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB 22; Length 684; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oestrogen-regulated LIV-1 family protein AAF50401_Dm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU74625 standard; Protein; 684 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                     49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYCA-) UNIV COLLEGE CARDIFF
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14-JUN-2000; 2000GB-0014493.
05-JUL-2000; 2000US-216349P.
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                                                                                                                                                                                                                                          (ABB57737-ABB72072).
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SHRHGHVHSP 514
                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                    684 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apoptosis
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                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SAPHO syndrome: synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA. inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
oestrogen-regulated gene) are useful for diagnosing a zinc homeostasis-related condition in a subject which involves contacting a sample from the subject with the recombinant protein and measuring the binding of antibody to the sample. The antibody is also useful for treating a zinc homeostasis-related condition. This sequence is a member of the LIV:1 family (a gene regulated by oestrogen levels) and is useful for creating recombinant proteins for diagnosing zinc-homeostasis related conditions, described in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Length 684;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB;
Pred. No. 32;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitcham JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU52691 standard; Protein; 82 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-2000; 2000US-199047P.
02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative
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L'maisonneuve J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating acne vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-616774/71.
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                                                                                                                                                                                                                                                                                                                                                                   684 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveltis; endophthalnatis; bone; joint, central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
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                                                                                                                                                                                                                   Score 43; DB 22; Length 82;
Pred. No. 6.6;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes immunogenic protein #2659.
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ter D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carter
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                                                                                                                                                                                                                                                                                                                                                                                                                   AA.
                                                                                                                                                                                                                                                                                                                                                                                                             AAU41763 standard; Protein; 88
                                                                                                                                                                                                                   47.38;
70.08;
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e J, Zhang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                 Query Match
Best Local Similarity 70.0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating acne vulgaris
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N-PSDB; AAS59515.
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                                                                                                                                                                                                                                                                                                          82 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200181581-A2.
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                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
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polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA).

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at tp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                          Score 43; DB 22; Length 88;
Pred. No. 7.1;
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                                                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                                                            47.38;
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Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                               7 YVHHRHARLRS 17
                                                                                                                                                                                                     88 AA;
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    888888888888x8
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Wed Nov 27 08:54:11 2002

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                                                                  November 27, 2002, 07:15:05; Search time 4.11197 Seconds (without alignments)
; 350.688 Million cell updates/sec
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Copyright (S) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                    283224 segs, 96134422 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              - protein search, using sw model
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S27482
S27482
D75212
AE2155
S61250
T00624
B82636
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Gapop 10.0 , Gapext 0.5
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91
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Perfect score:
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|--|-----------|--|----------------------|-------|------------------|---|
| 31 | | 44.0 | 710 | 7 7 | AE214/ T20635 | cytochrome c oxida hypothetical prote |
| | | 44.0 | 838 | 7 | A48440 | ring-infected eryt |
| | | 44.0 | 899 | 0 | H87513 | hypothetical prote |
| | | 44.0 | 1349 | ~ | T01699 | aldehyde oxidase (|
| | | 44.0 | 1495 | ~ | 860255 | transcription co-r |
| m | | 43.4 | 1167 | ~ | T42704 | hypothetical prote |
| | | 42.9 | 500 | 0 | S43068 | hypothetical prote |
| | | 42.9 | 296 | ~ | A40996 | phenylalanine 4-mo |
| | | 42.9 | 303 | ~ | E95374 | probable ABC trans |
| | | 42.9 | 323 | ~ (| E95877 | probable ABC trans |
| | | 42.9 | 349 | ~ | 843770 | phosphatidylcholin |
| | | 42.9 | 351 | ~ | S11519 | phosphatidylcholin |
| | | 42.9 | 805 | ~ (| E83/88 | galactose-1-phosph |
| | 5 0 | 42.0 | 548 562 | 70 | F70399 | probable asparagin hydrodenase redula |
| | | | | | ALIG | ALIGNMENTS |
| RESULT 1 | | | | | | |
| A10355 probable membrane protein YPO2924 [imported] | brane | prote | oin YPO | 292 | 4 [impor | ted] - Yersinia pestis (strain CO92) |
| C;Species: rersinia C;Date: 02-Nov-2001 | ov-20 | | pestis #sequence | re. | vision 0 | pestis #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001 |
| C, Accession: AI0355 | AI03 | | 5 | | | 00 74 60 80 0 E N |
| deno-Tarraga, A.M.: C) | . Σ | ren, r | s.w.; r. [llingwe | ort | b, T. C | Krearmilli, J.; Wien, b.w.; Inomeor, n.c., illuali, K.w.; Golden, M.: Co.; Francisce, M. deno-Tarrada, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. |
| 11, M.; Rutherford, | erfor | d, K | Simmo | gpu | , M.; Sk | a) |
| Nature 413, 523-527, 2001 | 523-5 | 77, 20 | 10T | 5 | a ta t | Nature 413, 523-527/, 2001 |
| A; Reference | numbe | r: AB(| 0001; M | | :2147041 | A)Reference number: AB0001; MUID:21470413; PMID:11386360 |
| A; Accession: AI0355 | AI03 | 55 | | | | |
| A; Status: preliminary | elimi | nary | | | | |
| A; Residues: 1-215 <kur></kur> | 1-215 | <kur:< td=""><td>^</td><td></td><td></td><td></td></kur:<> | ^ | | | |
| A; Cross-references: GB: AL590842; | rence | s: GB | : AL5908 | 42; | | PIDN:CAC92172.1; PID:g15980886; GSPDB:GN00175 |
| C;Genetics: A;Gene: YPO2924 | 924 | | | | | |
| | | | | | | |
| Query Match | h Simi | / Match | 49.58; | en er | Score | 45; DB 2; Length 215; No. 4 7: |

hypothetical protein F12E4.90 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 (Speciession: 148357 (Speciession: 148357 (Speciession: 148357 (Species) (Spe ö Gaps ; 0 5; Indels A:Residues: 1.F84 <BEV>
A:Cross-references: EMBL:AL162751
A:Experimental source: cultivar Columbia; BAC clone F12E4 Score 45; DB 7 Pred. No. 4.7; Mismatches Query Match Best Local Similarity 61.5%; Matches 8; Conservative 72 WAMTEGRREAHLR 84 1 WRMYFSHRHAHLR RESULT 2 T48357 ò g

ö Gaps ö 49.5%; Score 45; DB 2; Length 684; 70.0%; Pred. No. 17; 1; Indels iive 2; Mismatches 1; Indels Query Match 49.5 Best Local Similarity 70.0 Matches 7; Conservative A; Map position: 5 A; Note: F12E4.90

C; Genetics:

hypothetical prote hypothetical prote

hypothetical prote transcription fact

endo-1,4-beta-xyla

LPS biosynthesis p probable hemolysin

us-09-893-615-1.rpr

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V. Aucessiou: 10214,

Riyysotskala, V.S.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji, O.; Liu, S.;

rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel
submitted to the EMBL Data Library, August 1998
A. Description: Arabidopsis thaliana chromosome 1 BAC F8K4 sequence.

A. Reference number: 214574
A. Accession: T02147
A. Accession: T02147
A. Molecule type: DNA
A. Molecule ty
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R:Sato, N.; Fujiwara, S.; Kawaguchi, A.; Tsuzuki, M.
J. Biochem. 122, 1224-1232, 1997
A; Title: Cloning of a gene for chloroplast omega 6 desaturase of a green alga, Chlamy A; Reference number: JC5891; MUID:98158334; PMID:9498569
A; Reference number: JC5891; MUID:98158334; PMID:9498569
A; Status: nucleic acid sequence not shown
A; Residues: 1-424 <SAT>
A; Residues: 1-424 <SAT>
A; Comment: This enzyme catalyzes the desaturation of monoenoic to dienoic acids: C; Comment: This enzyme catalyzes the desaturation of monoenoic to dienoic acids: A; Gene: des6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           omega 6 desaturase (EC 1.14.99.-) precursor, chloroplast - Chlamydomonas reinhardtil
C;Species: Chlamydomonas reinhardtil
C;Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 20-Jun-2000
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C;Species: Zea mays (maize)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 28-Jul-2000
C;Accession: T01698
R;Sekimoto, H; Seo, M; Dohmae, N; Takio, K; Kamiya, Y.; Koshiba, T.
J; Biol. Chem. 272, 15280-15285, 1997
A;Title: Cloning and molecular characterization of plant aldehyde oxidase.
A;Reference number: 214401; MUID:97326103; PMID:9182554
A;Accession: T01698
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                     hypothetical protein F8K4.22 - Arabidopsis thaliana
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 22-Oct-1999
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C;Superfamily: omega-3 fatty acid desaturase
C;Keywords: chloroplast; oxidoreductase
F;1-40/Domain: transit peptide (chloroplast) #status predicted <TPS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 54.5%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 2; Length 743;
Pred. No. 27;
2; Mismatches '1; Indels
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70.08;
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Best Local Similarity 70.0'
Matches 7; Conservative
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|178 WRIKHNHHHAH 188
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418 HFSHQHHHLR 427
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                                                                                                                                                                                                                                                                                       C; Accession: T02147
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                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Bacillus subtilis Subtilis Subtilis C; Date: 05-Dec-1997 #text_change 20-Jun-2000 C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000 C; Bron. S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Changetre, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997 A; Hanbart, H.; Holsappel, S.; Habor, C.; Ferrari, E. Nature 390, 249-256, 1997 A; Hanbart, H.; Holsappel, S.; Habor, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Barro, V.; Doll, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A; Authors: Schletch, S.; Schroeter, R.; Scoffone, F.; Sekquchi, V.; Tanako, N.; Sadaie, Y.; Sato, T.; Sato, M.; Sadaie, Y.; Yasumoto, K.; Yas
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(Species: Arabidopsis thaliana (mouse-ear cress)
(Species: Arabidopsis thaliana (mouse-ear cress)
(Species: Arabidopsis thaliana (mouse-ear cress)
(Spacession: T04191
(Spaces
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C;Superfamily: Bacillus subtilis hypothetical protein yobF
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70.0%; Pred. No. 25;
tive, 2; Mismatches
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Best Local Similarity 70.03
Matches 7; Conservative,
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247 YAMYFKDRHSHL 258
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                                                           :|||:| |||
412 HFSHKHHHLR 421
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412 HFSHQHHHLR 421
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PIDN:CAC98929.1; PID:g16410254; GSPDB:GN00177
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A;Map position: 5
A;Introns: 288/1; 447/3; 478/3; 514/3; 541/1; 567/3; 883/2
      A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                   Score 42; DB 2
Pred. No. 17;
2; Mismatches
                                                                                                                                                       A; Residues: 1-252 <GLA>
A; Residues: 1-252 <GLA>
A; Cross-references: GB:NC_003210; PI
A; Experimental source: strain EGD-e
C; Genetics:
A; Gene: lmo0851
                                                                                                                                                                                                                                                                                                                                               46.2%;
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103 LYLAHTGRHERSP 115
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Best Local Similarity
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                                                                                               A; Status: preliminary A; Molecule type: DNA
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                                                                     A; Accession: AC1181
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C; Species: D5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C; Accession: C59849
R; Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Changerer 390, 249-256, 1997
A.Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
Lech, J.; Harwood, C.R.; Hematt, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A.Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucell
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Rosse, M.; Sadaio, Y.; Saton, T.; Scanlon,
A.Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, Y.; Satov, T.; Scanlon,
A.Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, Y.; Tosato, V.; Othiyama,
T.; Winters, P.; Wilpat, A.; Yamanoto, H.; Yamano, K.; Yasta, K.; Yoshida, R.
A.Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A.Reference number: A69580; MUID:98044033; PMID:9384377
A.Accession: C69849
A.Stesidues: 1-134 <KUN>
A.Residues: 1-134 <KUN
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A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitcurnam, A.; Ma ok, C.; Schlueter, T.; Simoes, N.; Tlerrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Berche, P.; Bloecker
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                       Across references: EMBL:D88451; NID:g2589161; PIDN:BAA23226.1; PID:g2589162
GGenetics:
A;Gene AO-1
C;Function:
A;Description: catalyzes oxidation of aldehydes into respective acids
C;Superfamily: xanthine dehydrogenase; ferredoxin [2Fe-25] homology
C;Superfamily: xanthine dehydrogenase; ferredoxin [2Fe-25] homology
C;Keywords: 2Fe-35; metalloprotein; oxidoreductase
F;31-81/Domain: ferredoxin [2Fe-25] homology cEDX>
F;30,55,58,80/Binding site: 2Fe-25 cluster (Cys) (covalent) #status predicted
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                               Score 43; DB 2; Length 1358;
Pred. No. 75;
3; Mismatches 2; Indels
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C;Superfamily: Bacillus subtilis hypothetical protein yjdH
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58.3%;
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                                                                                                                                                                                                                                                                                                                                               Query Match 47.3
Best Local Similarity 58.3
Matches 7; Conservative
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619 IYSTHPHAHVRS 630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 8; Conserv
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A; Residues: 1-1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Richaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlan, K.D.; Falhl, D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ok, C.; Schlueter, T.; Simoes, N.; Tlerrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla A;Tille: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-252 <GLA>
A;Residues: 1-252 <GLA>
A;Cross-references: GB:AL592022; PIDN:CAC96076.1; PID:g16413295; GSPDB:GN00178
A;Experimental source: stra4n-Clip11262
C;Genetics:
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hypothetical protein lin0844 (imported) – Listeria innocua (strain Clip11262)
                                C;Species: Listeria innocua
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 252;
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R; Woessner, J.; Bradshaw, H.
submitted to the EMBL Data Library, March 1996
A; Description: The sequence of C. elegans cosmid C01B7.
A; Reference number: 220581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C01B7.1 - Caenorhabditis elegans
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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2; Mismatches
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Gaps

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transcription regulator AraC/XylS family homolog yobg - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Dac-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C;Accession: G6989
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capueno, V.; Carter, N.M.;
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Hosono, S.; Hullo, M.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurite, K.; Lapidus, A.; Lardino
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Perro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanl
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekkguchi, J.; Sakowska, A.; Se
Akuthors: Voshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tarako, M.; Tarako, M.; Yata, K.; Yoshida
T.; Winters, Poshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
A;Reference number: A6980; MUID:98044033; PMID:9384377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   formate dehydrogenase (EC 1.2.1.2) O gamma chain - Haemophilus influenzae (strain Rd C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: B64042
C;Accession: B64042
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage GGodyne, J.D.; Scott, J.; Silriey, R.; Liu, L.I.; Glodek, A.; Kalley, J.M.; Weldman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: B64042
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-257 
A;Cross-references: GB:L42023; TIGR:H10008
C;Superfamily: formate dehydrogenase gamma chain
C;Keywords: NAD: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-241 <KUNA A;Coss-references: GB:Z99114; GB:AL009126; NID:92634230; PIDN:CAB13797.1; PID:e11853 A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 2; Length 241;
Pred. No. 24;
3; Mismatches 1; Indels
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Pred. No. 26;
0; Mismatches
Pred. No. 21;
2; Mismatches
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60.0%;
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Best Local Similarity 85.7%;
Matches 6; Conservative
   52.9%;
                                                                                                  1 WRMYFSH--RHAHLRSP 15
                                                                                                                                             ||| |: | ||:| |
81 WRMRSSNPIRRAHIRRP 97
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                                   9; Conservative
Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
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18 RLYHSHKHAY 27
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
Nakasa, B. 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Escherichia coll
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 08-Oct-1999
C;Accession: J01340; 510661
R;Cram, D.S.; Loh, S.M.; Cheah, K.C.; Skurray, R.A.
Gene 104, 85-90, 1991
A;Title: Sequence and conservation of genes at the distal end of the transfer region on A;Reference number: J01338; MUID:92009201; PMID:1916281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: DNA
A; Residues: 1-248 <CRA>
A; Residues: 1-248 <CRA>
A; Residues: 1-248 <CRA>
A; Cross-references: GBN38048; NID:g151835; PIDN:AAA98314.1; PID:g151836
A; Cross-references: GBN38048; NID:g151835; PIDN:AAA98314.1; PID:g151836
A; Experimental source: plasmid R6-5
B; Yoshioka, Y:; Fujita, Y:; Ohtsubo, E.
J; Mol. Biol. 214, 39-53, 1990
A; Title: Nucleotide sequence of the promoter-distal region of the tra operon of plasmid A; Reference number: S10658; MUID:90317835; PMID:2164585
A; Accession: S10661
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A; Residues: 1-208 < KUR>
A; Cross-references: GB:BA000019; PIDN:BAB76280.1; PID:g17133717; GSPDB:GN00179
A; Experimental source: strain PCC 7120
C; Genetics:
                                                                      Gaps
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A; Residues: 1-248 <YOS>
A; Cross-references: EMBL: X55815; NID: 942620; PIDN: CAA39339.1; PID: 942625
A; Experimental source: plasmid R100
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   Length 929
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                                                                      4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: transmembrane protein
F;39-55/Domain: transmembrane #status predicted <TMl>
Score 42; DB 2;
Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41.5; DB Pred. No. 21; 2; Mismatches
                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                               trax protein - Escherichia coli plasmids
46.28;
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Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                   6; Conservative
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75 WGLNLS-RHAHIRQP 88
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453 LFVAHRHGHRASP 465
                                                                                                                                      3 MYFSHRHAHLRSP 15
                            Best Local Similarity
Matches 6; Conserv
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A;Genome: plasmid
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A;Gene: all4581
   Query Match
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AE2378
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1 WRMYFSH 7 || || || || 159 WRQYFSH 165 oy Op

Search completed: November 27, 2002, 07:24:07 Job time : 12:112 secs

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us-09-893-615-1.rsp

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OM protein - protein search, using sw model

November 27, 2002, 05:39:34; Search time 2.14286 Seconds (without alignments) 290.334 Million cell updates/sec Run on:

US-09-893-615-1 91 1 WRMYFSHRHAHLRSP 15 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|-----------|--------|-------------|------------|------------|------------|------------|-----------|------------|--------------------|------------|--------------------|------------|------------|------------|------------|--------------------|------------|------------|------------|------------|-------------|------------|------------|------------|------------|-----------|-----------|------------|--------------------|------------|--------------------|------------|----------------|----------|-------------|
| SUMMARIES | | QI | CCT1_MOUSE | TNF5_CHICK | TRX2_ECOLI | FDXI_HAEIN | SYN_PYRAB | AG22_SHEEP | SGF3_BOMMO | RIK2_HUMAN | NCR2_HUMAN | HEPC_MORCS | DESA_SYNY3 | GALT_BACHD | RIK2_MOUSE | MASY_CUCMA | MASY_CUCSA | CARE_HUMAN | Y2R2_DROME | DPOL_PYRSD | -RL35_ECOLI | MEPA_ECOLI | RECF_PASMU | KC2A_THEPA | CG23_YEAST | SYN_PYRFU | SYN_PYRHO | RSP6_CHLRE | SUOX_HUMAN | HELI_HSVEB | HELI_V2VD | ODO1_AZOVI | YCF2_PINTH | POLG_WNV | POLG_KUNJM |
| | | DB : | - | - | 7 | - | - | - | - | Н | - | - | - | ~ | Н | - | - | _ | - | - | Ä | - | П | - | П | - | П | - | - | - | - | - | , , | - | - |
| | | Length | 724 | 272 | 248 | 238 | 434 | 260 | 351 | 540 | 2517 | 82 | 351 | 208 | 539 | 266 | 268 | 1004 | 1021 | 1312 | 9 | 274 | 358 | 420 | 427 | 434 | 434 | 459 | 488 | 881 | 881 | 943 | 2054 | 3430 | 3433 |
| • | Query | Match | | • | • | 45.1 | • | 44.0 | • | | | | | 42.9 | | | | | 42.9 | | | 41.8 | | 41.8 | | 41.8 | | | | ٠ | | • | 41.8 | | |
| | | Score | 45 | 4 | 41.5 | 41 | 41 | 40 | 40 | 40 | 40 | 39 | 39 | 39 | 39 | 39 | 39 | 39 | 39 | 39 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 | 38 |
| | Result | 8 | - | ~ | m | 4 | Ŋ | 9 | 7 | 80 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 50 | 21 | 22 | 23 | 24 | 22 | 56 | 27 | 28 | 53 | 30 | 31 | 32 | 33 |

| P08771 zea mays (m P39973 saccharomyc Q37626 prototheca P03934 caenorhabdi P38677 neurospora Q9r0n6 mus musculu P38703 saccharomyc P96081 thermus aqu P3569 schizosacch Q9ulm2 homo sapien P34672 caenorhabdi O14829 homo sapien |
|--|
| YAC1_MAIZE YEI4_YEAST NU6M_PROWI TC1A_CAEEL CMLE_NEUCR SYT8_MOUSE IAG1_YEAST IAG1_YEAST GSHB_SCHPO YE99_HUWAN YO22_CAEEL PPEI_HUMAN |
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| 1102 2011 2012 2013 395 4411 693 653 653 |
| 044444444 00004444444 0000000000000000 |
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| 44444444444444444444444444444444444444 |

ALIGNMENTS

| SULT 1 L_MOUSE CCT1_MOUSE STA QQQWV9; Q9ZOU7; 16-0CT-2001 (Re) | 16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, Cyclin T1 (Cyclin T) (Cyclin T) | | | P SEQUENCE FROM N.A. STRAILBALLB/C. X MEDIITNE-90169742: Dubhmed-9643510. | | governs the species specificity of HIV-1 Tat."; EMBO J. 17:7056-7065(1998). | | SEQUENCE FROM N.A. S STRAIN-C57BL/6; TISSUE-Brain; | | Rice A.P., Littman D.R., Jones K.A.; | | Cycrl protein."; | L Genes Dev. 12:3512-3527(1998). | | TISSUE-Spleen; MEDLINE-99263519; PubMed-10329126; | Kwak Y.T., Ivanov D., Guo J., Nee E., Gaynor R.B.; | | | | - | | "Interactions between human cyclin T, Tat, and the tra | | Proc. Natl. Acad. Sci. U. | | ELONGATION FACTOR B (P-TEFB), WHICH I | | SUBUNIT OF RNA POLYMERASE II (RNAP II), DOES NOT BIND EFFICIENTLY TO THE TRANSACTIVATION DOMAIN OF THE HIV-1 NUCLEAR TRANSCRIPTIONAL | |
|--|---|------|-----|---|------|--|----|--|----------|--------------------------------------|----|------------------|----------------------------------|----|--|--|-----|----|-----|---|-----|--|----|---------------------------|-----|---------------------------------------|------|--|----|
| A P C C E | SETTE | 8888 | Z Z | RP RC | RA F | R. I.S. | RN | ğ δ | RA RA | RA | RT | R. | Z Z | RP | 2 X | RA | Z Z | R. | A A | 2 | X 6 | R. | RT | R. Y. | នូវ | ខ្ល | ខ្លួ | ខ្ល | ប្ |

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DOMAIN
TRANSMEM
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Matches
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                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                 MGD; MGL...

A InterPro; IPR0043u,

R Ffam; PF00134; cyclin; 1.

DR SMART; SM00385; CYCLIN; 1.

DR PROSITE; PS00292; CYCLINS; FALSE_NEG.

KW Cyclin; Cell cycle; Cell division; Colled coil;

KW Cyclin; Cell cycle; Cell division; Nuclear protein.

NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

253 270 TAT:TAR RECOGNITION MOTIF (TRM).

PAR:TAR RECOGNITION MOTIF (TRM).

PAR:TAR RECOGNITION MOTIF (TRM).

PAR:TAR RECOGNITION MOTIF (TRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 5 (CD40 ligand) (CD40-L) (CD154 protein).
TUNFSF5 OR CD40LG OR CD40L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=White leghorn: TISSUE-Spleen;
STRAIN=White leghorn: TISSUE-Spleen;
STRAIN=White leghorn: TISSUE-Spleen;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Cytokine that binds to TNFRSF5. Mediates B-cell proliferation in the absence of co-stimulus as well as IgE production in the presence of IL-4. Involved in immunoglobulin class switching (By similarity).
-!- SUBUNIT: Homotimer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type II membrane protein. Also exists as extracellular soluble form (By similarity). PTM: The soluble form derives from the membrane form by protecultic processing (By similarity).
SUBUNIT: ASSOCIATES WITH CDK9 TO FORM P-TEFB. CYCLIN T1 IS THE PREDOMINANT CYCLIN ASSOCIATED WITH CDK9.
SUBGELLULAR LOCATION: Nuclear (By similarity).
SIMILARITY: BELONGS TO THE CYCLIN FAMILY. STRONG TO CYCLIN C
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
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6.9;
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7396E428F5A8B91B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 45; DB
Pred. No. 6.9;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                   EMBL; AF095640; AAD13656.1; --
EMBL; AF109179; AAD19654.1; --
EMBL; AF087662; AAD17798.1; --
EMBL; AF113951; AAD17205.1; --
MGD; MGI:1328363; Ccntl.
InterPro; IPR004366; Cyclin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 41, Created)
(Rel. 41, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                        80565 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                              49.5%;
58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
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522 HHSHRHSHLQLP 533
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                                                                                                                                                                                                                                                                                                                                                                                                        724 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                       516
565
715
48
                                                SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002
15-JUN-2002
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHICK
                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNF5_CHICK
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                                                                                                                use by non-profit institutions as long as its content is in o way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/annqunce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TUMOR NECROSÍS FACTOR LIGAND SUPERFAMILY, MEMBER 5, MEMBRANE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 5, SOLUBLE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLASMID-IncFII R100;
MEDLINE-90317835; PubMed-2164585;
Yoshikoka Y., Fuljta Y., Ohtsubo E.;
"Nucleotide sequence of the promoter-distal region of the tra operon of plasmid R100, including tra! (DNA helicase I) and trab genes.";
J. Mol. Biol. 214:39-53(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
5409F24A8E53CCD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 1; Length 272;
Pred. No. 7.5;
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CLEAVAGE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Signal-anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cram D.S., Loh S.M., Cheah K.C., Skurray R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ed. No. 7.5;
Mismatches
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Plasmid IncFII R100, and Plasmid R6-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92009201; PubMed-1916281;
                                                                                                                                                                                                                                                                        HSSP; P29965; 1ALY.
InterPro; IPR003263; TNF_5.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
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W
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ProDom; PD008600; TNF_5; 1.
SMART; SM00207; TNF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE, PS00251; TNF_1; 1. PROSITE; PS50049; TNF_2; 1. Cytokine; Transmembrane; Gly
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109 FEMHRSHEHPHLKS 122
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124
146
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272 AA;
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es 7; Conserv
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15-DEC-1998 (Rel.
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P22710;
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STRAIN-GE5 / Orsay;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pyrococcus.
NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                             140 WRQYFSH 146
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                                                                                                                                                                                                                                                                                                                              1 WRMYFSH 7
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Q9V251;
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                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseelab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 White O., Clayton R.A., Kerlavage A.R., Fleischmann R.D.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: ALLOWS TO USE FORMATE AS MAJOR ELECTRON DONOR DURING
ANAEROBIC RESPIRATION. SUBUNIT GAMMA IS PROBABLY THE CYTOCHROME
BS56(FDO) COMPONENT OF THE FORMATE DEHYDROGENARE (BY SIMILARITY).
-!- SUBUNIT: FORMATE DEHYDROGENASE IS A MEMBRANE-BOUND COMPLEX, FORMED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Formate dehydrogenase, cytochrome B556 subunit (Formate dehydrogenase
"Sequence and conservation of genes at the distal end of the transfer region on plasmids F and R6-5.";
Gene 104:85-90(1991).
                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIRAIN-Rd / KW20 / ATCC 51907;

MEDLINE-95350630; PubMed-7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L. I., Glodek A., Kelley J.M., Weidman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                    -! - FUNCTION: RESPONSIBLE FOR THE N-TERMINAL ACETYLATION OF F PILIN.
                                                                                                                                                                                                                                                                                                                                                                   ij
                                                  -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                       Score 41.5; DB 1; Length 248; Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                  POTENTIAL.
12B4C36DE4529B2E CRC64;
                                                                                                                                                                                                                                                                                                                                                      Pred. No. 8.1;
2; Mismatches . 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 AA.
                                                                                                                                                                                                                                                                        POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FDH gamma subunit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                27307 MW;
                                                                                                                                                                                           EMBL; X55815; CAA39339.1; -. EMBL; M38048; AAA98314.1; -.
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                            1 WRMYFSHRHAHLRSP 15
                                                                                                                                                                                                                                                                                                                                                                                                          1 : | ||||:| |
75 WGLNLS-RHAHIRQP 88
                                                                                                                                                                                                                                             Plasmid; Transmembrane.
TRANSMEM 39 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haemophilus influenzae
                                                                                                                                                                                                                     PIR; JQ1340; JQ1340.
PIR; S10661; S10661.
                                                                                                                                                                                                                                                                                                              248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDXI OR HI0008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /enter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemoph1 lus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FDXI_HAEIN
P44451;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
                                                                                                                                                                                                                                                                          PRANSMEM
                                                                                                                                                                                                                                                                                      FRANSMEM
                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                   FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FDXI_HAEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- CATALYTIC ACTIVITY: ATP + L-asparagine + tRNA(Asn) = AMP + diphosphate + L-asparaginyl-tRNA(Asn).
-1- SUBCELLUTAR L-CATION: CYLOPlasmic.
-1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Asparaginyl-tRNA synthetase (EC 6.1.1.22) (Asparagine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transport; Heme; Iron; Transmembrane; Complete proteome.
BY SUBUNITS ALPHA, BETA AND GAMMA.
-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
-!- SIMILARITY: ORTHOLOG OF BOTH E.COLI FDNI AND FDOI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.1%; Score 41; DB 1; Length 238; 85.7%; Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4D0744AA342066A2 CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         434 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002106; AATRNA_11gaseII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPRO04364; TRNA-Synt_2.
IPR002312; TRNA-Synt_asp.
IPR004365; TRNA_anti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 PC
80 PC
140 PC
175 PC
27758 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004365; tRNA_anti
Pfam; PF00152; tRNA-synt_2; 1.
Pfam; PF01336; tRNA_anti; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ248283; CAB49147.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U32686; AAC21686.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR004522; AsnS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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SGF3 OR POU-M1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P14859
                                                                                                                                                                                                                                                                   SGF3_BOMMO
Q17237;
 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom;
                                                                                                                                                                                                                                                 SGF3_BOMMO
                                                                                              Matches
                                                                                                                                                                                                                              RESULT 7
 SO
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                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                      6
             TIGRFAMS; TIGR00457; asnS; 1.
PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robillard J.E., Page W.V., Mathews M.S., Schutte B.C., Nuyt A.M.,
                                                                                                                                                                      ö
                                                                                                                             45.1%; Score 41; DB 1; Length 434;
46.2%; Pred. No. 18;
tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR000276; GPCR_Rhodpsn.
Pfam: PF00001; 7tm_1; 1.
PROSTE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSTIE: PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                        434 AA; 50242 MW; 9A08BBCE2458A6A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL). 4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Type-2 anglotensin II receptor (AT2) (Fragment).
                                                                                                                                                                                                                                                                                                                                            260 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (POTENTIAL
                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-96169644; PubMed-8618791;
PRINTS; PR01042; TRNASYNTHASP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; S81979; AAB36404.1; -.
                                                                                                                                                                     6; Conservative
                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                               3 MYFSHRHAHLRSP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ovis aries (Sheep).
                                                                        Complete proteome. SEQUENCE 434 AA;
                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P34996
                                                                                                                                                                                                                                                                                                                                        AG22_SHEEP
Q28929;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
TRANSMEM
                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                          AG22_SHEEP
                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                      RESULT
SKERDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-Kinshu X Showa; TISSUE-Silk gland;
MEDLINE-93374935; PubMed-7690034;
Eukuta M., Matsuno K., Hui C.-C., Nagata T., Takiya S., Xu P.-X.,
Ueno K., Suzuki Y.;
"Molecular cloning of a POU domain-containing factor involved in the
"molecular cloning of a POU domain-gene.";
J. Blol. Chem. 268:19471-19933.
-I-FUNCTION: INVOLVED IN THE TRANSCRIPTIONAL REGULATION OF SERICIN-1
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pancrustacea; Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- SUBCELLULAR LOCATION: Nuclear.
-:- TISSUE SPECIFICITY: RESTRICTED TO THE MIDDLE SILK GLAND.
-:- TISSUE SPECIFICITY: EXPRESSION DIFFERENTIALLY REGULATED IN THE POSTERIOR AND MIDDLE SILK GLANDS DURING THE FOURTH MOLIT/FIFTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arrihropoda; Mandibulata; Pancrustacea; Hexapoda, Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY. CLASS-3 SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00027; HOMEOBOX_1; 1.
PROSITE; PS50071; HOMEOBOX_2; 1.
PROSITE; PS00035; POU_1; 1.
PROSITE; PS000465; POU_2; 1.
PROSITE; PS000465; POU_2; 1.
Nuclear protein; Neurogenesis; POU.
                                                                                      Length 260;
                                                                                                                                                Indels
                        29549 MW; BB5B48FF029A0B42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Silk gland factor 3 (SGF-3) (POU domain protein MI).
                                                                                  DB 1;
15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: CONTAINS 1 HOMEOBOX DOMAIN.
                                                                                                                                                Mismatches
                                                                                  Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000327; POU_domain.
Pfam; PF00046; homeobox; 1.
Pfam; PF00157; pou; 1.
                                                                                                                                             <u>ښ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD000010; Homeobox; 1.
PD000583; POU_domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSFAC; T00746; ... InterPro; IPR001356; Homeobox
                                                                                  44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M64781; AAA27841.1; -. HSSP: P14859; 10CT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POUDOMAIN.
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bombyx mori (Silk moth).
                                                                                                                                                                                                       1 WRMYFSHRHAHLRSP 15
                                                                                                                                                                                                                                         | |:|||: |
53 WATYYSHRYDWIFGP 67
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SMART; SM00352; POU; 1
260 AA;
                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7091;
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pancreas and lymph node
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                                                                                                                                                                                                                                                                                                                                                                                             MIM; 603455;
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MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
NP_BIND
BINDING
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MUTAGEN
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NCR2_HUMAN
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MEDLINE-98241596; PubMed-9575181;
Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;
RICK, a novel protein kinase containing a caspase recruitment domain,
interacts with CLARP and regulates CD95-mediated apoptosis.";
J. Biol. Chem. 273:12296-12300(1998).
                                                                                                 Gaps
                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Receptor-Interacting serine/threonine protein kinase 2 (EC 2.7.1.-)
(RIP-11ke interacting CLARP kinase). (Receptor-interacting protein 2)
(RIP-2) (CARD-containing interleukin-1 beta converting enzyme associated kinase) (CARD-containing IL-1 beta ICE-kinase).
Homo sapieng (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mattmann C., Tschopp J.; "Identification of CARDIAK, a RIP-like kinase that associates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- TISSUE SPECIFICITY: Detected in heart, brain, placenta, lung, peripheral blood leukocytes, spleen, kidney, testis, prostate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Endothelial cells;
MEDITINE-98107936; Pubmard-9642260;
MCGATHY JV., MI J., Dixit V.M.;
"RIP2 is a novel NF-kappaB-activating and cell death-inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND MUTAGENESIS OF ASP-146.
MEDLINE-98381580; Pubmed-9705938;
Thome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
                                                         DB 1; Length 351;
                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Platzer M., Varon R.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ozersky P., Holmes A., Broy M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                38591 MW; A6DFA4A59E9322B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-47.
                                                                                                                                                                                                                                                                           540 AA
                                                                                               1; Mismatches
                                                                         21;
                                                       44.0%; Score 40;
54.5%; Pred. No.
  HOMEOBOX
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                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Curr. Biol. 8:885-888(1998).
                                                                                               6; Conservative
                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor complex.
241 3
351 AA;
                                                                                                                                    1 WRMYFSHRHAH 11
                                                                                                                                                            | |: | |||
64 WAMHQHHAHAH 74
                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                           RIK2_HUMAN
043353;
DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     caspase-1
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                                                                                                                                                                                                                                    RESULT 8
RIK2_HUMAN
                                                                                             Matches
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09Y618; 09Y500; 013354; 000613; 015416;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nuclear receptor co-repressor 2 (N-COR2) (Silencing mediator of retinoic acid and thyroid hormone receptor) (SMRT) (SMRTe) (Thyroid-retinoic-acid-receptor-associated co-repressor) (T3 receptor-associating factor) (TRAC) (CTG26).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K->M: REDUCES FAS-MEDIATED APOPTOSIS.
D->N: ABOLISHES KINASE ACTIVITY.
575A692239505792 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    -1- PTM: Autophosphorylated.
    -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
    -1- SIMILARITY: CONTAINS 1 CARD DOMAIN.

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PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE; PS001007; PROTEIN_KINASE_ATP; TALSE_NEG.
TRANSFER; PS001008; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 540;
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ATP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       min, Joseph PR001315; CARD.
InterPro; IPR001315; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR004040; STY_pkinase.
Pfam; PF00619; CARD; 1.
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                                                                                                                                                                                                                                                                                                                      EMBL; AF027706; AAC34970.1; --
EMBL; AF076530; AAC2722.1; --
EMBL; AF064824; AAC25668.1; --
EMBL; AC004003; AAC24561.1; --
EMBL; AF117829; AAD04634.1; --
AAD04634.1; --
AAD04634.1; --
AAD04635.1; --
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EMBL; AC004003; AAC24561.1;
EMBL; AF117829; AAD04634.1;
GEMBL; BC004553; AAH04553.1;
Genew; HGNC:10020; RIPK2.
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DOMAIN 18 294
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SMART; SM00221; STYKC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Conservative
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Best Local Similarity
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Usage

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MIM; 600848;
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Sande S., Privalsky M.L.;
"Identification of TRACs (T3 receptor-associating cofactors), a family
of cofactors that associate with, and modulate the activity of,
MEDLINE-99178941; PubMed-10077563; Ordentlich P., Downes M., Xie W., Genin A., Spinner N.B., Evans R.M.; Ordentlich P., Downes M., Xie W., Genin A., Spinner N.B., Evans R.M.; "Unique forms of human and mouse nuclear receptor corepressor SMRT."; Proc. Natl. Acad. Sci. 05.A. 96:2639-2644(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAINS (ID1 AND ID2).

DOMAINS THE TWO INTERACTION DOMAINS (ID) CONTAIN A CONSERVED SEQUENCE REFERRED TO AS THE CORNR BOX. THIS MOTIF IS REQUIRED AND SUFFICIENT TO PERMIT BINDING TO UNLIGANDED TR AND RARS. SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE SPECIFICITY: UBIQUITOUS. HIGH LEVELS OF EXPRESSION ARE DETECTED IN LUNG, SPLEEN AND BRAIN.
INDUCTION: RECULATED DURING CELL CYCLE PROGRESSION.
DOMAIN: THE N-TERMINAL REGION CONTAINS REPRESSION FUNCTIONS THAT ARE DIVIDED INTO THREE INDEPENDANT REPRESSION DOMAINS (RDL, RD2 AND RD3). THE C-TERMINAL REGION CONTAINS THE NUCLEAR RECEPTORING DOMAINS THAT ARE DIVIDED IN TWO SEPARATE INTERACTION
                                                                                                                                                                               TISSUE-Cervical adenocarcinoma;
MEDILNE-9608552; PubMed-7566127;
Chen J.D., Evans R.M.;
"A transcriptional co-repressor that interacts with nuclear hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 SANT-A DOMAIN.
SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
SIMILARITY: CONTAINS 2 CORNE BOXES.
SIMILARITY: BELONGS TO THE N-COR NUCLEAR RECEPTOR COREPRESSORS
                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Brain cortex;
MEDLINE=97369492; PubMed=9225980;
Margolis R.L., Abraham M.R., Gatchell S.B., Li S.H., Kidwai A.S.,
Braschel T.S., Stine O.C., Callahan C., McInnis M.G., Ross C.A.;
"CDNAs with long CAG trinucleotide repeats from human brain.";
Hum. Genet. 100:114-122(1997).
                                                                                             Park E.J., Schroen D.J., Yang M., Li H., Li L., Chen J.D.; "SMRTe, a silencing mediator for retinoid and thyroid hormone receptors-extended isoform that is more related to the nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLANKING THE CORNR BOX DETERMINE NUCLEAR HORMONE RECEPTOR
                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 96:3519-3524(1999).
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM TRAC-1).
TISSUE-Fetal liver;
                                                                        FISSUE=Cervical adenocarcinoma;
MEDLINE=99199215; PubMed=10097068;
                                                                                                                                                                                                                                                                                                                                              Mol. Endocrinol. 10:813-825(1996).
                                                            SEQUENCE FROM N.A. (ISOFORM SMRT).
                                                                                                                                                                   SEQUENCE OF 1023-2517 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 428-613 FROM N.A.
                                                                                                                                                                                                                                                                                                                                    nuclear hormone receptors
                                                                                                                                                                                                                             receptors.";
Nature 377:454-457(1995)
                                                                                                                                   'eceptor corepressor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTIREPRESSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIFICITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50090; WNB_3; 1.

Nuclear protein; Transcription regulation; DNA-binding; Repressor; Coiled coil; Alternative splicing.

Coiled Coiled coil; Alternative splicing.

Coiled Coile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> PEDIPAPTES (IN REF. 2).
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G -> L (IN REF. 2).
S -> F (IN REF. 2).
G -> R (IN REF. 2).
G -> R (IN REF. 2).
SRSPAPPA -> MEAWDAHP (IN REF. 3).
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Morone chrysops x Morone saxatilis (White bass x Striped bass).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISSING (IN ISOFORM TRAC-1).
MISSING (IN ISOFORM TRAC-1).
L -> P (IN REF. 2).
L -> W (IN REF. 2).
L -> W (IN REF. 2).
MISSING (IN REF. 2).
A -> P (IN REF. 2).
SS -> EF (IN REF. 5).
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K -> T (IN REF. 4).

P -> A (IN REF. 4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40; DB 1; Le
Pred. No. 1.7e+02;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS -> EF (IN REF. 5
S -> T (IN REF. 2).
MISSING (IN REF. 2)
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORNR BOX OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLY - PRO.
POLY - PRO.
POLY - GLY.
POLY - PRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLY-LYS
                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001005; Myb_DNA_binding.
Pfam; PF00249; myb_DNA-binding; 2.
SMART; SM00395; SANT; 2.
                                                                                                                            EMBL; AF113003; AAD20946.1; -.
EMBL; AF125672; AAD22973.1; -.
EMBL; U37146; AAC50236.1: -.
                                                                                                                                                                                                           EMBL; U37146; AAC50236.1; -. EMBL; S83390; AAB50847.1; -. EMBL; U80750; AAB91446.1; -. TRANSFAC; T04689; -. Genew; HGNC:7673; NCOR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2482
1702
2398
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1034
1894
2494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ¥Ą;
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Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHRHAHLRSP 15
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SEQUENCE OF 1-450 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WRMYFSHRHAH 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fuji F., Hiran
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GALT_BACHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                       Shike H., Lauth X., Westerman M.E., Ostland V.E., Carlberg J.M., Van Olst J.C., Shimizu C., Bulet P., Burns J.C.; "Bass hepcidin is a novel antimicrobial peptide induced by bacterial
                                                                                                                                              -i- FUNCTION: Seems to act as a signaling molecule involved in the maintenance of iron homeostasis. Seems to be required in conjunction with HFE to regulate both intestinal iron absorption and iron storage in macrophages (By similarity).
 Acanthomorpha; Acanthopteryg11; Percomorpha; Perciformes; Percoide1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-90370121; Pubmed-2118597;
MEDALINE-90370121; Nurata N.;
Wada H., Gombos Z., Murata N.;
Wada H., Gombos Chilling tolerance of a cyanobacterium by genetic manipulation of fatty acid desaturation.";
Nature 347:200-203(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                           SEQUENCE FROM N.A., SEQUENCE OF 65-85, TISSUE SPECIFICITY, AND ANTIBIOTIC ACTIVITY.
                                                                                                                                                                                                                              -1- TISSUE SPECIFICITY: Predominantly expressed in liver.
-1- MASS SPECTROMETRY: WW-2255.97; WETHOD-WALDI; RANGE-65-85.
-1- INDUCTION: By bacterial challenge.
-1- SIMILARITY: BELONGS TO THE HEPCIDIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fatty acid desaturase (EC 1.14.99.-) (Delta 12 desaturase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
OFEASSCF0AS22C84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 1;
Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL,
                                                                                                                                                                                                                                                                                                                                                                                                                              HEPCIDIN.
                                                                                                                                    Biochem. 269:2232-2237(2002).
                                                                                                                                                                                                                     -1- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                TISSUE-Gill, and Skin;
MEDLINE-21982021; Pubmed-11985602;
                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF394246; AAM28440.1; -. Antiblotic; Hormone; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.9%;
                                                                                                                                                                                                                                                                                                                                                                                                              64
85
72
83
82
79
79
79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WRMYFSHRHAHLRSP 15
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49 WKMPYNNRHKRHSSP 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                         such as E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
85 AA;
            Moronidae; Morone NCBI_TaxID=45352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR SLR1350.
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P20388;
                                                                                                                          challenge
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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SEQUENCE FROM N.A.

MEDLINE—97061201; PubMed=8905231;
A Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
A Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
A Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
A Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
A Miyajima N., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
A Namura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
A Saquence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
Synechocystis sp. strain PCC6803. II. Sequence determination of the
Type entire genome and assignment of potential protein-coding regions. It
E DNA Res. 3:109-136(1996).
C. FUNCTION: CAN INTRODUCE A SECOND CIS DOUBLE BOND AT THE DELTA 12
C. FUNCTION OF FATTY ACID BOUND TO MEMBRANES GLYCEROLIPIDS. THIS
ENZYME IS INVOLVED IN CHILLING TOLERANCE BECAUSE THE PHASE
THE DESCREE OF USPATURE OF LIPIDS OF THE MEMBRANE DEPENDS ON
THE DESCREE OF USPATURATION OF FATTY ACID DESATURASE FAMILY.
C. I- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Membrane; Complete proteome.
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09KDV3; Q9KC74;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10) (Gal-1-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki K., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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EMBL; D90312; b...
EMBL; D90312; s...
PIRS, 211519.
InterPro; IPR001225; FA_desaturase; 1.
A Pfam; PF00487; FA_desaturase; 1.
Brobom; PD001081; FA_desaturase; 1.
Ardoreductase; Fatry acid blosynthesis; Membrane; Comp...
Brostle: Argoreductase; Argoreductase; Membrane; Comp...
Brostle: Argoreductase; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 39; DB 1; Length 351; Pred. No. 30;
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1; Mismatches
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MEDLINE-20512582; PubMed-11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 42.9
Best Local Similarity 45.5
Matches 5; Conservative
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5.
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ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                        Pred. No. 48;
5; Mismatches
                                                                                                                                                                                                                                                                                                                          Score 39;
SIMILARITY: CONTAINS 1 CARD DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                             CARD.
                                                                                                                                    EMBL; AF461040; AAL96436.1; -.
                                                                                                                                                                                                                                                                                                  60400 MW;
                                                                                                                                                                                                                                                                                                                           42.9%;
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                                                                                                                                                 PROSITE; PS50209; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                      5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                               1 WRMYFSHRHAHLRSP 15
                                                                                                                                                                                                                                                                                                                                                                                                         54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         northern blot analysis.
                                                                                                                                                                                                                                                                                                                                                                                                PIR; S15387; S15387
PIR; S14601; S14601
                                                                                                                                                                                                                                                                                                  539 AA;
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MASY_CUCMA
P24571;
                                                                                                                                                                                                                                                                                     ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                           NP_BIND
BINDING
                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
MASY_CUCMA
                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chin A.I., Dempsey P.W., Bruhn K., Miller J.F., Xu Y., Cheng G., "Involvement of receptor-interacting protein 2 in innate and adaptive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOTALION: ACTIVITIES PRO-CASPASE-1 and pro-CASPASE-8. Potentiates CASP-8-mediated apoptosis. Activates NF-kappaB (By similarity). SUBUNIT: Binds to CFLAR/CLARP and CASPI via their CARD domains. Binds to BIRG3/c-1AR1 and BIRC3/c-1AR2, TRAFI, TRAF2, TRAF5 and TRAF6. May be a component of both the TNFRSFIA and TNRFSF5/CD40 subcellular Location. Cytoplasmic (Probable). FIW: Autophosphorylated (By similarity). SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Receptor-interacting serine/threonine protein kinase 2 (EC 2.7.1.-).
  STRAIN-C-125 / JCM 9153;
MEDLINE-99411980; Pubmed-10484179;
Takani H., Takaki Y., Naksone K., Sakiyama T., Maeno G., Sasaki R., Hirama C., Fuji F., Masui N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                   "Genetic analysis of the chromosome of alkaliphilic Bacillus halodurans C-125."

Extremophiles 3:227-233(1999)

-:- CATALYIC ACTIVITY: UTP + alpha-D-galactose 1-phosphate = diphosphate + UDP-galactose.

-:- PATHWAY: Galactose metabolism; second step.

-:- SUBCELLUIAR LOCATION: Cytoplasmic (Potential).

-:- SIMILARITY: BELONGS TO THE GALACTOSE-1-PHOSPHATE URIDXLXLTRANSFERASE FAMILX 2.
                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01163; GAL_P_UDP_TRANSF_II; 1.
Transferase; Nucleotidyltransferase; Galactose metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 1; Length 508;
Pred. No. 45;
1; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       508 AA; 57989 MW; 16AF6F607FCEAE2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; , 539 AA.
                                                                                                                                                                                                                                                                                                                          InterPro: IPR000880; GalP_UDP_transf.
InterPro: IPR000766; GalP_transf_II.
Pfam: PF01087; GalP_UDP_transf; I.
Pfam: PF02744; GalP_UDP_tr_C: I.
TIGRFAMS; TIGR01239; galT_Z: I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-21891093; PubMed-11894097;
                                                                                                                                                                                                                                                                                                     EMBL; AP001510; BAB04828.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 50.00,
                                                                                                                                                                                                                                                                                                                 EMBL; AB024554; BAA83925.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 416:190-194(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               451 WALAIKERHAHL 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WRMYFSHRHAHL 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 508 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1mmune responses."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIK2_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P58801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIK2_MOUSE
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01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-2000 (Rel. 32, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
Malate synthase, glyoxysomal (EC 4.1.3.2)
Cucurbita maxima (Pumpkin) (Winter squash).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudioctyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eur. J. Blochem. 197:331:336(1991).
                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation; Apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 539; 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
42951BF97CA15DFA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cucumis sativus (cucumber).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MBL; MACONTECT STRVENCY.

JIR, 200550; SYRVENCY.

INTERPROJ IRROBAGES.

PÉAM; PF01274; MALATE_SYNTHASE; 1.

PROSITE; PS00310; MALATE_SYNTHASE; 1.

PROSITE; PS00510; MALATE_SYNTHASE; 1.

PROSITE; PS00510; MALATE_SYNTHASE; 1.

PROSITE; PS00510; MCROBODIC Caid cycle; Lyase; Glyoxysome.

Glyoxylate bypass; Tricarboxylia caid cycle; Lyase; Glyoxysome.

Glyoxylate bypass; Tricarboxylia caid cycle; Lyase; Glyoxysome.

Glyoxylate bypass; Tricarboxylia caid cycle; Lyase; Glyoxysome.

Glover Company of the company of the
Pfam; PF01274; Malate_synthase; 1. .
PROSITE; PS00342; MICROBODIES_CTER; 1.
PROSITE; PS00510; MALATE_SYNTHASE; 1.
Glyoxylate bypass; Tricarboxylic acid cycle; Lyase; Glyoxysome.
S1TE 564 566 MICROBODY TARGETING SIGNAL (POTENTIAL).
SEQUENCE 566 AA; 64635 MW; B77F77D1D593834A CRC64;
                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=CV. LONG GREEN RIDGE;
MEDLINE=91370851; PubMed=2491683;
Graham I.A., Smith L.M., Brown J.W.S., Leaver C.J., Smith S.M.;
"The malate synthase gene of cucumber.";
Plant Mol. Biol. 13:673-684(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                              1 42.9%; Score 39; DB 1; Length 566; Similarity 54.5%; Pred. No. 50; 6; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1988 (Rel. 08, Created)
01-APR-1990 (Rel. 14, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Malate synthase, glyoxysomal (EC 4.1.3.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     568 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X15425; CAA33465.1; -.
EMBL, M16219; AAA33123.1; -.
PIR; SO7560; SYKVMA.
InterPro; IPR001465; Malate_synthase.
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209 LYFFHNHANFR 219
                                                                                                                                                                                                                                                                                                                 3 MYFSHRHAHLR 13
                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
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P08216;
     DR DR DR SO FT
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Qy 3 MYFSHRHAHLR 13
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Db 210 LYFFHNHANFR 220
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Search completed: November 27, 2002, 07:18:52 Job time : 13.1429 secs

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November 27, 2002, 06:27:07; Search time 8.33977 Seconds (without alignments) 370.599 Million cell updates/sec
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                    671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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91
1 WRMYFSHRHAHLRSP 15
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_rvirus:* sp_bacteriap:* sp_archeap:* sp_plant:* sp_rodent:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | Q9k1b0 porphyromon | Q8zcp9 yersinia pe | Q9vsl7 drosophila | Q91zf4 arabidopsis | 034780 bacillus su | Q9zsb4 arabidopsis | 080707 arabidopsis | Q8s7k3 oryza sativ | Q9sbu4 chlamydomon | 048663 chlamydomon | O23887 zea mays (m | Q8xvz0 ralstonia s | Q9n0j0 bos taurus | Q8tqu6 methanosarc | 031649 bacillus su | Q92dg9 listeria in |
|-----------|-------------------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|
| SUMMARIES | . OI | Q9KIB0 | Q8ZCP9 · | O9VSL7 | Q9LZF4 | 034780 | Q92SB4 | 080707 | Q8S7K3 | Q9SBU4 | 048663 | 023887 | Q8XV20 | . 0f0N60 | OSTQU6 | 031649 | Q92DG9 |
| | DB | 7 | 16 | S | 10 | 16 | 10 | 10 | 10 | 10 | 10 | 10 | 16 | 9 | 17 | 16 | 16 |
| | % Query Match Length DB | 757 | 215 | 684 | 684 | 307 | 703 | 743 | 644 | 421 | 424 | 1358 | 92 | 111 | 120 | 134 | 252 |
| , | Query Match | 51.6 | 49.5 | 49.5 | 49.5 | 48.4 | 48.4 | 48.4 | 47.8 | 47.3 | 47.3 | 47.3 | 46.2 | 46.2 | 46.2 | 46.2 | 46.2 |
| | Score | 47 | 45 | 45 | 45 | 44 | 44 | 44 | 43.5 | 43 | 43 | 43 | 42 | 42 | 42 | 42 | 42 |
| | Result No. | п | 7 | Э | ₹ | 2 | 9 | 7 | æ | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 |

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δ Q

| Q898b5 listeria mo Q9v613 drosophila Q99x11 mus musculu Q99x11 mus musculu Q17548 caenorhabdi Q96x9 colorado ti Q84v4 eyach virus Q75691 homo sapien Q9afy9 shigella fi Q8vsa9 shigella fi Q8vsa9 shigella fi Q9afy9 shigella fi Q9afy9 shigella fi Q9nx9 shigella fi Q9nx9 shigella fi Q9ny1 anabaena sp Q9nmi pasteurella Q34901 bacilius su Q9hv33 pseudomonas Q9n9d3 physarum po Q9n9d3 physarum po Q9n9d3 physarum po Q910d2 physarum po Q | 51 | r; 757 AA. red) sequence update) annotation update) annotation update) annotation update) annotation update) annotation update) sequence update) annotation update) sequence update) sequence acceptor PG13. sequence acceptor PG13. redies acids."; //GenBank/DDBJ databases. sequence acids."; //GenBank/DDBJ databases. 24B6D65264F9D62 CRC64; re 47; DB 2; Length 757; re 47; DB 2; Length 757; di No. 19; wismatches 4; indels 0; Gaps 0; |
|--|-----------|--|
| 42 46.2 252 16 QBYBP5 42 46.2 486 5 Q9VQT3 42 46.2 917 11 Q99XL1 42 46.2 917 11 Q99XL1 42 46.2 1435 12 Q9DSQQ 42 46.2 2785 4 Q75691 11.5 45.6 278 2 Q9XQT8 41 45.1 228 16 Q9XNI4 41 45.1 241 16 Q34QDI 41 45.1 241 16 Q34QDI 41 45.1 370 16 Q9AYPB 41 45.1 370 16 Q9AYPB 41 45.1 370 16 Q9AYPB 41 45.1 45.1 45.2 4 Q9CQQC 41 45.1 45.1 370 16 Q9AYPB 41 45.1 45.1 45.2 4 Q9CQCC 41 45.1 45.1 45.2 4 Q9CQCC 41 45.1 45.1 833 12 Q6GSGC 41 45.1 45.1 833 12 Q6GSGC 41 45.1 60GSGCC 41 45.1 60GSGCC 41 45.1 60GSGCC 41 45.1 60GSGCCC 41 45.1 60GSGCCC 41 45.1 60GSGCCCC 41 45.1 60GSGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC | ALIGNMENT | PRELIMINARY; PRT; 75 000 (TrEMBLrel. 15, Last sequen 001 (TrEMBLrel. 15, Last sequen 001 (TrEMBLrel. 19, Last annota 1021 tonb-linked outer membrane monas gingivalis (Bacteroldets; Bac monas. 10-837; FROM N.A. 50; Barr I., Patterson M., Aglus C 10-8137; FROM N.A. 50; CFEB-2000) to the EMBL/GenBan FROM N.A. 50; CAR AFR1416.1; CAR AFR17 MW; 224B6D65 237558; AAR81416.1; COSS93; TONB_DOXC; 1. 757 AA; 84517 MW; 224B6D65 51.6%; Score 47; Similarity 61.5%; Pred. No. |
| 1188 1222222222222222222222222222222222 | | RESULT 1 09KIB0 TO 09KIB0 DAC 09KIB0, DT 01-0CT-2000 DT 01-0CT-2000 DT 01-DEC-2001 DE 01-DEC-2001 DE 01-DEC-2001 OS POTPHYTOMORA OC BACTETIS; CF OC POTPHYTOMORA OX NCBL_TAXID=0 OX NCBL_TAXID=0 OX NCBL_TAXID=0 RA NCSS B., BAIR RA HOCKING D., RT P. gingival RA HOCKING D., RT P. gingival RA HOCKING C.; RA ROSS B.C.; RA HOCKING RACHING R |

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Hypothetical
SEQUENCE 68
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Il P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Il P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Il P.W., Hoskins R.A., Galle R.F.,
Abril G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Pleischmann W.,
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=CO-92 / BIOVAR ORIENTALIS;
MEDLINE-21470413; PubMed-11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Brentice M.B., Sebaihia M., Dawies R.D., Churcher C., Mungall K.L.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamila N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Yersinia pestis, the causative agent of plague.";
Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45; DB 16; Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein; Complete proteome.
SEQUENCE 215 AA; 24920 MW; EF312DBBAC15B3BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.5%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, 026-817) protein.
                                                                                                              01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                    Putative membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WRMYFSHRHAHLR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
                                                                                                                                                                                                                                    Versinia pestis
                                                                                                                                                                                                                                                                                                     NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                   Yersinia
                                                                                          08ZCP9;
                                                                 Q8ZCP9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9VSL7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                    RESULT 2
Q8ZCP9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O9VSL7
                                                                                            ACCOCCOS NATIONAL SOLUTION OF THE STATE OF T
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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Rardorde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harts M., Harvey D., Helman T.J., Hernandez J.R., Houck J., Houston K.A., Howland T.J., Hernandez J.R., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C., Ralali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., R. Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Kull D., Lai Z., Rala Lu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D., R. Merlov G., Milshina N.C., Morbary C., Morris J., McShrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., R. Palazcalo M., Pittman G.S., Pan S., Poollard J., Puri Y., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Spieler E., Spradling A.C., Stapleron M., Stupski M.P., Smith T., Spieler B.C., Siden-Kiamos I., Simpson M., Stupski M.P., Smith T., Aspirkas R., Tector C., Turner R., Venter E., Wang A., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., R. Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., R. W. Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., R. W. Woodage T. Worley K.C., Wu D., Yang S., Yao Q.A., R. W. Woodage T. Worley K.C., Wu D., Yang S., Yao Q.A., R. W. Woodage T. Worley K.C., Wu D., Yang S., Yao Q.A., R. W. Woodage T. Worley K.C., Wu D., Yang S., Yao Q.A., R. W. Woodage T. Worley K.C., Wu D., Yang S., Zhao Q.A., R. W. Woodage T. Worley K.C., Wu D., Yang S., Zhao Q.A., R. W. Woodage T. Worley K.C., Wu D., Yang S., Zhao Q.A., R. W. Woodage T. Worley K.C., Wu D., Yang S., Zhao Q.A., The genome sequence of Drosophila melanogaster.";

R. Welley A. Woodage T. Woolland W. Zhou G. Shao Q. Shing B. Wills, R. Woolland R. W. Woolland W. Zhou G. Shing B. W. Woodage T. Woolland W. Zhou G. Shing B. W. Woodage T. Wasselland G., Zhao Q., Zhao Q. Shing B. W. Woodage T. Woolland W. Zhao G. Shing B. W. Woolland W. Zhao G. Shing B. W. Woolland W. Zhao G. Shing B. W. Woodage T. Woolland W. Zhao G. Shing B. W. Woodage T. Woolland W. Zhao G. Shing B. W. Woodage T. Woolland W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Posta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W., Rudd
Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL162751; CAB83292.1; -.
Interpro: IPR004146; DCI.
Interpro: IPR001841; Znf_ring.
Pfam; PF03107; DCI; 3.
SMART; SM00184; RING; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75037 MW; A7272B67C342B988 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79746 MW; C872720DD26E133E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; eudicotyledons; core eurosids II; Brasslcales; Brasslcaceae; Arabidopsis. NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9LZF4;
01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 79.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ä
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Pred. No. 36;
2; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      684 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 45; DB
Pred. No. 36;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003689; Zn_trnprt_Zip.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0024236; foi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 70.00
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF02535; Zip; 1
SEQUENCE 684 AA; 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al protein.
684 AA; 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||||| |: ||
505 SHRHGHVHSP 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 SHRHAHLRSP 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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247 YAMYFKDRHSHL 258

q

4 YFSHRHAHLR 13

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Hypothetical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                            092SB4
                                                                                                                                                                                                                                                                                          WASHU
                              RESULT 6
                                            Q92SB4
                                                                           A Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,

RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borriss R., Boursier L., Brans A., Braun M., Brighell S.C., Bron S.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Deviner K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Choi S.K., Calaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Fitz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,

RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kunta K., Ladidus A., Lau H., Masuda S., Mauel C., Medigue C.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Moone D., O'Relliy M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

RA Rieger M., Rivolta C., Roche B., Rose M., Sadaie Y.,

RA Rieger M., Rivolta C., Roche B., Rose M., Sadaie Y.,

RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,

RA Sato T., Scallan E., Schleich S., Schroeter R., Scoffone F.,

RA Sato T., Tamakoshi H., Tanaka T., Takahashi H., Takemaru K.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier P., Tognoni A.,

RA Winters P., Wandut R., Wadler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler E., Wedler H., Waltersengger T.,

RA Winters P., Walber A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

RA Winters P., Walber E., Wedler E., Wedler H., Weitzenegger T.,

RA Winters P., Walber E., Wedler E., Wedler H., Weitzenegger T.,

RA Winters P., Walber E., Wedler E., Wedler
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                           Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Lapidus A., Galleron N., Sorokin A., Ehrlich D.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF027868; AAB84459-1; --
EMBL; 299114; CAB13781.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 AA; 35348 MW; BF3974AA51D0F762 CRC64;
                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.4%; Score 44; DB 16;
58.3%; Pred. No. 24;
11ve 2; Mismatches 3
                                                                                      307 AA
                                                                                                                      Created)
                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98044033; PubMed-9384377;
                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Conservative
                                                                                      PRELIMINARY;
                                                                                                                                                                                                           Bacteria; Firmicutes;
Bacillaceae; Bacillus.
Best Local Similarity
                                                                                                                                                                                             Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 307 AA;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                         NCBI_TaxID=1423;
                                                                                                                                                               RADC homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-168;
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                                                                                                        034780;
                                                                                      034780
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                                                        RESULT 5
034780
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                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II: Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Bevan M., Wedler H., Wedler E., Wambutt R., Bancroft I., Mewes H.W.,
Mayer K.F.X., Schueller C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Laplant Y., Spalding L.;
"The sequence of A. thaliana F3H7.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ARI1822; ARAD03421; -.
EMBL; AL049523; CAB40022.1; -.
EMBL; AL04551; CAB78179.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The A. thaliana Genome Sequencing Project."; Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases
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703 AA; 81396 MW; 6EC241534E870B41 CRC64;
                        092SB4;
01-WAY-1999 (TrEMBLrel. 10, Created).
11-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
703 AA.
PRT;
                                                                                                                                           F3H7.4 protein.
F3H7.4 OR T4F9.20 OR AT4G10560.
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InterPro; IPR001841; Znf_ring.
Pfam; PF03107; DC1; 3.
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PRELIMINARY;
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STRAIN-CV. COLUMBIA;
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412 HFSHQHHHLR 421
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Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
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D009A65DD8EABC75 CRC64;
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67700 MW;
                                   47.8%;
50.0%;
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                                                                                                                               6; Conservative
                                                                         Conservative
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                                                                                                       1 WRMY-FSHRHAHLRSP 15
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                    Query Match
Best Local Similarity
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176 WRIKHNHHAH 186
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 644 AA;
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Best Local Similarity
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 SEQUENCE
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STRAIN-CY. COLUMBIA:
Vysotskala V.S., Schwartz J.R., Toriumi M., Kwan A., Yu G., Oji O.,
Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B.,
Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.J.,
Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
Theologis A.,
Arabidopsis thaliana chromosome 1 BAC FBK4 sequence.";
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                          Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative protein with similarityto protein phosphatase PP1 regulatory
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ONJAB SALÍVA (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryzea.
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Pred. No. 57;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Theologis A.'
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; ACO04392; ACC08230.1;
InterPro; IPR00219; DAG_PE-bind.
InterPro; IPR004146; DCI.
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                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
                                                                                            Created)
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ilarity 70.0%;
Conservative
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SMART; SM00109; C1; 2.
SEQUENCE 743 AA; 859
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418 HFSHQHHHLR 427
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Best Local Similarity
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080707
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
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Chlamydomonadaceae; Chlamydomonas.
NCBI_TaxID=3055;
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MEDLINE-98158343, PubMed-9498569;
Sato N., Fujiwara S., Kawaguchi A., Tsuzuki M.;
Sato N., Fujiwara S., Kawaguchi A., Tsuzuki M.;
"Cloning of a gene for chloroplast w6 desaturase of a green alga, "Cloning of a gene for chloroplast w6 desaturase of a green alga, "Cloning of a gene for chloroplast w6 desaturase of Bacchem, 122:1224-1232(1997).

BMBL; AB007640; BAA23881.1; ---

ThickPro. IPR001225; FA_desaturase.

Probom; PP001081; FA_desaturase; 2.
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  644;
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  Length
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                                               Indels
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                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Chloroplast w6 desaturase.
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  DB 10;
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                                                                                                                                                                                                                                                         421 AA
Score 43.5; D. Pred. No. 60; 4; Mismatches
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2; Mismatches
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InterPro; IPR001225; FA_desaturase.
Pfam; PF0048; FA_desaturase; 1.
ProDom; PD001081; FA_desaturase; 2.
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Gaps

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Length 92; Indels

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Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
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PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
                                                   Salanoubat M., Genins, Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Peissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Raistonia solanacearum.";
"Mature 415:497-502(2002).
"BMBL, ALG4071; Complete proteome.
"Phypothetical protein: Complete protecome.
SEQUENCE 92 AA; 10226 MW; DB6B4B409C8FC62B CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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Pred. No. 15;
1; Mismatches
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46.7%; Pred. No. 18;
Live 2; Mismatches
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                          STRAIN-GM11000;
MEDLINE-21681879; Pubmed-11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiotensin receptor 2 (Fragment).
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                                                                                                                                                                                                                            .28;
                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                         Conservative
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111 AA;
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es 7; Conserv
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Berisha B.;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                   Sekimoto H., Seo M., Dohmae N., Takio K., Kamiya Y., Koshiba T.; "Cloning and molecular characterization of plant aldehyde oxidase."; J. Blol. Chem. 272:15280-15285(1997).

-1. COFACTOR: BINDS A 2FE-25 CLUSTER (BY SIMILARITY).

EMBL; D8841; BAAA3226.1; --
HSSP; P80457; 1FIO.
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Bacteria; Proteobacteria; beta subdivision; Raistonia group;
Ralstonia.
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              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146682 MW; 82449227AFB14861 CRC64;
                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Aldehyde oxidase (EC 1.2.3.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
11-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein RSc2685.
RSC2685 OR RS00036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00288; 2Fe-25_bind.
InterPro; IPR00264; 2Fe25_ferredoxin.
InterPro; IPR000564; 2Fe25_ferredoxin.
InterPro; IPR0005107; Co_deh_flav_C.
InterPro; IPR0007107; Euk_Phinase.
InterPro; IPR000719; Euk_Phinase.
InterPro; IPR000719; Euk_Phinase.
InterPro; IPR000719; Euk_Phinase.
InterPro; IPR000719; Euk_Phinase.
InterPro; IPR0007041; Faredoxin.
Pfam; PF03178; Ald_Xan_dh_C2; 1.
Pfam; PF03185; Ald_Xan_dh_C2; 1.
Pfam; PF03189; Co_deh_flav_C; 1.
Pfam; PF00111; fer2; 1.
Pfam; PF01799; Fer2. 1.
ProDom; PD186071; 2Fe-25_bind; 1.
ProDom; PD186071; 2Fe-25_bind; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_I.
INTON-SUIFUR; Oxidoreductase.
SEQUENCE 1358 AA; 146682 MW; 82449227AFB14861 C.
              3;
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ilarity 58.3%; Pred. No. 1.5e+02;
Conservative 3; Mismatches 2;
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              Mismatches
 No. 47;
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MEDLINE-97326103; PubMed-9182554;
             5;
54.58;
              Conservative
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619 IYSTHPHAHVRS 630
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Best Local Similarity
7; Conserv
                                         1 WRMYFSHRHAH 11
Best Local Similarity
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08XVZ0;
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Length 111; Indels .

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Search completed: November 27, 2002, 07:22:39
Job time: 21.3398 secs
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE 21929760; PubMed-1193238;

MEDLINE-21929760; PubMed-1193238;

A alagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

A lalan N., Maylor J., Stange-Thoman N., DeArellano K., Johnson R.,

Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,

A Lammer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,

A Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,

Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,

Rerry J.G., Jarrell K.F., Jing H., Macarlo A.J.L., Paulsen I.,

M Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,

A Metcalf W.W., Birren B.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        he genome of Methanosarcina acetivorans reveals extensive metabolic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.2%; Score 42; DB 17; Length 120; 72.7%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                 Archaea, Euryarchaeota, Methanococci, Methanosarcinales, Methanosarcinaceae, Methanosarcina.
NCBI_TaxID=2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 AA; 13232 MW; 49AAB649268558FD CRC64;
                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and physiological diversity."
Genome Res. 12:532-542(2002).
EMBL; AE010814; AAM04857.1;
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20,
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                                    PRELIMINARY;
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01-JAN-1998 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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75 FSHRYAQLLSP 85
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SEQUENCE 120 AA
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RESULT 14
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A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
Robayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Rufita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medique C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Presean E., Pulic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Ra Persecan E., Pulic P., Purnelle B., Ropoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Santan E., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Schiuchi J., Sckowska A., Seror S.J., Schroeter R., Scoffone F.,
Schiuchi J., Schowska A., Seror S.J., Schroeter R., Scoffone F.,
Schiuchi J., Manmout R., Waller E., Wedler E., Westliss M., Vannameto K., Yasumoto K., Yata K.,
R. The complete genome sequence of the gram-positive bacterium Bacillus
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Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.2%; Score 42; DB 16; Length 134;
llarity 66.7%; Pred. No. 22;
Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; 299110; CAB13062.1; -.
Complete proteome.
SEQUENCE 134 AA; 15340 MW; 80F1E6CFC76B34E3 CKC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 390:249-256(1997).
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Matches 8; Conserv
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Hilbert H.,
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                                                   November 27, 2002, 07:17:51; Search time 2.72201 Seconds (without alignments) 162.139 Million cell updates/sec
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Sequence 2,
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Sequence 2,
Sequence 7,
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Sequence 4
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                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/taa/5A_COMB.pep:*
/cgn2_6/ptodata/1/taa/5B_COMB.pep:*
/cgn2_6/ptodata/1/taa/6A_COMB.pep:*
/cgn2_6/ptodata/1/taa/6B_COMB.pep:*
/cgn2_6/ptodata/1/taa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/taa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-114-001C-5632
US-09-128-6028-34
US-08-817-029-2
US-08-38-031-6
US-08-38-06725-6
US-08-530-8628-11
                                                                                                                                                                                fotal number of hits satisfying chosen parameters:
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US-09-069-023-27
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JS-08-271-364A-7
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-09-470-271-1
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                                                                                                                                                               262574 seqs, 29422922 residues
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Maximum Match 100%
Listing first 45 summaries
                                     OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                1 WRMYFSHRHAHLRSP 15
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Maximum DB seq length: 2000000000
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US-09-069-023-7

Sequence 7, Application US/09069023A

Sequence 7, Application US/09069023A

Patent No. 6348573

GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inohara, Naohiro
APPLICANT: Nunez, Cabriel
APPLICANT: Nunex, Cabriel
APPLICANT: Nonex, Cabriel
APPLICANT: Nonex, Cabriel
APPLICANT: Nonex, Cabriel
APPLICANT: Nonex, Composition Number in TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998 04-27
NUMBER OF SEQ ID NOS: 38

SOFTHARE: Patentin Ver. 2.0
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Sequence
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Sequence 4, Application US/0909041A

Patent No. 6346276

GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-076001

CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 300

TYPE: PRT
                     US-09-073-354-1
US-08-656-005A-1
US-09-363-055-1
US-09-418-005-1
US-09-408-005-1
US-09-206-800-9
US-09-206-800-1
US-09-206-800-1
US-08-989-299-9
US-08-974-549A-190
US-08-974-549A-54
US-08-851-843A-8
US-08-851-843A-8
US-08-851-843A-8
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US-09-430-323-8
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774
774
774
921
1164
1164
1164
1313
840
872
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RESULT 2
US-09-099-041A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 7
LENGTH: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       us-09-069-023-7
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Matches
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; ORGANISM: Homo sapiens US-09-099-041A-4

Sequence Sequence Sequence Sequence

Sequence

-09-133-962A-10

US-08-229-284A-2

PCT-US95-06725-2

40 WRVQVAVKHLHIHTP 54

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Sequence 1, Application US/09069023A
Patent No. 6348573
Regneral information:
APPLICANT: Nunez, Gabriel
APPLICANT: Noseki, Takeyoshi
APPLICANT: Koseki, Takeyoshi
APPLICANT: Koseki, Takeyoshi
APPLICANT: Koseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
FILE REFERENCE: UM-03333
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 531;
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Patent No. 6033855
GENERAL INFORMATION:
APPLICANT BETLIN. GENES ENCODING CASPASE RECRUITMENT TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTY: 0.54

ZIP: 0.2110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKetter
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSED for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,942
FILING DATE: 06-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40; DB 4;
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35.283
REFERENCE/DOCKET NUMBER: 07334/06
TELECOMMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
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31 WRVQVAVKHLHIHTP 45
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US-09-069-023-1
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Best Local Similarity
Local 5; Conserve
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LENGTH: 531
TYPE: PRT
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                                                  RESULT 5
US-09-069-023-1
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-09-019-942-1
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Sequence 4, Application US/09245281

Sequence 4, Application US/09245281

Sequence 4, Application US/09245281

Sequence 6.3659196

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY

TITLE OF INVENTION: NOVER: 1999-02-05

EARLIER PELICATION NUMBER: US 09/245, 281

CURRENT PILING DATE: 1999-12-08

EARLIER PELING DATE: 1998-12-08

EARLIER PILING DATE: 1998-06-17

EARLIER PILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 4

LENGTH: 300
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Length 300;
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Patent No. 6460140

GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROPERING FAMILY AND USES THEREOF
TILE REFERENCE: 0734-112001
CURRENT FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR APPLICATION NUMBER: US 09/099,041
PRIOR PRILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 47

SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 32;
5; Mismatches
        Score 40; DB 4;
Pred. No. 32;
                                                  Mismatches
          44.0%;
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Best Local Similarity 33.3%;
Matches 5; Conservative
                                                    Conservative
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                                                                                                                      40 WRVQVAVKHLHIHTP 54
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LENGTH: 300
TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
                          Best Local Similarity
Matches 5; Conserva
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Matches 5; Conserv
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             Query Match
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TOPOLOGY: linear

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Gaps

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GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION:
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY
TITLE OF INVENTION: NOVEL NOSS THEREOF
FILE REFERENCE: 0734/118001
CURRENT APPLICATION NUMBER: US 09/245,281
CURRENT FILING DATE: 1999-02-05
EARLIER APPLICATION NUMBER: US 09/209,041
EARLIER PILING DATE: 1998-06-17
EARLIER PILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-06-17
EARLIER FILING DATE: 1998-06-06
NUMBER OF SEO ID NOS: 44

SOFTWARE: RASESO FOR WINDOWS VERSION 4.0
SEO ID NO 2
LENGTH: 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4;
59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows 95
SOFWARE: FastESQ for Windows Version 2.0b
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/470,271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35.283
REFERENCE/DOCKET NUMBER: 07334/061
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/019,942
FILING DATE:
                    Sequence 2, Application US/09245281
Patent No. 6369196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-470-271-1
Sequence 1, Application US/09470271
Patent No. 6410689
GENERAL INFORMATION:
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TELEFAX: 20154
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 540 amino acids
""PE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WRMYFSHRHAHLRSP 15
                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-245-281-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 WRVQVAVKHLHIHTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserv
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STREET: 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: B
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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Patent No. 6148573
GENERAL INFORMATION:
APPLICANT: Nunez, Gabriel
APPLICANT: Inchara, Nachiro
APPLICANT: Roseki, Takeyoshi
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING APOPTOSIS
TITLE OF INVENTION: SIGNALING PATHWAY INHIBITORS AND ACTIVATORS
TITLE OF INVENTION: WORDER: US/09/069,023A
CURRENT APPLICATION NUMBER: US/09/069,023A
CURRENT FILING DATE: 1998-04-27
NUMBER OF SEQ ID NOS: 38
SSOFWARE: Patentin Ver. 2.0
SEQ ID NO 27
LENGTH: 540
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                                                         DB 3; Length 540;
59;
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Pred. No. 59;
5; Mismatches 5; Indels
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59;
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 07334-076001
CURRENT APPLICATION NUMBER: US/09/099,041A
CURRENT FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 09/019,942
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 540
                                                                                                    5; Indels
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                                                                                                  5; Mismatches
                                                           Score 40;
Pred. No.
                                                                                                                                                                                                                                                                         Sequence 2, Application US/09099041A Patent No. 6340576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.0%;
33.3%;
                                                         44:0%;
                                                       Query Match
Best Local Similarity 33.3
Matches 5; Conservative
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Best Local Similarity 33.3
Matches 5; Conservative
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; MOLECULE TYPE: protein US-09-019-942-1
                                                                                                                                       1 WRMYFSHRHAHLRSP 15
                                                                                                                                                             40 WRVQVAVKHLHIHTP 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-09-099-041A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRGANISM: Homo sapiens
US-09-069-023-27
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Matches 5; Conserv
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US-09-099-041A-2
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Gaps ö

Length 540; Indels

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Length 1019;
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Patent No. 5834285
GENERAL INFORMATION:
APPLICANT: Perler, Francine
APPLICANT: Perler, Francine
APPLICANT: Jack, William E.
TITLE OF INVENTION: RECOMBINANT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE FROM ARCHAEBACTERIA
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSE:
ADDRESSEE: INC.
ADDRESSEE: INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
GONDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 1; 1
Pred. No. 1.7e+02;
1; Mismatches 1;
                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/626,057
FILING DATE: 11-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/513,994
FILING DATE: 26-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REGISTRATION NUMBER: 30901
RECISTRATION NUMBER: NEB-101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/222,715B FILING DATE: 04-APR-1994 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING LACATION: 536
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/167,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: A. --
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/686,340
APPLICATION TOWNER: 17-APR-1991
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/626,057
FILING DATE: 11-DEC-1990
PRIOR APPLICATION DATA:
                 IMBER: US 07/686,340
17-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MASSACHUSETTS: US
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: un
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Patent No. 5756334
GENERAL INFORMATION:
APPLICANT: PERLER, FRANCINE B.
APPLICANT: SOUTHWORTH, MAURICE W.
TITLE OF INVENTION: RECOMBINANT THEROMSTABLE DNA POLYMERASE
TITLE OF INVENTION: FROM ARCHAEBACTERIA
                                                          Score 40; DB 4; Length 540;
Pred. No. 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.0%; Score 40; DB 4; Length 540; 33.3%; Pred. No. 59;
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 07334-112001
CURRENT FILING DATE: 1998-12-08
FRIOR PELICATION NUMBER: US 09/099,041
PRIOR FILING DATE: 1998-06-17
PRIOR FILING DATE: 1998-00-06
NUMBER OF SEQ ID NOS: 47
SOFTWARE: FASTSEO for Windows Version 4.0
                                                                                                      5; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/271,364A
FILING DATE: 06-JUL-1994
                                                                                                    5; Mismatches
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CORRESPONDENCE ADDRESS:
ADDRESSE: NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/811,421
FILING DATE: 18-DEC-1991
                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09207359B Patent No. 6469140
                                                          Query Match
Best Local Similarity 33.3%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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COUNTRY: US
; MOLECULE TYPE: protein US-09-470-271-1
                                                                                                                                             1 WRMYFSHRHAHLRSP 15
                                                                                                                                                                     40 WRVQVAVKHLHIHTP 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 5; Conserv
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US-08-271-364A-7
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US-09-207-359B-2
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LENGTH: 540
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Search completed: November 27, 2002, 07:25:10 Job time : 5.72201 secs
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Patent No. 6380370
GENERAL INFORMATION:
APPLICATION BOUGEtte-Stamm et al
APLICATION DOUCETTE ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-10-08
NUMBER OF SEQ ID NOS: 5674
SOURCE OF SEQ ID NOS: 5674
LENGTH: 305
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Patent No. 6342658
GENERAL INFORMATION:
APPLICANT: DeBonte, Lorin R.
APPLICANT: Shorrosh, Basil S.
APPLICANT: Shorrosh, Basil S.
APPLICANT: Shorrosh, Basil S.
CURENT APPLICATION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF FILE REFERENCE: 07148-063002
CURRENT APPLICATION NUMBER: US/09/354,231B
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR PILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 69
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Pred. No. 1.7e+02;
1; Mismatches 1; Indels
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42.9%; Pred. No. 70;
tive 3; Mismatches 5; Indels
                                                       NAME: Williams, Gregory D.
REGISTRATION NUMBER: 30901
REFERENCE/POCKET NUMBER: NEB-054C3FC2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
US 07/513,994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-5632
                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 1019 amino acids TYPE: amino acid
                                                                                                                                                                                                                        26:
                    FILING DATE: 26-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory L
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 42.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-222-7158-26
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289 YNVYVHHRDAHIES 302
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WRMYFSH 7
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US-09-134-001C-5632
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US-09-354-231B-34
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Gaps
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                                                                                                            Score 37; DB 4; Length 29;
Pred. No. 9.2;
                                                                                                                                                2; Indels
                                                                                                                                              2; Mismatches
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 34 LENGTH: 29
                                                                                                              Query Match
Best Local Similarity 60.0%;
Matches 6; Conservative
                                                 ; TYPE: PRT; ORGANISM: Ricinus communis
US-09-354-231B-34
                                                                                                                                                                                4 YFSHRHAHLR 13
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5 YFSWKHSHRR 14
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us-09-893-615-87.rag

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November 27, 2002, 05:38:32; Search time 67.9112 Seconds (without alignments) 241.342 Million cell updates/sec
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646
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          908470 segs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                        · protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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381 heavy chain va 381 single chain a Anti-HerZhene singl Lead binding MAb 6 Murine mAb 1D9 hea Murine 1D9 antibod Murine antibody 1D H. pylori 26 kba p Mouse heavy chain Lead binding MAb 2 Description AAR90829 AAR90837 AAY70111 AAW01587 AAU09919 AAE06947 AAE07033 AAB10022 AAO14978 AAW01593 ΙĐ Length DB Query Match 1 85.0 85.0 85.0 83.0 82.4 80.3 80.3 779.6 779.6 532 519 519 519 514.5 510 Score Result œ S

| 11 493 76.3 117 22 AAU09930 12 493 76.3 117 22 AAE06957 14 489 75.7 117 22 AAU09929 15 489 75.7 117 22 AAE06956 16 489 75.5 117 23 AAE06956 18 489 75.5 117 23 AAE06957 20 487 75.4 117 22 AAE06957 21 487 75.4 117 22 AAE06957 22 4487 75.4 117 22 AAE06957 23 483 75.4 117 22 AAE06973 24 487 75.4 117 22 AAE06971 25 476 73.0 126 22 AAE06973 26 471.5 73.0 126 22 AAE06972 27 468 72.4 256 23 AAU72866 28 467.5 72.4 256 23 AAU72866 29 467.5 72.4 256 23 AAU72866 20 467.5 72.4 256 23 AAU72866 21 468 72.1 127 22 AAE07008 31 462.5 71.3 281 18 AAW27560 32 460.5 71.3 281 18 AAW27560 33 460.5 71.3 281 18 AAW39451 40 448 69.3 122 21 AAY50975 41 447 69.3 121 20 AAW6122 44 447 69.3 121 20 AAW39551 447 69.3 146 120 18 AAW39551 447 69.3 146 120 19 AAW395869 447 69.2 142 18 AAY39869 | Humanised 1D9 heav Humanised murine 1 Humanised 1D9 heav Humanised 1D9 heav Humanised murine 1 Humanised murine h Humanised murine h Humanised murine h | ised 109 hears and murine ised murine ised murine in 109 antibo antibo acid sequen heavy chain | single c single c (P5-23 bi heavy c lybridoma Ab heav insus sin adipocyt | Lead binding MAD 4 Human FVIII antibo Human FVIII heavy Humanised anti-CD2 Protein sequence o Antibody ABX-CBL h Chimeric humanised Chimeric humanised SM3 heavy chain va MAD Br-3 heavy cha |
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| 11 | 200000000000000000000000000000000000000 | | 2004444400 | |
| 11111111111111111111111111111111111111 | ω | 488 488 488 488 47. | 46 67. 67. 67. 60. 60. | 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 |
| | 11 12 13 14 15 16 17 | 55 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 | 78888888498844 48888488848848 | 2 6 6 6 6 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 |

Lead binding MAb 2B4 heavy chain variable region. AAW01593 standard; Protein; 115 AA 22-AUG-1997 (first entry) AAW01593 RESULT 1 AAW01593

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ALIGNMENTS

Monoclonal antibody; Fd fragment; lead cation; perfume; cosmetic; pharmaceutical; health care; skin treatment; pesticide; herbicide; heavy metal.

95US-0541373. 96WO-US09258 (BION-) BIONEBRASKA INC. Mus musculus 05-JUN-1996; 10-OCT-1995; 05-JUN-1995; WO9639518-A1 12-DEC-1996

DNA encoding heavy metal binding polypeptide sequences - used for N-PSDB; AAT58267

Wylie DE;

Lopez O, Murray PJ, WPI; 1997-043140/04.

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Claim 8; Page 50-51; 106pp; English.
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                                                                                                                                                                                                                                                                                                The present sequence represents the heavy chain variable region for monoclonal antibody (MAb) 2B4, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from mouse hybridoma cells. The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfames, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials for electronic components. The products can provide for applications involving minute amounts of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
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            detecting, removing, adding or neutralising heavy metals, such as
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6
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Pred. No. 2.6e-46;
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                                                                                                                                                                                         Claim 12; Page 89; 125pp; English.
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N-PSDB; AAT15725.
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Best Local Similarity
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AAR90829-39 are monoclonal antibodies or a binding fragments produced by using insect guts, partic. insect brush border membranes (BBMs), esp. corn rootworm, as antigen; immunising a donor animal with the antigen; isolating immunised animal; fushing bisolating immunocompetent B cells from the immunised animal; fushing B cells with a tumour cell line; isolating the fused cells, culturing them and cloning positive hybrid cells; and screening the hybrid cells for prodn. of the required Mabs. The Mabs bind to the gut of a target insect but do not bind to mammalian BBMs. The DNA sequence can be operably linked to a toxin moiety, esp. selected from e.g. Bacillus toxins, lymenoptera and control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g. maize.
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Pred. No. 1e-45;
5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          85.0%;
86.3%;
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Matches 107; Conservative
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N-PSDB; AAT15733.
                                                                                                                                                                                                                                                                                                                                                                                                       119 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carozzi NB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insecta sp.
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR90837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antibody
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using insect guts, partic. insect brush border membranes (BBMs), esp. corn rootworm, as antigen; immunising a donor animal with the antigen; isolating immunocompetent B cells from the immunised animal; fusing B cells with a tumour cell line; isolating the fused cells, culturing the and cloning positive hybrid cells; and screening the hybrid cells for prodn. of the required MABs. The MABs bind to the gut of a target insect but do not bind to mammalian BBMs. The DNA sequence can be operably linked to a toxin molety, esp. selected from e.g. Bacillus toxins, Pseudomonas exotoxin and phytolaccin, etc. The Abs are useful for control of insect pests, e.g. Colcoptera, Dibtera, Hymenoptera and Lepidoptera. The pesticidal compsn. is pref. applied to a plant, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent discloses a novel retroviral vector, particularly Spleen Necrosis Virus (SNV) vector, having target cell specificity. The vector has a targetting envelope which is a chimeric protein consisting of an antigen binding site of an antibody (e.g. anti-DNP-scFv) or another
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retroviral vector; cell specific gene transfer; Spleen Necrosis Virus; SNV; antibody-envelope fusion protein; retroviral envelope protein; gene therapy; antigen binding site; single chain antibody; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDY-AMDYWGQGTSL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                            215 SYGDSVKDRFTVSRDDSQSMFYLQMNNLKTEDTAMYXCVR-----VVYGAMDYWGQGTSV 269
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                    1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell specific gene transfer using retroviral vectors containing antibody-envelope fusion proteins and wild type envelope proteins
                                                                                                                                                                                                                                                                                                                              ;
9
                                                                                                                                                                                                                                                                                       85.0%; Score 549; DB 17; Length 599;
86.3%; Pred. No. 6.6e-45;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY70111 standard; Protein; 333 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-Her2neu single chain antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Her2neu cell surface marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0135121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                          Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example; Fig 8; 45pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-224358/19.
                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                  599 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ51115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200009730-A2
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270 TVSS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 TVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dornburg RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY70111;
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                         Query Match
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peptide that binds to a specific cell surface protein, fused to the carboxy terminal part of the retroviral envelope protein. The presence of the wild type envelope protein serves as a helper molecule to improve or supplement a functional membrane fusion domain. The antigen binding site replaces the natural viral receptor binding site. The retroviral vector is used for cell specific gene transfer, especially in gene therapy. The invention overcomes the restricted host range limitation of retroviral vectors. The present sequence is an anti-Herzneu single chain antibody (scA). The coding sequence of this antibody was used in the construction of plasmid pAJ7 which contains a tagetting vector comprising the anti-Herzneu scA fused to the SNV-Env(envelope)-TM(transmembrane) coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents the heavy chain variable region for monoclonal antibody (MAb) 6F5, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from mouse hybridoma cells.
                                                                                                                                                                                                                                                                                                                                                                                                                    144 EVQLEESGGGLVQPKGSLKLSCAASGFTFNTYAMNWVRQAPGKGLEWLVRIRSKSNNYAT 203
                                                                                                                                                                                                                                                                                                                                                                                                 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDY---AMDYWGQGT 117
                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cosmetic;
herbicide;
                                                                                                                                                                                                                                                                                                                                EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy : tals, such as lead cations
                                                                                                                                                                                                                                                             Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Monoclonal antibody; Fd fragment; lead cation; perfume; pharmaceutical; health care; skin treatment; pesticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lead binding MAb 6F5 heavy chain variable region.
                                                                                                                                                                                                                                                             83.0%; Score 536; DB 21;
83.3%; Pred. No. 6.2e-44;
                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW01587 standard; Protein; 110 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 77; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wylie DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96WO-US09258
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95US-0462798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                              Matches 105; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BION-) BIONEBRASKA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lopez O, Murray PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-043140/04
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                               333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT58261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::||||
TVTVSS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SLTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9639518-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            heavy metal.
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                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118
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AAW01587
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The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-conductor and integrated circuit components and production materials for electronic components. The products can provide for applications involving minute amounts of specific heavy metals.
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                  ESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYATFYADS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Complementarity determining region 1 (CDR1)" 50..68 /note= "Complementarity determining region 2 (CDR2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101..106
/note= "Complementarity determining region 3 (CDR3)"
                                                                                                                                                                                                                                                                                                                                                VKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLTVSS 123
                                                                                                                                                                                                                                                                                                                                                                1 ESGGGLVQPKGSLKLSCAASGFTFNTYAMNWVRQAPGKGLEWVARIRSKSNNYATYYADS
                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                   Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine mAb 1D9 heavy chain variable region protein sequence.
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mAb 1D9 heavy chain variable region; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiinflammatory; collagen disease; immunosuppressive antiasthmatic; insulin-dependent diabetes mellitus; inflammatory bowel disease; ulcerative collitis; graft rejection; allergic disease; antipsoriatic; antiarthritic; nephrotropic; antithyrold; restenosis; dermatological; anaphylaxis; cell adhesion inhibitor; vascular injury; autoimmune disease; immunoglobulin; complementarity determining region; CDR; CDIB; CCR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27..30
/note= "Part of H1 structure loop"
                                                                                                                                                                                                                 Score 532; DB 18;
Pred, No. 4.2e-44;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU09919 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                 Query Match 82.4%;
Best Local Similarity 87.3%;
Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAR-2001; 2001WO-US08266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAR-2000; 2000US-0528267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Horvath CJ, Rao PE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-607511/69.
                                                                                                                                                                                     110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atherosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200170266-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUN-2002
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                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU09919;
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                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU0991
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The present invention relates to a new method of inhibiting stenosis or restenosis of a blood vessel following vascular injury in a subject. The new method comprises administering to the subject agents which inhibit the adhesion and/or recruitment of neutrophils and mononuclear cells to a site of vascular injury by binding CD18 or CCR2. The method of the invention inhibits stenosis or restenosis of a blood vessel following vascular injury arising from a vascular intervention procedure such as vascular injury arising from a vascular intervention procedure such as vascular injury arising from a vascular intervention procedure such as vascular injury arising from a narogary. The method is also useful for treating a subject having an inflammatory disease or condition and praft versus host disease. Chronic inflammatory diseases of the lung, collagen diseases, and insulin-dependent diabetes mellitus can also be treated. The method is further useful for treating inflammatory bowel diseases, such as ulcerative collitis. Additional diseases or conditions including systemic anaphylaxis of hypersensitivity responses, and inflammatory dermatoses, autoimmune diseases such as a rithitis, graft rejection and other diseases including atherosclerosis. The present sequence represents sequence contains three CDR's that can be used to inhibit stenosis or restenosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphjaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angloplasty; acquired immune deficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody; neointimal hyperplasia; VH; heavy chain variable region.
Inhibiting stenosis or restenosis of a blood vessel following vascular injury or angioplasty in a subject by administering agent which inhibits recruitment or adhesion of neutrophils, mononuclear cells to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EVQLVESGGGLVQPKGSLKLSCAASGFSFNAYAMNWVRQAPGKGLEWVARIFTFTKNNNYAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine 1D9 antibody heavy chain variable (VH) region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 519; DB 22;
Pred. No. 8.2e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE06947 standard; Protein; 117 AA.
                                                                                                                Claim 30; Fig 16; 108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 99; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSS 123
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                                                                    injury site
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Region
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us-09-893-615-87.rag

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free patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating CR2. They are useful for inhibiting or treating cell for inhibiting a real floking, for treating CCR2-mediated disorders such as renumatory disorder, autoimmune disorders such as rheumatorid arthritis and multiple sclerosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for traating CCR2 mediated disease. They are also useful for treating allergy, anaphylaxis, and in the manufacture of a medicament for treating allergy, anaphylaxis, and in the manufacture of a medicament for treating allergy, anaphylaxis, and in the manufacture of a medicament for treating allergy, anaphylaxis, and in the manufacture of a medicament for treating allergy, anaphylaxis, and in the manufactured allergic reaction, shock, stenosis, allograft rejection, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumanised antibodies are also useful for inhibiting narrowing of the luman of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is the heavy chain variable (VH) region of murine ID9 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                        Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 117;
50.68 /label- Complementarity_determining_region 101..106 /label- Complementarity_determining_region /label- Complementarity_determining_region
                                                                                                                                                                                                                                                                                                           O'Brien S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80.3%; Score 519; DB 22;
80.5%; Pred. No. 8.2e-43;
ive 11; Mismatches 7;
                                                                                                                                                                                                                                                                                                                Jones ST,
                                                                                                                                                                                                                                                                                                             Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 8; Fig 8; 183pp; English.
                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                 02-FEB-2001; 2001WO-US03537.
                                                                                                                                                                                                                          03-FEB-2000; 2000US-0497625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99; Conservative
                                                                                                                                                                                                                                                                                                           Horvath C,
                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-488888/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA;
                                                                                                    WO200157226-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 VSS 123
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                                                                                                                                             09-AUG-2001
                                                                                                                                                                                                                                                                                                             Larosa GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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neuroprotective; immunosuppressive; human immunodeficiency virus; half inflammatory cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumal, arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asherosclerosis; atherosclerosis; allograft rejection; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease, angloplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neolintimal hyperplasia; antibody 1D9 heavy chain variable region.
                                                                         Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'Keefe T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'Brien S,
                                                                                                                                                                                                                                     20.148
/note= "Murine mature antibody 1D9 kappa
light chain variable region"
                                                Murine antibody 1D9 heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Newman W, Jones ST,
                                                                                                                                                                                                                                                                                                         /label- Variable_region
                                                                                                                                                                                                                                                                                                                                   .abel - constant_region
                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         /note- "Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 21; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-FEB-2000; 2000US-0497625.
                                                                                                                                                                                                                                                                                                                                                                                                                                 02-FEB-2001; 2001WO-US03537
                       16-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                      138..148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Larosa GJ, Horvath C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-488888/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAD13178
                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                 WO200157226-A1
                                                                                                                                                                                                                                                                                                                                                                                                        09-AUG-2001.
AAE07033;
                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                Mus sp
                                                                                                                                                                                                                                                                                               Region
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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin manised antibodies are useful for inhibiting the interaction of a call expressing CCR2. They are useful for inhibiting the interaction of a call expressing CCR2. They are useful for inhibiting or treating I leukocyte trafficking, for treating CCR2-mediated disorders such as renamatory disorder, autoimmune disorders such as rheumatory disorder, autoimmune disorders such as rheumatorial and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgE. mediated allergic reaction, shock, stenosis, allogist rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (ALDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal-Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of

AAE07033 standard; Protein; 148 AA.

RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel method for the detection of a mammalian infection by an acid-resistant microorganism (A) by treating a faecal sample with at least two different monoclonal antibodies (MAD) (or their fragments or derivatives) or aptamers (collectively (I)) and detecting formation of a complex (C) between (I) and the corresponding antigen of (A). The first and second (I) bind to epitopes of different antigens (Ag). These epitopes are present, after passage through the intestines, in at least some mammals, and have either: (I) their native structure; or (II) a structure against which an antibody is produced by an animal infected or immunized with (A), or its extract, lysate, derived protein or fragment, or with a synthetic peptide. Practically all mammals display at least one of the specified epitopes. The method is used to detect infection by acid-fast bacteria, particularly of the genera Helicobacter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Detecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a faecal sample with two binding reagents for antigens that survive intestinal passage
a vessel in a mammal, preferably associated with vascular intervention. The present sequence is murine antibody 1D9 heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                   Acid-resistant microorganism; detection; faecal; intestine; infection; monoclonal antibody; heavy chain.
                                                                                                                                                                    61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
                                                                                                                                                                                  Gaps
                                                                                                                 1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                               20 EVQLVESGGGLVQPKGSLKLSCAASGFSFNAYAMNWVRQAPGKGLEWVARITFTKTKNNNYAT 79
                                                                                        ;
9
                                                                                                                                                                                                                                                                                                                                                                                           H. pylori 26 kDa protein-binding antibody heavy chain protein.
                                                             Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lakner M;
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cullmann G, Friedrichs U, Heppner P,
                                                             80.3%; Score 519; DB 22;
80.5%; Pred. No. 1.1e-42;
ive 11; Mismatches 7;
                                                                                                                                                                                                                                                                                                              AAB10022 standard; Protein; 125 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 4; 84pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-EP08212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98EP-0120517
98EP-0120687
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CONN-) CONNEX GMBH.
                                                                           Best_Local Similarity
Matches 99; Conserv
                                       148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAA40202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200026671-A1
                                                                                                                                                                                                                                       134 VSS 136
                                                                                                                                                                                                                                                                                                                                                                 01-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39-OCT-1999;
                                                                                                                                                                                                                       VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-1998;
06-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ringeis A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reiter C,
                                                                                                                                                                                                                                                                                                                                      AAB10022;
                                       Sequence
                                                                Query Match
                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse, graft rejection, CC chemokine receptor 2 antaqonist;
CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;
lung transplant; heart-lung transplant; pancreas transplant;
bowel transplant; heart transplant; graft versus host disease;
chronic graft rejection; antibody heavy chain variable region; mAb 1D9.
Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus, M. tuberculosis, C. jejuni and C. pylori. (1) may also be used therapeutically. The method is direct and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible degradation of antigens during passage through the intestines. This sequence represents the H. pylori 26 kba protein-binding antibody (DNS ACC2355) heavy chain which is used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 ADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVR-RGASGIDYAMDYWGQGTSLTV 121
                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 LLEESGGGLVQPTGSLKLSCAASGFTFNSYAMYWVRQAPGKGLEWVARIRSKSDNYATYY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 MLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYATFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         graft versus host disease or chronic graft, involves administering a CCR2
                                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                                                                                                                                                                                                                 21; Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                        13;
                                                                                                                                                                                                                                                                                                                                                                              .4e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                           8; Mismatches
                                                                                                                                                                                                                                                                                                                                              Score 514.5;
Pred. No. 2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; protein; 117 AA.
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                                                                                                                                                                                                                                                                                                                                           79.6%;
82.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-APR-2001; 2001US-0835087.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-APR-2000; 2000US-0549448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                           Query Match 79.6
Best Local Similarity 82.0
Matches 100; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 16pp;
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                                                                                                                                                                                                                                                                                 125 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US2002042370-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 SS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antagonist
                                                                                                                                                                                                                          .nvention
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                                                                                                                                                                                                                                                                                       Sequence
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1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT
                          Region
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Matches
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method of the invention is useful for inhibiting graft rejection - particularly allografts such as kidney, liver, lung, heart-lung, pancreas, bowel and heart. The method of the invention is also useful for inhibiting graft versus host disease and for inhibiting chronic rejection of a transplanted graft. The present amino acid sequence represents a mouse antibody heavy chain variable region (mAb 1D9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Substitution of Thr residue normally present
in human 4B4°CL sequence (AAU09926) by Ser
residue normally present in mouse mAb 1D9 heavy
chain sequence (AAU09919)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Substitution of Ser residue normally present
in human 4B4'CL sequence (AAU09926) by Asn
residue normally present in mouse mAb 1D9 heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain sequence (AAU09919). Specification states
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the mutation as N30S but as sequence has Asn at position 30 the mutation is likely to be S30N"
                                                                                                                                                                                        1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Substitution of Gly residue normally present
in human 484'CL sequence (AAU09926) by Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complementarity determining region 1 (CDR1),
                                                                                                                                                                                                                                                                                                                                                                                 Humanised 1D9 heavy chain variable region, 1D9RHD protein sequence.
                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  grafted from mouse mAb 1D9 heavy chain sequence (AAU09919)"
                                                                                                                                                                                                                                                                                                                                                                                                   Human; mouse; 4B4'CL heavy chain variable region; vasotropic; antiinflammatory; collagen disease; immunosuppressive; antiinsthmattc; insulin-dependent diabetes mellitus; inflammatory bowel disease; ulcerative colitis; ID9RHD; graft rejection; allergic disease; antipsoriatic; antiarthritic; nephrotropic; antiinyroid; restenosis; dermatological; anaphylaxis; cell adhesion inhibitor; vascular injury; autofimmune disease; immunoglobulin; complementarity determining region; CDR; CD18; CCR2;
                                                                                                   Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Part of H1 structure loop"
                                                                                                 78.9%; Score 510; DB 23;
79.7%; Pred. No. 6.1e-42;
ilve 11; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                               AAU09930 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atherosclerosis; mutant; mutein
                                                                                                                                                                                                                                                                                                                                                          18-JUN-2002 (first entry)
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric - Homo sapiens.
Chimeric - Mus sp.
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/note-
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- Synthetic.
                                                                                                           Local Similarity
nes 98; Conserv
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                                                                            117
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                                                                                                                                                                                                                                                         115 VSS 117
                                                                                                                                                                                                                                                                                                                                     AAU09930;
                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a new method of inhibiting stenosis or restenosis of a blood vessel following vascular injury in a subject. The new method comprises administering to the subject agents which inhibit the adhesion and/or recruitment of neutrophils and monounclear cells to a site of vascular injury by binding CD18 or CCR2. The method of the invention inhibits stenosis or restenosis of a blood vessel following vascular injury arising from a vascular intervention procedure such as vascular by-pass or transplantation surgery. The method is also useful mediated by neutrophil and monounclear cell activity e.g. asthma and graft versus host disease. Chronic inflammatory diseases of the lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen diseases, and insulin-dependent diabetes mellitus can also be treated. The method is further useful for treating inflammatory bowel alseases, such as ulcerative colitis. Additional diseases or conditions include inflammatory or allergic diseases and conditions, including systemic anaphylaxis of hypersensitivity responses, drug allergies, psoriasis and inflammatory dermatoses, autoimmune diseases such as arthritis, graft rejection and other diseases including atherosclerosis. This sequence represents the variable region of one of several humanised in 109 heavy chains (AAU09927-AAU09930). These heavy chains were used in
                                                                                                                                                                                                                                           "Substitution of Phe residue normally present
in human 4B4'CL sequence (AAU09926) by Tyr
residue normally present in mouse mAb 1D9 heavy
                                                                                                                                                                                                                                                                                                                                                                                                                  "Substitution of Thr residue normally present in human 4B4°CL sequence (AAU09926) by Val residue normally present in mouse mAb 1D9 heavy chaln sequence (AAU09919)"
residue normally present in mouse mAb 1D9 heavy chain sequence (AAU09919)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibiting stenosis or restenosis of a blood vessel following vascular injury or angloplasty in a subject by administering agent which inhibits recruitment or adhesion of neutrophils, monionuclear cells to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                       "Complementarity determining region 2 (CDR2), grafted from mouse mAb 1D9 heavy chain sequence (AAU09919)"
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Local Sam.
94;
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AAU09928
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                                                                                                                                                                                                                                       Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rehumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angloplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; ID9 antibody; necintimal hyperplasia; VH; heavy chain variable region; ID9RHD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting
                                Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
EVQLVESGGGLVKPGGSLRLSCAASGFSFNAYAMNWVRQAPGKGLEWVARIRTKNNNYAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O'Keefe T;
                     61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRKGASGIDYAMDYWGQGTSLT
                                                                                                                                                                                                                   Humanised murine 1D9 antibody heavy chain variable region, 1D9RHD.
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/label- CDR3
/note- "Complementarity determining region 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                            "Complementarity determining region 1"
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/label- CDR2
/note- "Complementarity determining region
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                                                                                                                                               AAE06957 standard; Protein; 117 AA.
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/label- CDR1
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    Homo sapiens.

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leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as riceumatoid arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating classes. They are also useful for treating callergy, anaphylaxis, malignancy, chronic and acute inflammatory, anaphylaxis, malignancy, chronic and acute inflammatory glomerulopethies, acquired immune deficiency syndrome (AIDS), restenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopethies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting nacrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention.

The present sequence is humanised murine ID9 antibody heavy chain
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in human 4B4'CL sequence (AAU09926) by Asn
residue normally present in mouse mAb 1D9 heavy
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in human 4B4'CL sequence (AAU09926) by Ser
residue normally present in mouse mAb 1D9 heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRKGASGIDYAMDYWGQGTSLT 120
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14; Mismatches 9; Indels (
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/note- "Part of H1 structure loop"
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Best Local Similarity
Matches 94; Conserv
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The present invention relates to a new method of inhibiting stenosis or restenosis of a blood vessel following vascular injury in a subject. The new method comprises administering to the subject agents which inhibit to the adhesion and/or recruitment of neutrophils and mononclear cells to a site of vascular injury by binding CD18 or CCR2. The method of the invention inhibits stenosis or restenosis of a blood vessel following vascular injury arising from a vascular intervention procedure such as vascular injury arising from a vascular intervention procedure such as vascular by-pass or transplantation surgery. The method is also useful for treating a subject having an inflammatory disease or condition mediated by neutrophil and mononuclear cell activity e.g. asthma and collated by neutrophil and mononuclear cell activity e.g. asthma and collated by neutrophil and mononuclear cell activity e.g. asthma and cell seated. The method is further useful for treating inflammatory bowel diseases, such as ulcerative collits. Additional diseases or conditions systemic anaphylaxis of hypersensitivity responses, drug allergies, psoriasis and inflammatory dermatoses, autoimmune diseases such as a trinities, graft rejection and other diseases including atherosclerosis. This sequence represents the variable region of one of several humanised the invention for the production of anti-CCR2 antibody or antigen-binding
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chain sequence (AAU09919). Specification states the mutation as N30S but as sequence has Asn at position 30 the mutation is likely to be S30N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting stenosis or restenosis of a blood vessel following vascular injury or angioplasty in a subject by administering agent which inhibits recruitment or adhesion of neutrophils, mononuclear cells to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                      "Complementarity determining region 1 (CDR1),
                                                                                                                                            "Complementarity determining region 2 (CDR2), grafted from mouse mab 1D9 heavy chain sequence (AAU09919)"
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                                                                                          grafted from mouse mAb 1D9 heavy chain sequence (AAU09919)"
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Best Local Similarity 75.6%
Matches 93; Conservative
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Injury site
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"Substitution of Ser residue normally present in human 4B4'CL sequence (AA.009926) by Asn residue normally present in mouse mAb 1D9 heavy chain sequence (AA.009919). Specification states the mutation as N30S but as sequence has Asn at position 30 the mutation is likely to be $30N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Substitution of Thr residue normally present
in human 4B4'CL sequence (AAU09246) by Ser
residue normally present in mouse mAb 1D9 heavy
chain sequence (AAU09919)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in human 4B4'CL sequence (AAU09926) by Ala
residue normally present in mouse mAb 1D9 heavy
chain sequence (AAU09919)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Substitution of Phe residue normally present in human 4B4/CL sequence (AAU09916) by Tyr residue normally present in mouse mAb 1D9 heavy chain sequence (AAU09919)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Substitution of Gly residue normally present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complementarity determining region 1 (CDR1), grafted from mouse mAb 1D9 heavy chain sequence (AAU09919)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complementarity determining region 2 (CDR2), grafted from mouse mAb 1D5 heavy chain sequence (AAU09919)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complementarity determining region 3 (CDR3), grafted from mouse mAb 1D9 heavy chain sequence (AAU09919)"
                                                                                                                                                                                                                                                                                                                                                                            Humanised 1D9 heavy chain variable region, 1D9RHC protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; mouse; 4B4'CL heavy chain variable region; vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiinflammatory; collagen disease; immunosuppressive; antiasthmatic; insulin-dependent diabetes mellitus; inflammatory bowel disease; ulcerative colitis; IDSNHC; graft rejection; allergic disease; antipsoriatic; antiarthritic; nephrotropic; antithyroid; restenosis; dermatological; anaphylaxis; cell adhesion inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunoglobul in;
                                                                                                             <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vascular injury; autoimmune disease; immunoglobulin
complementarity determining region; CDR; CD18; CCR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27..30
/note= "Part of H1 structure loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                  AAU09929 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atherosclerosis; mutant; mutein.
                                                                                                                                                                                                                                                                                                                     18-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric - Homo sapiens.
Chimeric - Mus sp.
Chimeric - Synthetic.
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/note=
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/note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 30 /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 49
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121 VSS 123
                                                      115 VSS 117
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                                                                                                                                           RESULT 14
                                                                                                                                                                    AAU09929
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The present invention relates to a new method of inhibiting stenosis or restenosis of a blood vessel following vascular injury in a subject. The new method comprises administering to the subject agents which inhibit the adhesion and/or recruitment of neutrophils and mononclear cells to a site of vascular injury by binding CD18 or CCR2. The method of the invention inhibits stenosis or restenosis of a blood vessel following vascular injury arising from a vascular intervention procedure such as vascular by-pass or transplantation surgery. The method is also useful for treating a subject having an inflammatory disease or condition mediated by neutrophil and mononuclear cell activity e.g. asthma and graft versus host disease. Chronic inflammatory diseases or condition mediated. The method is further useful for treating inflammatory bowel diseases, such as ulcerative collitis. Additional diseases or conditions include inflammatory or allergic diseases and conditions, including systemic anaphylaxis of hypersensitivity responses, drug allergies, systemic anaphylaxis of hypersensitivity responses, drug allergies, while some conditions and inflammatory dermatoses, autoimmune diseases such as a condition or arresponse to the condition of the condition of a condition or arresponse to the condition of a condition or arresponse to the condition of the condition of the condition of conditions and inflammatory dermatoses and condition of conditions and conditions and conditions are conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the variable region of one of several humanised 1D9 heavy chains (AAU09927-AAU09930). These heavy chains were used in the invention for the production of anti-CCR2 antibody or antigen-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic; neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
                                                                                                                                                                                                                                                                 Inhibiting stenosis or restenosis of a blood vessel following vascular
                                                                                                                                                                                                                                                                               injury or angioplasty in a subject by administering agent which inhibits recruitment or adhesion of neutrophils, mononuclear cells to injury site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE06956 standard; Protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 32; Fig 18; 108pp; English.
                                                                                                         (MILL-) MILLENNIUM PHARM INC.
15-MAR-2001; 2001WO-US08266
                                                    2000US-0528267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 AA;
                                                 17-MAR-2000;
                                                                                                                                                           Horvath CJ,
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fragment, having binding specificity for CC-chemokine receptor 2

(CCR2), comprising an antigen binding region of non-human origin
and at least a portion of an immunoglobulin of human origin. The
humanised antibodies are useful for inhibiting the interaction of
a cell expressing CCR2. They are useful for inhibiting or treating
CC HIV infection. The proteins of the invention are useful for inhibiting
CC HIV infection. The proteins of the invention are useful for inhibiting
CC HIV infection. The proteins of the invention are useful for inhibiting
CC arbitits and multiple solerobis, atherogenesis and atherosorslers such as
inflammatory disorder, autoimmune disorders such as rheumatoid
and for inhibiting restenosis. They are useful in therapy or diagnosis,
and for inhibiting restenosis. They are useful in therapy or diagnosis,
and for inhibiting restenosis. They are useful in therapy or diagnosis,
and in the manufacture of a medicament for treating allergy, anaphylaxis,
malignancy, chronic and acute inflammation, histamine and IgE.
CC disease. They are also useful for transine and IgE.
malignancy, chronic and acute inflammation, histamine and IgE.
(Fibrotic disease, asthma, inflammation, histamine and inhibiting narrowing of the
intervention, including angioplasty and/or stent placement in a mammal.
CC Humanised antibodies are also useful for inhibiting narrowing of the
luman of a vessel in a mammal, preferably associated with vascular intervention.
CC The present sequence is humanised murine ID9 antibody heavy chain
multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibroric disease; anaphoplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; 1D9 antibody; neoIntimal hyperplasia; VH; heavy chain variable region; 1D9RHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The patent discloses a humanised antibody or its antigen-binding
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                                                                                                                                                                                                                                       "Complementarity determinion region 1"
                                                                                                                                                                                                                                                                                                 /note= "Complementarity determining region 2"
101..106
                                                                                                                                                                                                                                                                                                                                                         /note- "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O'Brien S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.7%; Score 489; DB 22; 75.6%; Pred. No. 6.6e-40; iive 14; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones ST,
                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                                                                                                          /label= CDR2
                                                                                                                                                                                                                                                                                                                                    /label- CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            variable (VH) region, 1D9RHC
                                                                                                                                                                                                                    /label - CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-FEB-2000; 2000US-0497625.
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                                                                                                                      - Mus sp.
- Homo sapiens.
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Best Local Similarity
Matches 93; Conserv
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1 EVQLVESGGGLVKPGGSLRLSCAASGFSFNAYAMNWVRQAPGKGLEWVARIRTKNNNYAT 60
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1 EVMLVESGGGLVQPKGSLKL.....SGIDYAMDYWGQGTSLTVSS 123
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
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                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database

heavy chain pre heavy chain V r chain Description heavy SUMMARIES PH1093 B42575 S58213 S26462 S32186 S20775 AVMS06 A31485 D30540 MHMS76 S31107 H36005 S31678 520642 S44107 å Query Match Length DB 449.5 446 444 439 438.5 438.5 438 438 438 438 438 437 528.5 526.5 526.5 494.5 480.5 477 467.5 463.4 456 443.5 442.5 441.5 441 439.5 Score Result ŝ

||: VSA 141 121 VSS 123

139

δ g RESULT 2
542467
19 heavy chain V region precursor - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C; Accession: S42467
R; Shiyanov, P.A.; Bespalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
A; Reference number: S42466
A; Accession: S42467
A; Status: preliminary
A; Status: preliminary
A; Status: nelliminary
A; Residues: 1-137 <SHI>

A;Cross-references: EMBL:X78107; NID:9460798; PIDN:CAA54997.1; PID:9460799 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin F;34-119/Domain: immunoglobulin homology <IMM>

chain

| 436 67.5 115 1 AVMS82 Ig heavy chain 436 67.5 117 2 S31109 Ig heavy chain 435 67.3 160 2 S05271 Ig heavy chain 433 67.0 140 2 S31588 Ig heavy chain | 432 66.9 123 2 A36006 Igheavy chain 431.5 66.8 121 2 127887 Igheavy chain 431 66.7 118 2 520641 Igheavy chain 431 66.7 122 2 E27888 Igheavy chain 431 66.7 123 2 526794 Iqheavy chain | 66.7 125 2 \$30531 19 heavy 66.6 120 2 \$1686 19 heavy 66.6 120 2 \$4411 1 | RESULT 1 13213 132 | Query Match 81.8%; Score 528.5; DB 2; Length 141; Best Local Similarity 83.7%; Pred. No. 9.5e-42; 1 deps 1; Matches 103; Conservative 7; Mismatches 12; Indels 1; Gaps 1; 1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMWWRQAPGKGLEWVARIRSKSNNYAT 60 111111111111111111111111111111111111 |
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R;Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A;Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Reference number: PH0971; MUID:92381444; PMID:1512540
A;Reference type: mRNA
A;Residues: 1-110 <TIL>
A;Experimental source: B cell, strain [NZB x NZW]F1
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession: A27630
R; Kofler, R.
J: Immunol. 140, 4031-4034, 1988
R; Kofler, R.
J: Immunol. 150, MUID: 8629103; PMID: 3131427
R; Reference number: A27630; MUID: 9196220; PIDN: AAA38634.1; PID: 9196221; GB: M20825
R; Cross-references: GB: M21470; NID: 919610n; Immunoglobulin homology
C; Superfamily: immunoglobulin N region: Immunoglobulin homology C; MM>
F; 34-119/Domain: immunoglobulin homology <IMM>
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A;Residues: 1-110 <TIL.
A;Experimental source: B cell, strain [NZB x NZW]F1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                        Score 494.5; DB Pred. No. 1e-38; 4; Mismatches
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Best Local Similarity 84.3%;
Matches 97; Conservative
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Best Local Similarity
Matches 93; Conserv
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A;Reference number: A41940; MUID:92086633; PMID:1749770
A;Accession: A41940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: sequence extracted from NCBI backbone (NCBIP:70715)
R;Smith, R.G.; Voss Jr., E.W.
Mil. Immunol. 27, 463-470, 1990
A;Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from A;Reference number: PL0198; MUID:90309768; PMID:2114528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 07-May-1999
C;Accession: 441940; PL0201
R:Herron, J.N.; He, X.M.; Ballard, D.W.; Blier, P.R.; Pace, P.E.; Bothwell, A.L.; Voss
Proteins 11, 159-175, 1991
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C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PH1091
                                                                                                                                                                                                                                                            61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region G2b, autoantibody BV04-01 - mouse (fragment) N;Alternate names: anti-DNA autoantibody BV04-01, heavy chain V region
                                   Length 137;
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A.Residues: 1-118 <SMI>
A.Residues: 1-118 <SMI>
A.Sesidues: 1-118 <SMI>
A.Sesidues: 1-118 <SMI>
C.Superfamily: immunoglobulin V region; immunoglobulin homology C.Keywords: heterotetramer; immunoglobulin homology <IMM>
F:15-100/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:50-68/Region: complementarity-determining 2
F:101-110/Region: complementarity-determining 3
F:101-105/Region: D region
F:101-105/Region: JH region
                                                             ..4e-41;
nes 10;
                                      DB 2;
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82.9%; Pred. No. 3.2e-41;
iive 7; Mismatches 12;
                                                                                        6; Mismatches
                                Score 526.5;
Pred. No. 1.4
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                                81.5%;
82.9%;
                                Query Match 81.5
Best Local Similarity 82.9
Matches 102; Conservative
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Matches 102; Conservative
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||19 VSA 121
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Ig heavy chain V region (anti-F(ab')2) - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 13-Jan-1996 #sequence_revision 12-Apr-1996 #text_change 23-Jul-1999
C; Accession: S58213; S58212
R; Welschof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebel, S.; Breitlin submitted to the EMBL Data Library, July 1995
A; Description: Characterization of heavy and light chain immunoglobulin variable reging A; Accession: S58213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-127 < WELD.
A; Residues: 1-127 < WELD.
A; Residues: 1-127 < WELD.
A; Cross-references: EMBL: X89055; NID: 9929638; PIDN: CAA61442.1; PID: 9929639; EMBL: X890
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-100/Domain: immunoglobulin homology < IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AYAASVKGRFTISRDDSENTAYLQMNSLKIEDTAVYYCTRGSSMVRGVNGY-YGMDVWGQ 119
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  11 LVQPKGS--LKLSCAASGFTFNNYAMNWVRQAPGKGLEWVAFIRSKSNNYATFYADSVKD 68
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-92/Domain: immunoglobulin homology <IMM>
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Pred. No. 3.2e-35;
4; Mismatches 3; Indels
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                                                                       9.2e-36;
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71.9%; Pred. No. 9.2e-
ilve 11; Mismatches
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Best Local Similarity 71.99
Matches 92; Conservative
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R; Kavaler, J.
submitted to the EMBL Data Li
A; Reference number: S26459
A; Accession: S26462
A; Status: preliminary
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Best Local Similarity
Matches 91; Conserv
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A; Residues: 1-100 <KAV>
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C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Species: Musculus (house mouse)
R:Garcia, K.C.; Desiderio, S.V.; Ronco, P.M.; Verroust, P.J.; Amzel, L.M.
Science 277, 228-531, 1992
A:Title: Recognition of angiotensin II: antibodies at different levels of an idiotypic n. A; Reference number: A42575; MUID:92342952; PMID:1636087
A; Reference number: A42575; MUID:92342952; PMID:1636087
A; Residues: 1-101 cGAR>
A; Residues: 1-101 cGAR>
A; Residues: 1-101 cGAR>
A; Cross-references: GB:S40679; NID:9252098; PIDN:AAB22669.1; PID:9252099
A; Experimental source: BALB/c mice, myeloma cell line NS-1
A; Note: sequence extracted from NCBI backbone (NCBIN:109337, NCBIP:109338)
C: Superfamily: Immunoglobulin V region; immunoglobulin homology < IMM>
F; 7-92/Domain: immunoglobulin homology < IMM>
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C; Species: Mus musculus (house mouse)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Paterian Date: 30-Sep-1993 #sequence 17.N.
J. Exp. Med. 176, 761-779, 1992
A; Fitle: Both IgW and IgG anti-DNA antibodies are the products of clonally select
A; Reference number: PH0971; MUID:92381444; PMID:1512540
A; Reference number: PH0971; MUID:92381444; PMID:1512540
A; Residues: nucleic acid sequence not shown
A; Residues: 1-110 < TLL>
A; Residues: 1-110 < TLL>
C; Superfamental source: B cell, strain [NZB x NZW]F1
C; Superfamily: immunoglobulin vegion; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 15-100/Domain: immunoglobulin homology < IMM>
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                                                                            Length 110;
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Pred. No. 4.1e-37;
6; Mismatches 4; Indels
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Pred. No. 2.8e-36;
2; Mismatches 6;
                                                                       Score 480.5; DB 2
Pred. No. 1.9e-37;
3; Mismatches 10
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C;Keywords: heterotetramer; immunoglobulin F;15-100/Domain: immunoglobulin homology <IMM>
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1 Similarity 87.6%;
92; Conservative 7
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                                                                         74.48;
82.68;
                                                                                                                            Conservative
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Best Local S
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9 GGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYATFYADSVKD 68

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121 VSS 123
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C. Date: 20-Reb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C. Date: 20-Reb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C. Accession: S20775
R. Mortari, F.; Wang, J.; Schroeder, H.W.
Submitted to the EMBL Data Library, April 1992
A. Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A. Reference number: S20764
A. Recession: S20775
A. Status: preliminary
A. Molecule type: DNA
A. Residues: 1-124 < MOR>
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Ig heavy chain V region - mouse (fragment)
C;Species: Wus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999
C;Accession: S32186
                                                                                                                                                                 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-123 <IZU>
A;Cross-references: EMBL:X70093; NID:g288249; PIDN:CAA49698.1; PID:g288250
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-100/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                   25; Indels
                                                                                                                                                                                                                                                                                                                                         Query Match 69.7%; Score 450; DB 2; Best Local Similarity 69.9%; Pred. No. 1.4e-34; Matches 86; Conservative 12; Mismatches 25
                                                             C; Accession: S32186
R; Izul, S.
submitted to the EMBL Data Library, February 1993
A; Accession: S32186
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Best Local Similarity 71.0%
Matches 88; Conservative
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RESULT 13

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Ideavy chain V region - human (fragment)
C; Species: Homo saptens (man)
C; Species: Homo saptens (man)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C; Ccession: 523624
A; Med: 175, 831-842, 1992
A; Riche; Genetic analysis of self-associating immunoglobulin G rheumatoid factors fro A; Reference number: 523624
A; Accession: 523624
A; Accession: 523624
A; Residues: preliminary
A; Molecule type: DNA
A; Residues: 1-143 < OLE>
                                                                                                                                                                                                             two myeloma inulin-binding pro
Typecies: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: C92811; A02072
R;Johnson, N.; Slankard, J.; Paul, L.; Hood, L.
J. Immunol. 128, 302-307, 1982
A;Title: The complete V domain amino acid sequences of two myeloma inulin-bindin A;Reference number: A92811; MUID:82099361; PMID:6798111
A;Reference number: A92811; MUID:82099361; PMID:6798111
A;Residues: 1-115 < JOH>
C;Comment: This chain was isolated from a myeloma protein that binds inulin.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; Immunoglobulin homology C;Keywords: heterotetramer; Immunoglobulin homology ciMM>
F;22-98/Disulfide bonds: #status predicted
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Ig heavy chain V region - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 06.Jan-1995 #sequence_revision 06.Jan-1995 #text_change 20-Jun-2000
C; Accession: 538714
R; Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A; Reference number: 538713
A; Reference number: 538714
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-115 < CIM>A; Residues: 1-115 < CIM>A; CIM>CIM>C; Superfeances: EMBL: X76014; NID: 9416092; PIDN: CAA53601.1; PID: 91334076
C; Superfeanily: immunoglobulin v region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match

68.7%; Score 443.5; DB 2; Length 115;
Best Local Similarity 69.7%; Pred. No. 5.2e-34;
Matches 85; Conservative 14; Mismatches 16; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: November 27, 2002, 07:24:15 Job time: 35.7181 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 27, 2002, 05:39:34; Search time 17.5714 Seconds (without alignments) 290.334 Million cell updates/sec Run on:

US-09-893-615-87 646 1 EVMLVESGGGLVQPKGSLKL.....SGIDYAMDYWGQGTSLTVSS 123 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 Total number of hits satisfying chosen parameters:

112892 seqs, 41476328 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | P01801 mus | P01804 mus musculu | | enw | snw | P01797 mus musculu | P01805 rattus norv | P01798 mus musculu | P01800 mus musculu | P01794 mus musculu | P01783 mus musculu | P01790 mus musculu | P01768 homo sapien | mus | P01803 mus musculu | P01788 mus musculu | P01789 mus musculu | mus | mus | homo | บรกพ | P01792 mus musculu | | mus m | homo | P01769 homo sapien | homo | рошо | B mus m | PO1812 mus musculu | рошо | 767 homo | P01811 mus musculu |
|-----------|----------------|------------|--------------------|------------|------------|------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------|--------------------|--------------------|--------------------|------------|------------|------------|------------|--------------------|------------|------------|------------|--------------------|------------|------------|------------|--------------------|------------|------------|--------------------|
| SUMMARIES | ID | HV32_MOUSE | HV35_MOUSE | HV30_MOUSE | HV27_MOUSE | HV33_MOUSE | HV28_MOUSE | HV01_RAT | HV29_MOUSE | HV31_MOUSE | HV25_MOUSE | HV16_MOUSE | HV21_MOUSE | HV3G_HUMAN | HV18_MOUSE | HV34_MOUSE | HV19_MOUSE | HV20_MOUSE | HV22_MOUSE | HV26_MOUSE | HV3J_HUMAN | HV24_MOUSE | HV23_MOUSE | HV3T_HUMAN | HV17_MOUSE | HV3E_HUMAN | HV3H_HUMAN | HV3D_HUMAN | HV3K_HUMAN | HV38_MOUSE | HV42_MOUSE | HV3I_HUMAN | HV3F_HUMAN | HV41_MOUSE |
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| | Length | 11 | 111 | 113 | 113 | 115 | 113 | 142 | 113 | 113 | 123 | 136 | 122 | 122 | 123 | 113 | 123 | 122 | 123 | 144 | 121 | 123 | 123 | 116 | 117 | 120 | 122 | 115 | 126 | 119 | 117 | 119 | 115 | 117 |
| æ | Query Match | 0.69 | 0.89 | | 67.5 | | | | 65.9 | | | | | 63.5 | | | | | | 62.4 | | | | 6.09 | | - | | | | | | 58.4 | | |
| | Score | 4 | 439.5 | 438 | 436 | 436 | 430 | 427 | 426 | 422 | 421 | 416.5 | 411.5 | 410.5 | 407 | 406 | 4 | 405.5 | 405 | 403 | 399 | 398 | m : | 393.5 | 383 | വ | 385.5 | ന | 383.5 | ∞ . | 377 | 377 | 376 | 375 |
| | Result No. | - | 7 | ო | 4 | 'n | 9 | 7 | ω. | σ, | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 81 | 61 | 20 | 21 | 22 | 23 | 77 | 25 | 26 | 27 | 28 | 29 | 30 | 31 | 35 | 33 |

RESULT 2
HV35_MOUSE
ID HV35_MOUSE
AC PO1904
BD 1-15UL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

| homo sapien mus musculu mus musculu homo sapien mus musculu homo sapien homo sapien homo sapien homo sapien homo sapien | | n THAT | Gaps 1; | |
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| | tomi. | inulin | 8; NNYA 1111 | GTLV |
| P01764 P01810 P01810 P01762 P01763 P01773 P01777 | PRT; 115 AA. uence update) otation update) 06. Craniata; Vertebrata; Euteleostomi | s of two myeloma FROM A MYELOMA | Section 115 115 115 115 115 115 115 12810 MW; B67AD6638A121A5F CRC64; CRC64; | EVALDESGGGLVQFGGSMLSCVASGE IF SNIMMINWYRQSFENGLEWYAELRINSNINTATE STADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT |
| Į | PRT; 115 AA. uence update) otation update) 06. Craniata; Verte | | B67AD6638A121A5. Score 446; DB 1; Pred. No. 6.4e-41 ; Mismatches 1 SGFTFNNYAMWWRQAP | FAMYYC FAMYYC FGIYYC |
| HV3C HUMAN HV37_MOUSE HV40 MOUSE HV34_HUMAN HV36_MOUSE HV38_HUMAN HV56_MOUSE HV31_HUMAN HV31_HUMAN HV36_HUMAN HV36_HUMAN HV36_HUMAN | RT; 115 ence upda tation up 6. raniata; ciurognat | | 67AD6638A1 re 446; D d. No. 6.4 Mismatches TFNNYAMNWV | KTED |
| HV37, HV37, HV39, HV36, HV36, HV37, HV37, HV37, | D; PRT; Created) Last sequence u Last annotation egion J606. ordata; Craniati | ed-6798111; ., Paul L., amino acid 7(1982). S CHAIN WAS 9_MHC. 9_V. | SCON Prec 10; N | QMNNI |
| нансананана | ARD; , Created , Last se , Last an region J Chordata; | Med=679 J., Pau n aminn 07(1983) 15 CHAL 19_v. | 0 MV | MLYI |
| 1119 1119 1128 1128 1139 114 117 1119 1119 | RG. r, AR | жре он ни чою | 115 | RDDSQS : |
| 7.7.7.2 7.7.7.2 7.7.7.2 7.7.7 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 8.5 | STAN STAN (Rel. 0) (Rel. 0) (Rel. 1) (Rel. 1) (Rel. 1) (Rel. 1) (Rel. 2) (Rel. 3) (Rel. 4) (Rel. 4) (Rel. 4) (Rel. 4) (Rel. 5) (R | 9361, Slanka Slanka e V de etns." 128:30 NEOUS: ULIN. 1 IMCF RR00300 RR00300 RR00359 7; 19; | 115 AA; h Similarity 87; Conser MLVESGGGLVQ | SETIS SETIS |
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| 374 373.5 370.5 369.5 369.5 361.5 360.5 360.3 380.5 357.5 | MOUS 1; L-15 L-16 L-16 Vote | (1) SEQUENCE. MEDLINE-82099361; Pubbm Johnson N., Slankard J The complete V domain binding proteins."; J. Immunol. 128:302-30 - MISCELLANEOUS: THI. BINDS INULIN. PIR; C92811; AVMSO. HSSP; P01789; IMCP. InterPro; IPR003006; I InterPro; IPR003066; I InterPro; IPR00306; I INTERPRO; INTERPRO; I INTERPRO; I | E (1) ल (1) | |
| <pre></pre> | RESULT 1 1D HV32_MOUSE 1D PV32_ AC P0180 DT 21-JU DT 15-JU DF 15-JU DF 19 he OC EUKAT OC EUKAT | | NON_SEQUI | |
| | RES HVC DT DT DT DT OC OC | RN RXX RY RTT RTT RTT DDR DDR DDR DDR DDR FT | ES & & | 6 6 6 6 |
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Conservative
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P01802;
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HV33_MOUSE
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                                                                                                                        MEDLINE—81013937; PubMed=6251474;
MEDLINE—81013937; PubMed=6251474;
MEDLINE—81013937; PubMed=6251474;
MEDLINE—81013937; PubMed=6251474;
MEDLINE—81037; PubMed=625147;
MEDLINE—81037; PubMed=6251474;
ME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 ESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYATFYADS 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ESGGGLVQPGGSMKLSCVASGFTFSNYWMMWVRQSPEKGLEWVAEIRLKS-GYATHYAES 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE.
MEDLINE-77134726; PubMed-402936;
Vrana M., Rudikoff S., Potter M.;
"Heavy-chain variable-region sequence from an inulin-binding myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 VKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 VKGRFTISRDDSKSSVYLQMNNLRAEDTGIYYCTRPGVP-----DYWGQGTTLTVSS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HV30_MOUSE STANDARD; PRT; 113 AA.
P01799;
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Heavy chain V-III region ABE-47N.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
Ig heavy chain V-III region HPC76 (Fragment).
Was musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 68.0%; Score 439.5; DB 1; Length 111; 1 Similarity 72.9%; Pred. No. 3.1e-40; 86; Conservative 9; Mismatches 16; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 111 AA; 12304 MW; 0EDE98EC7348056A CRC64;
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Pred. No. 4.5e-40;
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70.2%;
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Best Local Similarity
Matches 86; Conserv
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                                                                         NCBI_TaxID-10090;
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HV30_MOUSE
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-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN.
PIR; A93818; ANWASH.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003156; Ig_V.
Pfam; PF00047; ig; 1.
SWART; SW00406; IGV; 1.
                                                                                                                                    61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
                                                                                                                                                              61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRKGASGIDYAMDYWGQGTSLT 120
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                                             EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                 Gaps
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Vrana M., Rudikoff S., Potter M.;
"Sequence variation among heavy chains from inulin-binding myeloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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18; indels
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                                                                                                                                                                                                                                                                                                                                     RESULT 4
HV27_MOUSE
ID HV22_MOUSE STANDARD; PRT; 113 AA.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1999 (Rel. 38, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG heavy chain V-III region A4.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
pheavy chain V-III region W3082.
Mus musculus (Mouse).
10; Mismatches
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Conservative
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Best Local Similarity
Matches 83; Conserv
   Best Local Similarity
Matches 84; Conserv
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                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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P01805;
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HV29_MOUSE
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-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS INULIN.
PIR; B93818; AVMS61.
HSPP: PO1810; ZFBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                        J. Immunol. 128:302-307(1982).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
                                                                                                                                                                                                                                                                                                                                                                             61 HYAESVKGRFTISRDDSKSSVYLRMNNLRPEDTGIYYCTTGFA------YWGQGTLVT 112
                                                                                                                                                                                                                                                                                                                                                                  FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRGASGIDYAMDYWGQGTSLT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIINE-78158406; PubMed-417344;
Vrana M., Rudikoff S., Potter M.;
"Sequence variation among heavy chains from inulin-binding myeloma
proteins.";
Eukaryota; Metazoa; Chordata; Craniata; Vertebrața; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                   two myeloma inuling
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Was musculus (Mouse).
Washaryota Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                          Length 115;
                                                                                                                                                                                                                                                                                              18; Indels
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115 115
115 AA; 12887 MW; 984517648C121C5A CRC64;
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                                                                      Johnson N., Slankard J., Paul L., Hood L.;
"The complete V domain amino acid sequences of
binding proteins.";
                                                                                                                                                                                                                                                                       67.5%; Score 436; DB 1;
69.1%; Pred. No. 7.6e-40;
iive 12; Mismatches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
12-JUL-1999 (Rel. 38, Last annotation update)
1g heavy chain V-III region U61.
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                                                            MEDLINE-82099361; Pubmed-6798111;
                                                                                                                                         PIR; D92811; AVMS82.
HSSP; P01810; 2FBJ.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                  Local Similarity 69.19 tes 85; Conservative
                                                                                                                                                                                       Pfam; PF00047; 1g; 1.
SMART; SM00406; 1Gv; 1.
Immunoglobulin V region.
DISULFID 22 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00047; 1g; 1. SMART; SM00406; IGv; 1. Immunoglobulin V region.
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113
113 AA;
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P01797;
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66.6%; Score 430; DB 1; Length 113;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig heavy chain V region IR2 precursor.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                               Gaps
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                                                                                                                                                         1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
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Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
"Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                                         .;
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-1- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN IGE-SECRETING IMMUNOCYTOMA THAT ARISES SPONTANEOUSLY IN LOU/C/WSL RATS.

PIR: A02075; EVRTR2.

HSSP: P01789; IMCP.

InterPro; IPR003006; Ig_MC.

InterPro; IPR003506; Ig_V.

Pfam: PF00047; ig; 1.

SMART; SM00406; IGv; 1.

Immunoglobulin V region; Signal.
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                                                     Indels
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3.3e-39;
ches 19;
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01, Last sequence update)
38, Last annotation update)
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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69.4%; Pred. No. 3.3e ive 10; Mismatches
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P01798;
21-JUL-1986 (
21-JUL-1986 (
15-JUL-1999 (
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Length 113;
              Query Match 65.3%; Score 422; DB 1; Best Local Similarity 68.6%; Pred. No. 2.3e-38; Matches 83; Conservative 10; Mismatches 20
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                              123 AA
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                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region HPCG14.
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P01794;
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HV16_MOUSE
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                                                                                                      Wrana M., Rudikoff S., Potter M.;

"Sequence variation among heavy chains from inulin-binding myeloma
"Sequence variation among heavy chains from inulin-binding myeloma
"The proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).

"In Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961(1978).

"In SCELLANBOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.

"IN PIR. C93818: AWSO9.

"RINES INULIN.

"IN INTERPROJ IPRO03596; Ig_W.

"IN SMART; SM00406; Ig_V.

"IN SMART; SM00406; IGv; 1.

"IN INDIALPER 113 113
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Rudikoff S., Potter M.;
*Inmunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment.";
J. Immunol. 127:191-194(1981).
--- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
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Ig heavy chain V-III region E109.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-OCT-1993 (Rel. 27, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 heavy chain V-III region T957.
Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                           65.9%; Score 426; DB 1; Length 113; 67.8%; Pred. No. 8.7e-39; ive 13; Mismatches 18; Indels
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                                                                                 SEQUENCE.
MEDLINE-78158406; PubMed-417344;
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BINDS INULIA.
PIR, A92810; AVMS57.
HSSP, P01810; 2FBJ.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_W.
Pfam; PF00047; ig; 1.
R SMART; SM00406; IGV; 1.
M Immunoglobulin V region.
2 98
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les 82; Conservative
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                                                      NCBI_TaxID-10090;
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P01800;
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HV31_MOUSE
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A Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
TigG antibodies to phosphorylcholine exhibit more diversity than their Igw counterparts.";
Their Igw counterparts.";
Auture 291:39-34(1981).
C -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WYELOMA PROTEIN THAT BINDS PHOSPHORYLCHOLINE.
DR RINDS PHOSPHORYLCHOLINE.
DR RINDS PHOSPHORYLCHOLINE.
DR RISP; PO1789; 1MCP.
InterPro; IPR003596; Ig_WHC.
DR InterPro; IPR003596; Ig_W.
DR Ffam: PF00047; 4g 1.
SMART; SMO0406; IGv; 1.
SMART; SMO0406; IGv; 1.
SMART; SMO0406; IGv; 1.
SWART; SMOULIN V region; Hybridoma.
SEQUENCE 123 AA; 13807 MW; A7584FB098B7785D CRC64;
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                                                   1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridue; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                 1 EVKLEESGGGLVQPGGSMKLSCVASGFTFSNYWMWWVRQSPEKGLEWVAEIRLKSHNYET
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01, Last sequence update)
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P01783;
21-JUL-1986 (Rel. 0]
21-JUL-1999 (Rel. 38
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(MOPC 511).";
Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
-!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHORYLCHOLINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-81054880; PubMed-6776528;
Robinson E.A., Appella E.;
"Complete amino acid sequence of a mouse immunoglobulin alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 heavy chain V-III region CAM.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location of a possible JH segment.";
Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF PATIENT WITH MACROGLOBULINEMIA.
PATIENT WITH MACROGLOBULINEMIA.
HSSP: PO1772; 2FB4.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR00475; 199; 1.
SWART; SW00406; IGy. 1.
Inmunoglobulin V region.
Ig heavy chain V region M511.
Ms musculus (Mouse).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYRROLIDONE CARBOXYLIC ACID.
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SEQUENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;
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122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;
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MEDLINE-81013859; Pubmed-6774332;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                     "Heavy chain variable region contribution to the NPb family of antibodies: somatic mutation evident in a gamma 2a variable region."; Cell 24:625-637(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
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Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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DN -> ND (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).
                                                                                                                                                                                                                                                                                MEDLINE-77100368; PubMed-401950;
Adetugbo K., Milstein C., Secher D.S.;
"Molecular analysis of spontaneous somatic mutants.";
Nature 265:299-304(1977).
   heavy chain V region MOPC 21 precursor (Fragment).
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01, Last sequence update)
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NON_TER 1 1 1 SIGNAL <1
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HSSP; P01772; ZFB4.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
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 Ig heavy cnain v ... Mus musculus (Mouse)
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136 AA;
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P01790:
21-JUL-1986 (Rel. 0)
21-JUL-1996 (Rel. 0)
15-JUL-1999 (Rel. 38
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MEDLINE-80199926; PubMed-6769593;
Early P., Huang H., Davis M., Calame K., Hood L.;
"An immunoglobulin heavy chain variable region gene is generated from three segments of DNA: VH, D and JH.";
Cell 19:981-992(1980).
                                                                                                                  61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVR-RGASGIDYAMDYWGQGTSL 119
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                                                                1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
Igg antibodies to phosphorylcholine exhibit more diversity than their IgM counterparts.";
Nature 291:29-34(1981).
-I. MISCELLANEOUS: ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.
-I. MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA AND
HYBRIDDMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.
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                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE (TEPC 15).
MEDLINE-76222762; PubMed-819932;
Rudikoff S., Potter M.;
Size difference among immunoglobulin heavy chains from phosphorylcholine-binding proteins.;
Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
                          Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.
Mus musculus (Mouse)
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63.5%; Score 410.5; DB 1; 64.5%; Pred. No. 4.3e-37;
                          23;
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Rudikoff S., Barstad P., Potter M., Hood L.;
Unpublished results, cited by:
Hood L., Campbell J.H., Elgin S.C.R.;
Annu. Rev. Genet. 9:305-353(1975).
                         18; Mismatches
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InterPro; 1PR003596; 1g_V.
Pfam; PF00047; 1g; 1.
SMART; SM00406; 1GV; 1.
Immunoglobulin V region; Hybridoma.
NON_TER 123 123
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HSSP; P01789; 1MCP.
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Rudikoff S., Potter M.; "Immunoglobulin heavy chains from anti-inulin myeloma proteins: "Immunoglobulin heavy chain joining segment."; J. Immunol. 127:191-194(1981).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT
                      1 EVKLVESGGGLVQPGGSLRLSCATSGFTFSDFYMEWVRQPPGKRLEWIAASRNKANDYTT
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 heavy chain V region AMPCI.
Mus musculus (Mouse).
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PIR, A02073; HYMSAM.
HSSP, P01789; 1MCP.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; 19_V.
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SMART; SM00406; IGv; 1.
Immunoglobulin V region.
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1: sp_archea:*
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3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_anammal:*
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Commission | | ID Description | 096BB9 | O8WU38 O8Wu38 homo sapten | Q9UL90 O9ul90 homo sapien | 09u191 homo | snm 6vgr80 . | Q9u171 homo | Q9u193 homo | | Q8wuk1 homo | Q9hcc1 homo | Q8tc77 homo | . 099ka4 mus | Q920e7 mus | Q9u184 homo | Q91wp5 mus r | 1000 |
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| | | Query Match Length DB | 597 | 573 | 113 | 118 | 469 | 121 | 116 | 494 | 613 | 112 | 471 | 487 | 119 | 122 | 479 | |
| | æ | Query | 6.99 | 66.3 | 65.2 | 64.9 | 64.9 | 64.6 | 64.4 | 64.0 | 64.0 | 63.7 | 63.5 | 63.4 | 62.7 | 62.6 | 62.4 | , |
| | | Score | 432 | 428.5 | 421 | 419.5 | 419.5 | 417 | 416 | 413.5 | 413.5 | 411.5 | 410.5 | 409.5 | 405 | 404.5 | 403 | 0 00 |
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| 402 62.2 131 4 09UL88 395.5 61.2 484 11 08VEAO 384.5 61.1 118 4 09UL72 380 58.8 486 11 09YS09 366 56.7 480 11 091XE1 356.5 55.2 437 11 09YRFO 356.5 55.2 437 11 09VRFO 356.5 55.2 437 11 09VRFO 336 52.0 484 11 099UR6 328.5 55.0 121 11 099UR6 328.5 50.9 121 11 099UR6 324 50.2 146 11 0924R4 324 50.2 146 11 0924R4 322.5 49.9 145 11 0924R4 321.5 49.8 143 11 0924R0 311.5 48.5 11 0924Q1 314.5 48.7 241 1 0924Q1 314.5 48.7 241 1 0924Q1 313.5 48.5 113 4 09UL94 313.5 48.5 113 4 09UL94 311.5 48.3 117 11 09QXFO | Q9u188 homo sapien Q8vea0 mus musculu Q9u172 homo sapien Q9u509 homo sapien Q9u509 homo sapien Q9uxel mus musculu Q9uxel mus musculu Q9up3 homo sapien Q9up3 homo sapien Q9up3 homo sapien Q9up3 homo sapien Q9up4 mus musculu Q9u44 mus musculu Q9u487 homo sapien Q9u487 homo sapien Q9u487 homo sapien Q9u487 homo sapien Q9u487 mus musculu Q9u447 mus musculu | nus nus nus nus nus nus nus nus nus |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Fragment).
Homo saplens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Young D.C.;
"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL: AF035024: AAD56260.1; -.
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                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC021276; AAH21276.1;
InterPro; IPR003599; 1g.
InterPro; IPR003599; 1g.
InterPro; IPR003596; Ig.AHC.
InterPro; IPR003596; Ig.AV.
Pfam; PF00047; 1g; 4.
SMART; SM00409; IGc; 1.
SMART; SM00406; IGC; 1.
SMART; SM00406; IGC; 1.
PROSITE: PS00290; IGC, 1.
PROSITE: PS00290; IGC, 1.
PHypothetical protein.
SEQUENCE 573 AA; 62967 MW; FD072344033AC530 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                             01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 63.0 kDa protein.
                                                                                      573 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003006; Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84; Conservative
                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                         NCBI_TaxID-9606
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                                                                                                                                                                                                                                                                                                                                                                 TISSUE-TONSIL;
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                                                                                                             Q8WU38;
                                                                                      08WU38
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                                         RESULT 2
Q8WU38
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                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                 1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
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                                                                                                                                                                                                                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                // coung U.C.;
// Myosin-reactive autoantibodies in rheumatic carditis and normal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
                                                                                                                                                                                  Length 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain.varlable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
NCBI_TaxID=9606;
                                                                                                                                                                                                                                  14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12843 MW; D0633949F2AC149D CRC64;
                                                                                                                                 113 AA; 12437 MW; ED57FDD19086D07F CRC64;
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Best Local Similarity 68.0%; Pred. No. 4.4e-36;
Matches 83; Conservative 15; Mismatches 19;
                                                                                                                                                                                65.2%; Score 421; DB 4; 66.7%; Pred. No. 2.9e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clin. Immunol. Immunopathol. 87:184-192(1998).
EMBL; AF035023; AAD56259.1; -.
HSSP; P01772; 2F84.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 AA.
                                                                                                                                                                                Query Match 65.2%; Score 421; DB Best Local Similarity 66.7%; Pred. No. 2.9e Matches 82; Conservative 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
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InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1. NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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NON_TER 118 1
SEQUENCE 118 AA;
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1 EVQLVESGGGVVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKGLFWVSLI--SGDGGST
                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                   Clin. Immunol. Immunopathol. EMBL; AF035021; AAD56257.1; -HSSP, P01772; 2FB4. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_V.
                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83; Conservative
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SM00406; IGv; 1.
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                                                                                                                                               PRELIMINARY;
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Best Local Similarity
Matches 83; Conserv
                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00047
                                                                 VSS 123
                                                                                       119 VSS 121
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| 115 SS 116
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NON_TER
SEQUENCE
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096к68;
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Q96K68
                                                                                                                          RESULT 7
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                  08R3V9;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 52.0 kba protein.
Mus musculus (Mouse).
Eukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo Sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myosin-reactive autoantibodies in rheumatic carditis and normal
                                                                                                                                                                                                                 DB 11; Length 469;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                               Ouery Match 64.9%; Score 419.5; DB 11; Length Best Local Similarity 65.9%; Pred. No. 2.5e-35; Matches 83; Conservative 14; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024405; AAH24405.1; -..
Hypothetical protein.
SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13154 MW; 2F045CCFA5D50736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64.6%; Score 417; DB 4;
65.9%; Pred. No. 8.2e-36;
iive 17; Mismatches 23.
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EMBL; AF035043; AAD56279.1; -.
HSSP; P01772; ZPB4.
Incerpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                   121 AA
          469 AA
          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81; Conservative
          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                             NCB1_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-9606;
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140 LVTVSA 145
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SEQUENCE
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62 YADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLTV 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 VQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISYDGSN--KY
                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Washaryota: Metazoa; Chordata: Craniata; Vertebrata: Euteleostom1;
Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Myosin-reactive autoantibodies in rheumatic carditis and normal
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-ELJ14473 fis, clone MAMMA1001080, highly similar to Homo
saplens SNC73 protein (SNC73) mRNA.
                                                                                                                                                                                                                                                                                                                                                                               Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64.4%; Score 416; DB 4; Length 116; 68.0%; Pred. No. 9.9e-36; ive 14; Mismatches 19; Indels
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 AA; 12434 MW; 0DA0348154DD6061 CRC64;
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PRELIMINARY;
                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                      112 AA;
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                                                                                                                                                                                               NCBI_TaxID=9606
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                                           111
137 VSS 139
                               121 VSS 123
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NON_TER
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Q9HCC1
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Q8TC77
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                  1909a1 T., Car T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Naqai K., Sugano S., Shiratori A., Sudo H., Mishikawa T., Naqai K., Sugano S., Shiratori A., Sudo H., Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Ninomiya K., Iwayanagi T., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AK027379; BAB55072.1.
                                                                                                                                                                                                                                                       61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASG-IDYAMDYWGQGTSL 119
                                                                                                                                                                                                                                                                   61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
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                                                                                                                                                                                                                 1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                            1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Pred, No. 1.5e-34;
Pred. no. 1.5e-34; Indels
                                                                                                                                                                                              22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC02040; AAH20240.1;
InterPro; IPR003599; Ig.
InterPro; IPR003597; Ig.cl.
InterPro; IPR003506; Ig.MHC.
InterPro; IPR003596; Ig.MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 67.3 kDa protein.
                                                                                                                                                                         64.0%; Score 413.5; DB 4 65.3%; Pred. No. 1.1e-34; ive 18; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19; Mismatches
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65.0%;
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           TISSUE-MAMMARY GLAND;
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Rest Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                            138 TVSS 141
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Q8WUK1;
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Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

An antibody fragment2A3 specific for native lysozyme: Isolaion from a synthetic phage display library and characterization.";

Thuman synthetic phage display library and characterization.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; ABG04915; BAB16829.1;

EMBL; ABG04915; BAB16829.1;

InterPro; IPR003506; Ig.

InterPro; IPR003506; Ig.

R InterPro; IPR003506; Ig.

R InterPro; IPR003506; Ig.

R SMART; SM00409; IG; 1.

SMART; SM00410; IG.11ke; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRKGASGIDYAMDYWGQGT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostom1;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databages.
EMBL; BC024289; AAH24289.1; ..
Hypothetical protein.
SEQUENCE 471 AA; 51791 MW; 388F7F4CF588660E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12243 MW; 24F1A45EC3B84788 CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 51.8 kba protein.
Homo sapiens (Human).
01-WAR-2001 (TrEMBLrel. 16, Created)
01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.7%; Score 411.5; DB 4; Best Local Similarity 67.5%; Pred. No. 2.8e-35; Matches 79; Conservative 17; Mismatches 14;
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                                                                                                      Single chain Fv (Fragment).
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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NON_TER
SEQUENCE
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Q9UL84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 SYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLRQLTSYWY-FDLWGRGTL 136
                                                                                         61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVR--RGASGIDYAMDYWGQGTS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                             Gaps
                                                          1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 EVQLVESGGGLVKPGGSLKLSCAASGFTFSSYAMSWVRQTPEKRLEWVATI-SDGGSY-T 77
                                                1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 487;
         Length 471;
       63.5%; Score 410.5; DB 4; Length llarity 66.4%; Pred. No. 2.1e-34; Conservative 20; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                      Strausberg R;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0040786.1;
HSPP; D0104072 2FBJ.
InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.
InterPro; IPR003609; Ig_like.
InterPro; IPR0036009; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;
                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical 5.2 6 kpa protein.
Hypothetical 6.2 6 kpa protein.
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(TrEMBLrel. 19, Last sequence update)
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SMART: SM00409; 1G; 3.
SMART; SM00406; 1G; 3.
SMART; SM00406; 1Gc1; 3.
SMART; SM00410; 1G_11ke; 1.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
                                                                                                                                                                                                           PRELIMINARY;
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                 Local Similarity
nes 83; Conserv
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137 VTVSS 141
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01-DEC-2001 (
01-DEC-2001 (
        Query Match
Best Local S
Matches 83
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Q920E7
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61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
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                                                                                                                                                                                                            Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.; "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                             (Fragment).
Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9UL84;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable region
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Pterin-mimicking anti-idiotope heavy chain variable region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21; Indels
                                                                                                                                                                                                                                                                                  122 AA; 13579 MW; 36054D41366545B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 62.7%; Score 405; DB 11;
Best Local Similarity 65.9%; Pred. No. 1.4e-34;
Matches 81; Conservative 17; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 404.5; DB 4
Pred. No. 1.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fetus.";
Clin. Immunol. Immunopathol. 87:184-192(1998)
EMBL; AF035030; AAD56266.1; -.
INSEP: POIT72: 2FB4.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_v.
Pfan; PF00047; ig; 1.
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1 Similarity 66.4%;
83; Conservative 15
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Best Local Similarity
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                                            61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVR--RGASGIDYAMDYWGQGTS 118
                                                              20 EVQLVESGGGLVKPGGSLKVSCAASGLTFSNYAMSWVRQSPEKRLEWVAAINSNGGN--T 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                     091WP5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 51.6 kDa protein.
Hypothetical 51.6 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             Straubberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC013656; AAH13656.1;
InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 4.
SNART; SM00408; IGc2; I.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
Hypothetical protein; Immunoglobulin domain.
SEQUENCE 479 AA; 51603 WW; ECB2D0877748584F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
62.4%; Score 403; DB 11;
Best Local Similarity 64.2%; Pred. No. 1.3e-33;
Matches 79; Conservative 18; Mismatches 18;
                                                                                                                                                                                                                        479 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: November 27, 2002, 07:22:53 Job time : 74.3861 secs
                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                             :||||
118 VTVSS 122
                                                                                                           119 LTVSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 VSS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               132 VSS 134
                                                                                                                                                                                                                        091WP5
                                                                                                                                                                                         RESULT 15
Q91WP5
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                              OM protein - protein search, using sw model
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November 27, 2002, 07:17:51; Search time 22.3205 Seconds (without alignments) 162.139 Million cell updates/sec Run on:

US-09-893-615-87 Title:

646 1 EVMLVESGGGLVQPKGSLKL.....SGIDYAMDYWGQGTSLTVSS 123 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_AA:* Database :

/cgn2_6/ptodata/1/laa/5A_COMB.pep:*
/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | | | Appl | | App11 | Appl | Appl | Appl | Appli | Appl | Appl | | 7 | | Appl | Appl | Appli | Appli | Appl | Appl | Appl | Appl | Appl | Appli | App11 | App11 | Appl | Appl | Appl |
|-----------|---------------|---|-----------|-----------|----------|----------------|------------------|----------|------------------|-------------------|-------------------|--------------------|----------|------------------|------------|----------------|-----------------|------------------|-------------------|------------------|------------------|------------|------------|------------|-------------|------------|------------------|--------------|----------|
| | 5 | | 36, | 7 | ~ | 18 | 18, | 24, | 7 | 38, | 63, | 178 | 28, | 26, | 10, | 38, | m | 9 | 24, | 70, | 93, | 70, | 93, | 4 | 4 | 4, | 35 | 15, | 15, |
| | Description | | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence |
| | D | | 03 | 02 | נט | 0) | U, | 0,1 | • | 0,1 | | 0, | 0,1 | U) | | 0,1 | , | J. | 01 | 0, | 0, | 0, | 0, | 0, | U 2 | 0, | u, | 0, | U) |
| CIES | | | 7-128-36 | 2-542-2 | 5-469-2 | 2-542-18 | US-08-765-469-18 | 7-128-24 | JS-08-483-749A-2 | US-09-025-769B-38 | US-09-025-769B-63 | US-09-025-769B-178 | 7-128-28 | US-08-767-128-26 | 3-749A-10 | 7-128-38 | US-09-069-821-3 | US-09-420-592A-6 | US-09-025-769B-24 | US-08-478-039-70 | US-08-478-039-93 | 5-349A-70 | 5-349A-93 | 1-373C-4 | 7-642B-4 | 5-206C-4 | US-08-983-607-32 | -392-338A-15 | 5-750-15 |
| SUMMAKIES | | | US-08-767 | US-08-442 | -08-76 | US-08-442-542- | -08-76 | -08-767 | -08-48 | -09-02 | -09-02 | -09-02 | -08-767 | -08-767 | US-08-483- | US-08-767-128- | 90-60- | -09-42(| -09-02 | -08-478 | -08-478 | US-08-476- | US-08-476- | US-07-934- | US-08-437-6 | US-08-146- | :-08-38 | US-08-39 | -09-166 |
| | q | | ns | Sn | SS | SO | S | ns | ns | Sn | ns | ns | S | S | a | ns | S | Sn | S | SO | S | Sn | S | S | S | ns | ns | S | us |
| | DB | | ٣ | - | m | - | m | ო | m | 4 | 4 | 4 | m | c | m | m | 4 | 4 | 4 | - | - | - | - | ~ | m | 4 | 4 | ~ | m |
| | Length DB | | 115 | 119 | 119 | | | | 122 | 120 | 120 | 281 | 120 | 119 | 114 | 124 | 263 | 283 | 117 | 130 | 130 | 130 | 130 | 120 | 120 | 120 | 140 | 250 | 250 |
| | Query | : | 5.9 | 0 | 0. | 0.5 | 0.0 | ₹. | 1.6 | ۳. | 1.3 | 1.3 | 70.4 | 0. | 8.8 | 8. | 8. | 68.8 | | 7. | .7 | .7 | 68.7 | ۳. ع | 68.3 | 8.3 | ۳. س | 8.3 | 8.3 |
| æ | Ouery | - | 80 | 8 | 8 | æ | æ | 8 | 7 | 7 | 7 | 7 | 7 | 9 | 8 | 3 | 39 | 39 | 3 | 8 | ö | ₩ | <u>~</u> | 9 | <u> </u> | 3 | <u>ت</u> | <u> </u> | <u>ن</u> |
| | Score | | 555 | 549 | 549 | 549 | 549 | 532 | 462.5 | 460.5 | 460.5 | 460.5 | 454.5 | 4 | 444.5 | 444.5 | 444.5 | 444.5 | 444 | 443.5 | 443.5 | 443.5 | 443.5 | 441.5 | 441.5 | 441.5 | 441.5 | 441.5 | 441.5 |
| | Result No. | 1 | - | 7 | m | 4 | S | 9 | 7 | 80 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 |

INFORMATION FOR SEQ ID NO: 36:

| Appl Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl | Appl |
|--------------------------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|------------------|------------------|------------------|-------------------|------------------|------------------|
| 15, | 15, | 17, | 17, | 17, | 17, | 17, | 14, | 23, | 14, | 23, | 23, | 23, | 23, | 13, | 13, | 13, |
| Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Sequence | Seguence | Sequence | Seguence | Sequence | Sequence | Sequence |
| US-09-166-093-15 US-09-172-019-15 | US-09-166-094-15 | US-08-392-338A-17 | US-09-166-750-17 | US-09-166-093-17 | US-09-172-019-17 | US-09-166-094-17 | US-08-224-591-14 | US-08-392-338A-23 | US-08-926-789-14 | US-09-166-750-23 | US-09-166-093-23 | US-09-172-019-23 | US-09-166-094-23 | US-08-392-338A-13 | US-09-166-750-13 | US-09-166-093-13 |
| ოო | ო | ~ | ٣ | 3 | m | ٣ | 7 | 7 | 7 | ٣ | m | ო | ٣ | 7 | ٣ | m |
| 250 250 | 250 | 253 | 253 | 253 | 253 | 253 | 242 | 242 | 242 | 242 | 242 | 242 | 242 | 244 | 244 | 244 |
| 68.3 68.3 | 68.3 | 68.3 | 68.3 | 68.3 | 68.3 | 68.3 | 67.7 | 67.7 | 67.7 | 67.7 | 67.7 | 67.7 | 67.7 | 67.7 | 67.7 | 67.7 |
| 441.5 | 441.5 | 441.5 | 441.5 | 441.5 | 441.5 | 441.5 | 437.5 | 437.5 | 437.5 | 437.5 | 437.5 | 437.5 | 437.5 | 437.5 | 437.5 | 437.5 |
| 28 29 | 30 | 31 | 32 | 33 | 34 | 32 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |
| | | | | | | | | | | | | | | | | |

ALIGNMENTS

```
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
Sequence 36, Application US/08767128
Patent No. 6111079
GENERAL INFORMATION WILLE, DWANE E.
APPLICANT: UOPEZ, OSVALDO
APPLICANT: GOEBEL, PETER JOSEPH
APPLICANT: GOEBEL, PETER JOSEPH
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: UOLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/51,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILLIG DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 612/371-5278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 612/332-9081
TELEX:
                                                                                                                                                                                                                                                                                                                                                           STATE: MN
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RESULT 3
US-08-765-469-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
Query Match
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                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08442542

Patent No. 566600

GENERAL INFORMATION:

APPLICANT: Carcai, Nadine B.

TITLE OF INVENTION: Antibodies which Bind to Insect Gut

TITLE OF INVENTION: Proteins and their Use

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Clba-Geigy Corporation

STREET: 7 Skyline Drive
                                                                                                                                                                             Length 115;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,542
FILING DATE: 16 MAY-1995
CLASSIFICATION 530
PRIOR APPLICATION 1994
ATYONEY/AGENT INFORMATION:
NAME: 28-JUN-1994
ATYONEY/AGENT INFORMATION:
NAME: SPILILI, W MULTRAY
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION INFORMATION:
TELEPRAK: 919-541-8689
TELEFRAK: 919-541-8689
                                                                                                                                                                 ; DB 3; Len
. 1.6e-49;
5;
                                                                                                                                                                             Score 555; DB Pred. No. 1.6e-2; Mismatches
                                                                                                                                                                             85.9%;
87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 amino acids
               : 115 amino acids
amino acid
                                                                                                                                                                                                          Matches 108; Conservative
                                                                                                                  FRAGMENT TYPE: internal ORIGINAL SOURCE:
 SEQUENCE CHARACTERISTICS
                                             single
                                                                       MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                         linear
                                                                                                                                                                             Query Match
Best Local Similarity
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                                          STRANDEDNESS:
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                                                        TOPOLOGY:
                                                                                                       ANTI-SENSE:
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               LENGTH:
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                                                                                                                                                61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDY-AMDYWGQGTSL 119
                                                                                                                                                                   1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                       Gaps
                                                                        1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                            .
9
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Length 119;
                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08765469
Patent No. 6069301
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine B.
APPLICANT: Koziel, Michael G.
ATILE OF INVENTION: Antibodies which Bind to Insert Gut TITLE OF INVENTION: Proteins and their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 549; DB 3;
Pred. No. 6.8e-49;
5; Mismatches 6
 85.0%; Score 549; DB 1;
86.3%; Pred. No. 6.8e-49;
                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Spruill, W. Murray
REGISTATION UNBER: 32,943
REFERENCE/DOCKET NUMBER: CGC TELECOMMUNICATION INFORMATION:
TELEFAN: 919-541-8615
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85.0%;
86.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/267
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 85.0
Best Local Similarity 86.3
Matches 107; Conservative
                      Best Local Similarity 86.3
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                        120 TVSS 123
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1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3: Merchant, Gould, Smith, Edell, Welter & Schmidt 3100 No. 6111079west Center, 90 South Seventh St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
  Antibodies which Bind to Insect Gut
Proteins and their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 549; DB 3;
Pred. No. 4.3e-48;
5; Mismatches 6
TITLE OF INVENTION: Antibodies which
TITLE OF INVENTION: Proteins and the
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGC 1750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 24, Application US/08767128 Patent No. 6111079 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/267,641
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFRENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 85.0%;
Best Local Similarity 86.3%;
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 599 amino acids
TYPE: amino acid
                                                                                                  STREET: 7 Skyline Drive
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-765-469-18
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minneapolis
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                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 QVKLQESGGGLVQPKGSLKLSCAASGFTFNNFAMWWYRQAPGKGLEWVARIRSKSNNYAT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 SYGDSVKDRFTVSRDDSQSMFYLQMNNLKTEDTAMYXCVR-----VVYGAMDYWGQGTSV 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDY-AMDYWGQGTSL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Carozai, Machael G.

APPLICANT: Carozai, Michael G.

TITLE OF INVENTION: Antibodies which Bind to Insect Gut

TITLE OF INVENTION: Proteins and their Use

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Clba-Geigy Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 85.0%; Score 549; DB 1; Best Local Similarity 86.3%; Pred. No. 4.3e-48; Matches 107; Conservative 5; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/442,542
FILING DATE: 16-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/267,641
FILING DATE: 28-JUN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGC 1750
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Patent No. 6069301
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine B.
APPLICANT: Koziel, Michael G.
                                                                                                                                           Sequence 18, Application US/08442542 Patent No. 5686600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REPRENCE/DOCKET NUMBER: CGC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 599 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                        116 TVSS 119
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120 TVSS 123
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US-08-765-469-18
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                                                                                                                      US-08-442-542-18
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61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRKGASGIDYAMDYWGQGTSLT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 122;
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COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    MEDIUM TYPE: Floppy disk
    COMPUTER: DE-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
    CURRENT APPLICATION DATA:
    APPLICATION UNMBER: US/09/025,769B
    FILING DATE: 18-FEB-1998
    PRIOR APPLICATION NUMBER: EP 95 11 3021.0
    FILING DATE: 18-AUG-1995
    ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      c/o Fish & Neave
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Patent No. 6300064

GENERAL INFORMATION:
APPLICANT: Raappik, Achim
APPLICANT: Ilaq, Vic
APPLICANT: Ilaq, Vic
APPLICANT: Pluck Noroney, Simon
APPLICANT: Pluckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
UNMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.6%; Score 462.5; DB 3 Best Local Similarity 73.2%; Pred. No. 4.4e-40; Matches 90; Conservative 10; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: James F. Haley, Jr., Esq. STREET: 1251 Avenue of the Americas CITY: New York STATE: New York
                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0508.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   James F. Haley, Jr., Esq.
                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-483-749A-2
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US-09-025-769B-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 VKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRFA-----YWAQGTLVTVSA 110
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Patent No. 6054561
GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
CITY: EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.4%; Score 532; DB 3; Length 110; Best Local Similarity 87.3%; Pred. No. 3.3e-47; Matches 103; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                           CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
FILING DATE: 06-JUN-1995
FILING DATE: 05-JUN-1995
ATTONNEY, AGENT INFORMATION:
ANALY: CAGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/331-5278
TELEFAX: 612/332-9081
               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 110 amino acida TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             internal
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COMPUTER READABLE FORM:
             COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                   Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TBM PC Compatible
COMPUTER: TBM PC Compatible
COPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-FUR 1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., ESG.
NAME: James F. Haley, Jr., ESG.
NAME: James F. Haley, Jr., MORPHO/5
                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: James F. Haley, Jr., Esq. c/o Fish \kappa Neave 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 178, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Roappik, Achim
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Plackthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                DB 4;
                                                                              71.3%; Score 460.5; DB 4 72.4%; Pred. No. 6.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 460.5; DB 4
; Pred. No. 1.8e-39;
14; Mismatches 17
                                                                            Query Match
71.3%; Score 460.5; Best Local Similarity 72.4%; Pred. No. 6.9e Matches 89; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.3%;
72.4%;
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(212)596-9090
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Best Local Similarity 72.49
Matches 89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (212)596-909
INFORMATION FOR SEQ ID NO:
                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                       US-09-025-769B-63
                                                                                                                                                                                                                                                                                                                     121 VSS 123
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                              1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                                                              Length 120;
                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Knappik, Achim
APPLICANT: Rose, Peter
APPLICANT: 11ag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
                                                                                                                                                                                                                                                                            71.3%; Score 460.5; DB 4
72.4%; Pred. No. 6.9e-40;
                                                                                                                                                                                                                                                                                                                     14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-A0G-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/025,769B FILING DATE: 18-FEB-1998
                    MORPHO/5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 63, Application US/09025769B Patent No. 6300064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
REGISTRATION NUMBER: 27,794
                  REFERENCE/DOCKET NUMBER: MC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9090
TELEFAX: (212)596-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 63: SEQUENCE CHARACTERISTICS:
                                                                                                                                      LENGTH: 120 amino acids TYPE: amino acid
                                                                        TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (212)596-9090
                                                                                                                                                                                                                                                                                                Best Local Similarity 72.49
Matches 89; Conservative
                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
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: New York
RY: USA
                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                      US-09-025-769B-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 VSS 123
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US-09-025-769B-63
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                                                                                                                                                            TYPE:
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                                       26 EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGG--ST 83
                                                                                                                                                                                                                                               US-08-767-128-28

Sequence 28, Application US/08767128

Sequence 28, Application US/08767128

Sequence 28, Application US/08767128

Sequence 28, Application US/08767128

GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
APPLICANT: GOEBEL, PETER JOSEPH
APPLICANT: GOEBEL GOEBEL
STREET: 3100 No. 6111079west Center, 90 South Seventh St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
RROR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
FILING DATE: 10-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Carter, Charles G.
REGISTATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: FSALSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 120 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-767-128-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                             121 VSS 123
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                                                                                                                          Gaps
                                                                                                  1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
         Length 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSYALDO
APPLICANT: MURRAY PETER JOSEPH
APPLICANT: GOEBEL, PETER
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: UCCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
         70.4%; Score 454.5; DB 3; 70.7%; Pred. No. 2.8e-39; ive 11; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA.
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION NUMBER:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
APPLICATION NUMBER: 08/462,798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 8648.49USF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOCTWARE: FRASLSEQ VERSION 1.5
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-767-128-26; Sequence 26, Application US/08767128; Patent No. 6111079; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35,093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
Query Match
Best Local Similarity 70.7%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Carter, Charles G
REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 amino acids
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SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3100 No. (CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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61 HYAESVKGRFTASRDDSKSSIYLQMNNLRTEDTGIYFCT-----FWDYWGRGTTLT 111
                                                                                                                                                                                                                                                                  APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: MAICHART, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8648.49USF1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
CSOFTWARE: FASKED VERSION 1.5
CSOFTWARENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
                                                                                                                                                                                      Sequence 38, Application US/08767128 Patent No. 6111079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35,093
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                     DWANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Carter, Charles G
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 124 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Minneapolis
                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: WYLIE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FRAGMENT TYPE: 1
; ORIGINAL SOURCE: US-08-767-128-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55402
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                                                                            112 VSS 114
                                           121 VSS 123
                                                                                                                                                                   US-08-767-128-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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                                                                                                                                                                                                                                                                                                                  61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
                                                                                                                                                                                                                                                                                            61 FYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRRGASGIDYAMDYWGQGTSLT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Gaps
                                                                                                                                                                                                                               9; Gaps
                                                                                                                                                                                                            1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVRQAPGKGLEWVARIRSKSNNYAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MANIGEN BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
NUMBER OF SEQUENCES: 33
CORRESPONDENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
CITY: EMERYVILLE
STATE: CA
COUNTRY: USA
ZIP: 94662-8097
COMPUTER: IBM PC COMPALIBLE
COMPUTER: FLOPPY disk
COMPUTER: FLOPPY disk
COMPUTER: PACABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PACABLE FORM:
MEDIUM TYPE: PLOPPY disk
COMPUTER: PACABLE FORM:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 114;
                                                                                                                           DB 3; Length 119;
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                                                                                                                       Ouery Match 69.0%; Score 446; DB 3; Length 11 Best Local Similarity 70.7%; Pred. No. 2e-38; Matches 87; Conservative 12; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.8%; Score 444.5; DB 3; 69.1%; Pred. No. 2.8e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 10, Application US/08483749A Patent No. 6054561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INPORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/CDCKET NUMBER: 0508
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 69.18
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: RING, DAVID B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS LENGTH: 114 amino acio
                                         internal
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                   ; ANTI-SENSE: NO
; FRAGMENT TYPE: 1
; ORIGINAL SOURCE:
US-08-767-128-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE:
US-08-483-749A-10
HYPOTHETICAL:
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Gaps

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Sequence 3, Application US/09069821

Patent No. 632332

GENERAL INFORMATION:
APPLICANT: WANG, MACLIANG
APPLICANT: WHICK, MOBERT
APPLICANT: WHICK, MOBERT
APPLICANT: LEE, LIHSYNG S.
ITILE OF INVENTION: CAPABLE OF GLYCOSYLATION, PRODUCTION AND USES THEREOF
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STRRET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2,
                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 30-APR-1998
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 60/067,341

FILING DATE: 02-DEC-1997

PRIOR APPLICATION NUMBER: US 60/063,074

FILING DATE: 27-0CT-1997

FILING DATE: 27-0CT-1997

PRIOR APPLICATION NUMBER: US 60/050,472

FILING DATE: 33-JUN-1997

APPLICATION NUMBER: US 60/044,449

FILING DATE: 30-ARR-1997

APPLICATION NUMBER: US 60/044,449

FILING DATE: 30-ARR-1997

ATTORNEY/AGENT INFORMATION:

NAME: KIM, JUDITH U:

RECISTRATION NUMBER: 40,679

REFERENCE/DOCKET NUMBER: 0977.2280003

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)371-2560

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 263 amino acids
amino acid
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not relevant
E: peptide
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TOPOLOGY: not
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20002
                                                                                                                                                                      120 TVSS 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: DC
                                                                                                                                                                                                                                                                            RESULT 15
US-09-069-821-3
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        Qy
        1 EVMLVESGGGLVQPKGSLKLSCAASGFTFNNYAMNWVQAPGKGLEWVARIRSKSNNYAT 60

        Db
        130 EVQLVESGGGLVQPKGSLKLSCAASGFTFSSYAMSWYRQAPGKGLEWVSVISGKTDGGST 189

        Qy
        61 FYADSVKDRFTISRDSQSMLYLQWNNLKTEDTAMYYCVRRGASGID-----YAMDY 112

        Db
        190 YYADSVKGRFTISRDNSKNTLYLQMNNLKTEDTAMYYCVRRGASGID-----YAMDY 112

        Cy
        113 WGGGTSLTVSS 123

        Db
        249 WGGTSLTVSS 123

        Db
        249 WGGTLVTVSS 259

        Search completed: November 27, 2002, 07:25:12

        Job time: 24.3205 secs
```

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

OM nucleic - nucleic search, using sw model

| | | 90 | |
|--|----------------------|-----------------------------------|--|
| November 27, 2002, 03:36:38; Search time 1460.96 Seconds | (without alignments) | 7350.598 Million cell updates/sec | |
| 002, 03 | | | |
| 27, 2 | | | |
| November : | | | |
| Run on: | | | |

| 7350.598 Million cell updates/sec Title: US-09-893-615-86 Perfect score: 369 Sequence: 1 GAAGTGATGCTGGAGTC |
|--|
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2054640 seqs, 14551402878 residues Gapop 10.0 , Gapext 1.0 Searched:

4109280 Fotal number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Gen Embl:

| | • | | | | | | | | | | | |
|-----------|------------|-------------|------------|--------|--------|---|------------|----|--------|-------------|--------------|-----|
| Genemb1:* | 1: gb_ba:* | 2: gb_htg:* | 3: gb_in:* | ą g | q b | ď | 7: gb_ph:* | qb | q 6 | 10: gb_ro:* | 11: gb_sts:* | 10. |
| tabase : | | | | | | | | | | | | |

| gb_sy:* | *:un_db | gb_vi:* | em_ba: | em_fun:* | em_hum: * | em_in:* | em_mu:* | em_om: * | em_or: * | em_ov:* | em_pat: * | em_ph: * | em_p1:* | em_ro:* | em_sts:* | em_un: | 4. 4 |
|---------|---------|---------|--------|----------|-----------|---------|---------|----------|----------|---------|-----------|----------|---------|---------|----------|--------|------|
| 12: | 13: | 14: | 15: | 16: | 17: | 18: | 19: | 50: | 21: | 22: | 23: | 24: | 25: | 56: | 27: | 28: | . 90 |

em_vi:* em_htg_hum:* em_htg_inv:*

em_htg_other: *
em_htg_mus: *
em_htg_pln: *
em_htg_rod: *

em_htg_mam:*
em_htg_vrt:*
em_sy:*
em_htgo_hum:*
em_htgo_nus:*
em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| 1 | 2 | 5 | r |) • | | |
|---------------|-------|-------|--------------------------|--------|------------|--------------------|
| | | ď | | | SUMMARIES | |
| Result No. | Score | Query | Query Match Length DB | DB | ID | Description . |
| 7 | 309.8 | 84.0 | 370 | 101 | 865980 | S65980 IQ VH193020 |
| 7 | 305 | 82.7 | 366 | 10 | MUSIGH339A | L30140 Mus Musculu |
| m | 304 | 82.4 | 475 | 10 | MUSIGHAAAC | |
| 4 | 303.4 | 82.2 | 499 | 10 | MUSIGHAAAB | M60021 Mouse Ig he |
| 2 | 301 | 81.6 | 443 | 10 | MUSIGHXS | M21469 Mouse Ig un |
| 9 | 301 | 81.6 | 444 | 10 | MMIGHRF2 | X16801 Mouse MRL-R |
| 7 | 300.4 | 81.4 | 357 | 9 | 173737 | I73737 Sequence 1 |
| 80 | 300.4 | 81.4 | 1797 | 9 | 173745 | I73745 Sequence 17 |
| σ | 298.6 | 80.9 | 366 | 10 | AF178591 | AF178591 Mus muscu |
| 10 | 297 | 80.5 | 366 | 10 | AF178595 | AF178595 Mus muscu |
| 11 | 297 | 80.5 | 366 | 10 | AF178596 | AF178596 Mus muscu |
| 12 | 291 | 78.9 | 408 | 10 | AF045483 | AF045483 Mus muscu |
| 13 | 289.6 | 78.5 | 366 | 10 | MUSIGH125A | L31512 Mus musculu |
| 14 | 288.8 | 78.3 | 360 | 10 | MUSIHCVRA | D50376 Mouse mRNA |
| 15 | 288.6 | 78.2 | 345 | 9 | AR108686 | AR108686 Sequence |
| 16 | 287.8 | 78.0 | 351 | 10 | AF006586 | AF006586 Mus muscu |
| 17 | 286.2 | 77.6 | 663 | 10 | AF064445 | AF064445 Mus muscu |
| 18 | 285.8 | 77.5 | 474 | 10 | MUSIGKCLT | M20829 Mouse IgG2a |
| 19 | 284.4 | 77.1 | 330 | 9 | AR108680 | AR108680 Sequence |
| 20 | 283.8 | 76.9 | 375 | 9 | AX025327 | AX025327 Sequence |
| 21 | 283.4 | 76.8 | 663 | 10 | AF064443 | AF064443 Mus muscu |
| c 22 | 283.4 | 76.8 | 185591 | 7 | AC073561 | AC073561 Mus muscu |

AC073561 MUS MUSCU
M59948 MOUSE IG aC
AF468835 MUS MUSCU
AF066835 MUS MUSCU
AC10669 MUS MUSCU
AC11869 MUS MUSCU
S63182 IG VH-ant.1
AF31939 MUS MUSCU
AC90843 MUS MUSCU
AC75546 MUS MUSCU
AC75546 MUS MUSCU
AC75546 MUS MUSCU
AC7661 AF1fffclal
C22093 M.domesticu
AX208067 Sequence
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AX208067 Sequence AF321939 MMIGGIHV MDIGMVAR AC090843 MUSIGHACT MMU55546 MMU55545 AF064442 AF064444 AX208064 S72511 MMU55544 360 202704 282.4 282.2 282.2 280.6 279.4 279.2 279.2 279.2 O U

ALIGNMENTS

| S65980 | | | | | | | |
|------------|------------|--|----------|------------|-------------|-----------------|--|
| LOCUS | S65980 | | 370 bp | mRNA | mRNA linear | ROD 24-NOV-1993 | |
| DEFINITION | Ig VH1930; | DEFINITION IG VH193020-anti-insulin 193020 monoclonal antibody heavy chain | 193020 m | onoclonal. | antibody | heavy chain | |
| | variable | region [mice, NO | D spleen | and myeld | oma cells, | nonobese | |
| | diabetic, | diabetic, mRNA Partial, 370 nt]. | 70 nt]. | | | | |
| ACCESSION | 865980 | | | | | | |
| VERSION | S65980.1 | S65980.1 GI:425687 | | | | | |

RESULT 1

| | - (DI D) |
|-----------|---------------------------------------|
| ACCESSION | 865980 |
| VERSION | S65980.1 GI:425687 |
| KEYWORDS | |
| SOURCE | Mus sp. nonobese diabetic NOD spleen |
| ORGANISM | Mus sp. |
| | Eukaryota; Metazoa; Chordata; Craniat |
| | Mammalia; Eutheria; Rodentia; Sciurog |
| | |

and myeloma cells.

ta; Vertebrata; Euteleostomi; gnathi; Muridae; Murinae; Mus.

1 (bases 1 to 370) Pleau,J.M., Marche,P.N., Serrano,M.P., Boitard,C. and Bach,J.F.

REFERENCE AUTHORS

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VERSION
KEYWORDS
SOURCE
ORGANISM
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LOCUS
                                           ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361
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                                                                                REFERENCE
                                                                                            AUTHORS
                                                                                                                                             JOURNAL
                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                              CDS
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                                                                                                                                                                                              /gene="Ig VH193020"
/note="anti-insulin 193020 monoclonal antibody heavy chain
variable region"
                                                                                                                                                                                                                                                                                             /product="anti-insulin 193020 monoclonal antibody heavy chain variable region"
/protein_id="AAB28466.1"
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                                                                            GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 138351] from the original journal article. This sequence comes from Fig. 1a.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 370;
Evidence for antigen driven selection in two monocle auto-antibodies derived from nonobese diabetic mice Mol. Immunol. 30 (14), 1257-1264 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 309.8; DB 10; Length
Pred. No. 8.4e-86;
0; Mismatches 37; Indels
                                                                                                                                                                                                                                                        /gene="Ig VH193020"
/note="This sequence comes from Fig. la"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                              89 t
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L30140
L30140 GI:466280
V region; immunoglobulin heavy chain.
                                                                                                                                                  /db_xref="taxon:10095"
1. 370
/partial
                                                                                                                                                                                                                                                                                                                                                                                              97 9
                                                                                                                                 1. .370 /organism="Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.0%;
Matches 332; Conservative 0
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MUSIGH339A
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VERSION
KEYWORDS
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/product-"immunoglobulin heavy chain v region"
/protein_id-"AAA37931.1"
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/translation-"EVOLVETGGGLVQPKGSLKI.SCAASGFTFNTNVMSWVRQAPGKG
LGWYARIRSKSNNFGTYTABSVKDRFTISRDBSQSMLYLQMNNLKTEDTAMYYCVRHL
GGWDYAMDYWGQGTYVVSS"
76 c 99 9 91 t
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MOUSE Ig heavy chain mRNA V-D-J region, 5' end.
M60022
M60022.1 GI:194550
C-region; D-region; V-region; immunoglobulin heavy chain.
Mouse (strain C57BL/6) spleen cell hybridoma 222, cDNA to mRNA.
MUSIGHAACOLUB
                                                            Vertebrata; Euteleostomi;
hi; Muridae; Murinae; Mus
                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostor
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1
1 (bases 1 to 366)
Casadevall.A., Deshaw,M., Fan,M., Dromer,F., Kozel,T.R. and
Pirofski,L.-A.
Molecular and idiotypic analysis of antibodies to Cryptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
181 TATTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAGAGTATG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 305; DB 10;
Pred. No. 2.7e-84;
); Mismatches 30;
                                                                                                                                                                                                                                                                                                                 /sub_species="domesticus"
/db_xref="taxon:10090"
/cell_line="339"
/cell_type="B-cell"
                                                                                                                                                                                                                            Location/Qualiflers
1. 366
/organism="Mus musculus"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="hybridoma"
<1. .>36
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 82.7%;
Best Local Similarity 91.1%;
Matches 336; Conservative
                                                                                                                                                                                                          Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neoformans
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ROD 29-OCT-1994

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/codon_start=1
/product="immunoglobulin heavy chain"
/product="immunoglobulin heavy chain"
/protecin_id="An51055.1"
/db_xref="G1:194549"
/db_xref="G1:194549
                                                                                                                                                                                                                                 C-region; D-region; J-region; V-region; immunoglobulin heavy chain.
Mouse (strain C57BL/6) spleen cell hybridoma 244, cDNA to mRNA.
Mus musculus
                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 499)
Brigdoo,M. M. and Stollar,B.D.
Brigdoo,M. M. and Stollar,B.D.
Two induced anti.2-DNA monoclonal antibodies use VH gene segments related to those of anti-DNA autoantibodies
J. Immunol. 146 (6), 2005-2009 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATTATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 499;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product="immunoglobulin heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                            MUSIGHAAAAB 499 bp mRNA
Mouse Ig heavy chain mRNA V-D-J region, 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 303.4; DB 10,
Pred, No. 8.6e-84;
0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="chromosome 12"
/cell_line="hybridoma 244"
/tissue_type="liver"
/dev.stage="fetus"
1. 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .499
/organism="Mus muscu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.2%;
90.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="IgH"
77. .499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77. .133
/gene="IgH"
134. .499
/partial
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/gene="IgH"
434. .448
/gene="IgH"
449. .499
/gene="IgH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="IgH"
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                                                                                                                                                                                                              M60021.1 GI:194548
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Matches 335; Conserv
                          475
    468 TCTCCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
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                                                                                                                                                                  DEFINITION
                                                                                                                    MUSIGHAAAB
                                                                                                                                                                                                                                                                               ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MLLGLKWVFFVVFYQGVHCKVQLVESGGGLVQPKGSLKLSCAAS
GFNFNTYAMNWVRQAPGKGLEWVARIRSKSNNYATYYADSMKDRFTISRDDSENMLYL
OMINLKAEDTAMYYCVRQAYSNYGAMDYWGQGISVTVSS"
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                   l (bases 1 to 475)
Brigido, M.M. and Stollar, B.D.
Two induced anti-2-DAM monoclonal antibodies
related to those of anti-DAM autoantibodies
91170743
1900879
  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                291 ATTATGCCGATTCAATGAAAGACAGATTCACCATCTCCAGAGATGATTCAGAAAACATGC 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 CATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 CAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATTATGCAACAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAGAC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 TTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AAGTGATGCTGGTGGAGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCT
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/partial
/gene="IgH"
/product="immunoglobulin heavy chain"
110. .409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="immunoglobulin heavy chain"
/protein_id="AAA51056.1"
/db_xref="GI:194551"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 304; DB 10;
Pred. No. 5.5e-84;
0; Mismatches 30;
                                                                                                                                                                                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
/map="chromosome 12"
/cell_line="hybridoma 222"
Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Rodentia;
                                                                                                                                                                                                                                                                                                                                              /tissue_type="liver"
/dev_stage="fetus"
1. .475
                                                                                                                                                                                                           Location/Qualifiers
1. .475
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                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="19H"
53. .475
/partial
/gene="1gH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110. .409
/gene="IgH"
410. .424
/gene="IgH"
425. .475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="IgH"
110. .475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 82.4%;
Best Local Similarity 91.0%;
Matches 335; Conservative
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/gene="Igh"
91 c
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                                                                                                                                     JOURNAL
MEDLINE
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                                                                   AUTHORS
TITLE
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255 TATTATGCCGATTCAGTGAAAGACAGATTCACCATCTCCAGAGATGATTCACAAAGCATG 314
                                                                             /note="
                                                                                                                                                                                                                                                                                                  Mus musculus.
Mus musculus
                                                                                                                                            GICTCCTCA 443
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Best Local Similarity
Matches 333; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2887512
MRL-RF24 }
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                                                                                                                             361 GICTCCICA
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ORGANISM
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                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
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TITLE
JOURNAL
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TITLE
                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
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                                                                                                                                                       435
                                                                                                                                                                                             RESULT 6
MMIGHRF2
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Bukaryota wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dases 1 to 443)

Kroemer, G., Faessler, R., Strohal, R., Wick, G. and Kofler, R.

Evidence for a new murine immunoglobulin heavy chain variable region gene family

Finannol. Invest. 16 (2), 107-116 (1987)

87306735

2887512
                                                                                                                                                                                                                                                                                                                          Mouse spleen hybridoma (cell line MRL-RF24; haplotype Igh-j) cDNA
                                                                                                                                                                                                                                                         Mouse Ig unproductively rearranged H chain mRNA V-region.
M21469 M20825
M21469.1 GI:196219
C-region; V-region; immunoglobulin heavy chain; processed gene;
pseudogene.
                                                                                                 TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
             241 CTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAGA 300
                                                              TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATAATATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Draft entry and computer readable copy of sequence [1] kindly submitted by R.Kofler 28-JUL-1988.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Ig heavy chain MRL-DNA4BH V-region precursor (V-DSP2.7-JH4)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGTGATGCTGGTGGAGTGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            443 bp mRNA linear ROD 2 unproductively rearranged H chain mRNA V-region.
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Pred. No. 4.8e-83;
0; Mismatches 35; Indels
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19. 75
/note="Ig heavy chain signal peptide"
76. .>443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Ig heavy
92 c 108
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90.2%;
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Matches 333; Conservative
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                                                                                                                                                                   GTCTCCTCA 369
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VERSION
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ROD 07-MAY-1992
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                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (abases 1 to 444)
Kofler,R.
                                                                                                                                                                                                                                                                    Submitted (24-JUL-1989) Kofler.R., General and Experimantal Pathology, University of Innsbruck,, Fritz-Pregl-Str. 3, A-6020
                                                                                                                                                                                                                                                                                                    2 (bases 2 to 444)
Kroemer,G., Faessler,R., Strohal,R., Wick,G. and Kofler,R.
Evidence for a new murine immunoglobulin heavy chain variable immunol. Invest. 16 (2), 107-116 (1987)
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Mouse MRL-RF24BG nonfunctional Ig heavy chain transcript.
X16801
X16801.1 G1:52049
Ig D-segment; Ig heavy chain; joining region; pseudogene; variable region.
MNS musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="(pseudo) Ig heavy chain precursor protein"
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Pred. No. 4.8e-83;
0; Mismatches 35;
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77. .375
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/note="JH4 joining region"
92 c 108 g 126
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/strain="MRL/Mp-lpr/lpr.'
/db_xref="taxon:10090"
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20. .>444
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106. .107
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llarity 90.2%;
Conservative (
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AF178591 366 bp mRNA linear ROD 22-MAY-2000 Mus musculus 23-7 immunoglobulin heavy chain variable region mRNA, partial cds.
AF178591.1 GI:5853171
                                                                           03-APR-1998
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
I (Dasea 1 to 36)
Putterman, C., Deocharan, B. and Diamond, E.
Molecular analysis of the autoantibody response in peptide-induced
                                                                                                                                                                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         704 TCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAG-- 761
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Pred. No: 8e-83;
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                                                                                                                                                               l (bases 1 to 1797)
Carozal, N.B. and Kozlel, M.G.
Antibodies which bind to insect gut
Patent: US 5686600-A 17_11-NOV-1997;
                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                         1797 bp
US 5686600.
                                                                                                                                                                                                                                           402
                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                /organism="unknown"
488 c 452 g
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                                                                                    Sequence 17 from patent I73745
                                                                                                                                                                                                                                                                            81.4%;
91.0%;
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Matches 335; Conservative
                                                                                                                                          Unknown.
Unclassified.
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          136 TCATGTGCCCCTCTGGTTTCACCTTCAATACCTATGCCATGAACTGGGTCCGCCAGGGT 195
                                          CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATATGCAACA 180
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                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 357)
Carozzi, N.B. and Koziel, M.G.
Antibodies which bind to insect gut proteins and their use
Patent: US 5666600-A 1 11.NOV-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 TTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATGC
TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
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Pred. No. 7.3e-83;
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Sequence 1 from patent US 5686600.
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76 c 91 g
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ilarity 91.0%;
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Best Local Similarity
Matches 335; Conserv
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AF178596
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                                                                                                                                                                                                                                                      /product="immunoglobulin heavy chain variable region"
/protein_id="AAD54347.1"
/protein_id="AAD54347.1"
/protein_id="ABD54347.1"
/protein_id="ABD54347.1"
/translation="VNVVVESGGGLVOPKGSLKLSCAASGFTENTYAMNWVRQAPGKGLEWVARIRSKSNNYATYYADSVKDRFTISRDDSQSMLXLQMNNLKTEDTAMYXCVRHS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                           Direct Submission
Submitted (17-MG-1999) Rheumatology/Medicine, Albert Einstein
College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATTATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATATGCAACA 180
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                                                                                                                                                                                                                                                                                                                                                                       80.9%; Score 298.6; DB 10; Length 366; ilarity 90.0%; Pred. No. 2.7e-82; Conservative 0; Mismatches 34; Indels 3;
                                                                                                                                                                  /db_xref="taxon:10090"
/cell_line="23-7"
/cell_type="hybridoma"
/note="from peptide-immunized mouse"
                                                 2 (bases 1 to 366)
Putterman, C., Deocharan, B. and Diamond, B.

    .>366
    /note="anti-peptide antibody"

autoimmunity
J. Immunol. 164 (5), 2542-2549 (2000)
20143847
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    366 /
/organism="Mus musculus"
/strain="BALB/c"

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Mus musculus
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                                      10679092
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366 bp mRNA linear ROD 22-MAY-2000
partial cds.
AF178596
AF178596.1 GI:5853181
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LEWVARIRSKSNNYATYYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRHG
LGRYWYFDVWGAGTTVTVSS"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 366)
Putterman,C., Deocharan,B. and Diamond,B.
Molecular analysis of the autoantibody response in peptide-induced
                                                                                                                                           1 (bases 1 to 366)
Putterman,C., Deocharan,B. and Diamond,B.
Direct Submission
Submitted (17-40G-1999) Rheumatology/Medicine, Albert Einstein
College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAAATAATTATGCAACA 180
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                                                                                                                                                                                                                                                              1. 366
/organism="Mus musculus"
/organism="Taxon"
/db_xref="taxon:10090"
/cell_line="89.3"
/cell_type="hybridoma"
/note="from peptide-immunized mouse"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 297; DB 10;
Pred. No. 8.4e-82;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product=1mmunoglobulin heavy
/protein_id="AAD54351.1"
/db_xref="GI:5853180"
                                                                                                                                                                                                                                                                                                                                                                                            autoimmunity
J. Immunol. 164 (5), 2542-2549 (2000)
20143847
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Best Local Similarity 89.7
Matches 331; Conservative
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/translation="WVLGIKWVFFVVFYOGYHCEVOLVESGGGLVQPKGSLKLSCAAS
GFTFWTYAMHWVRQAPGKGLEWVARIRSKSSNYATYYADSVKDRFTISRDDSQSMLYL
OMNNLKTEDTAMYYCVRSDAMDYWGQGTSVTVSS"
                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 408)
Li.J., Fernandez, L., O'Connor, K.C., Imanishi-Kari, T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"anti-poly(dC) monoclonal antibody heavy chain"
/protein_id="AAC04511.1"
/db_xref="GI:2906050"
                                                                                                                                                                                                                                                                                                                                                                   3 (bases 1 to 408)
O'Connor,K.C., Farrell,T.P., Morikawa,A. and Stollar,B.D.
Direct Submission
Submitted (02-FB-1998) Biochemistry, Tufts University School of
Medicine, 136 Harrison Avenue, Boston, MA 02111, USA
                                                                                                                                                                                        The rearranged V(H) domain of a physiologically selected anti-single-stranded DNA antibody as a precursor for formation IgM and IgG antibodies to diverse antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATGTGCACCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
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musculus dCl anti-poly(dC) monoclonal antibody heavy chain
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                                                                                                                                                                                                                                                                                                      O'Connor, R.C., Farrell, T.P., Morikawa, A. and Stollar, B.D. Anti-DNA antibodies of normal mice immunized with poly(dC) structurally similar to natural autoantibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 408;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="C57BL/6"
/db.xref="taxon:10090"
/chromosome="12"
/clone="dc1"
/cel_line="spleen cell hybridoma"
/l. >408
/gene="IgH"
/l. >408
/gene="IgH"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 291; DB 10;
Pred. No. 6.4e-80;
0; Mismatches 20;
             variable region, (IgH) mRNA, partial cds
AF045483
AF045483.1 GI:2906049
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llarity 89.7%;
Conservative
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58. 357
/gene="Igh"
358. 375
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376. .408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="immunoglobulin heavy chain variable region"
/protein_id="AAD54352.1"
/db_xref="01:5853182"
/translation="DVKVVVSGGGLVQPKGSLKL.SCAASGFTFNTYAMNWVRQAPGKG
LEWVARIRSKSNNYATYADSVKDRFTISRDDSQSMLYLQMNNLKTEDTAMYYCVRHG
LGRYWYFDVWGAGTTYTVSS"
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                                                                                             Putterman, C., Deocharan, B. and Diamond, B. Molecular analysis of the autoantibody response in peptide-induced
                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                        2 (bases 1 to 366)
Putterman,C., Deocharan,B. and Diamond,B.
Direct Submission
Submitted (17-40G-1999) Rheumatology/Medicine, Albert Einstein
College of Medicine, 1300 Morris Park Ave., Bronx, NY 10461, USA
Location/Qualifiers
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Pred. No. 8.4e-82;
0; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                     /cell_type="hybridoma"
/note="from peptide-immunized mouse"
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                                                Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Rodentia; Sciurognat
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="anti-peptide antibody"
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                                                                                                                                             Immunol. 164 (5), 2542-2549 (2000)
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/cell_line="39-9"
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TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                                                                                                                                                                                                             Mus musculus
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Best Local Similarity
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 181
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                                                                                                                                                                                                                   RESULT 14
MUSIHCVRA
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/product="immunoglobulin heavy chain V region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ή:
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                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (abses 1 to 366)
Casadevall, A., Deshaw, M., Fan, M., Dromer, F., Kozel, T.R. and
              240
                                                                                                               L31512
L31512.1 GI:468344
V region; immunoglobulin heavy chain.
Wus musculus (strain BALB/c, sub_species domesticus) hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                         Pirofski,L.-A.
Molecular and idlotypic analysis of antibodies to Cryptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 TATTATGCCGATTCACTGAAAGACAGATTCACCATCTCCAGAGATGATTCACAAAGCATG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
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Pred. No. 1.7e-79;
0; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="BALB/c"
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75 c 93 9
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Location/Qualifiers
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88.3%;
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Best Local Similarity 88.3
Matches 326; Conservative
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MUSIHCVRA 360 bp mRNA linear ROD 26-MAR-2002 Mouse mRNA for immunoglobulin heavy chain variable region, partial sequence.
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/cell_type="hybridoma producing anti-human procollagenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 360)
Yamanaka, H.I., Kiril, Y. and Ohmoto, H.
Yamanaka, H.I., Kiril, Y. and Ohmoto, H.
An improved phage display antibody cloning system using newly designed PCR primers optimized for Pfu DNA polymerase
J. Biochem. 117 (6), 1218-1227 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (21-APR-1995) Hachiro Yamanaka, New Drug Research
Laboratorises, Kanebo Ltd.; 5-90 Tomobuchi-cho 1-chome,
Miyakojima-ku, Osaka, Osaka 534, Japan (Tel:06-921-1281(ex.3609),
Fax:06-923-3381)
                                                                                                               300
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/product="immunoglobulin heavy chain variable region"
/db_xref="IMGT/LIGM:D50376"
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Mus musculus (strain BALB/c) hybridoma producing anti-human
procollagenase antibody, cell-line KlE6 cDNA to mRNA.
                                                                                        CTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGAGA
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Hachiro Yamanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-5-90 Tomobuchi-cho Miyakojima-ku
Osaka, Osaka 534
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/note="PCR primer"
complement(339, .360)
/note="PCR primer"
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97.7%;
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D50376.1 GI:804892
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Yamanaka, H.
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November 27, 2002,

Search completed: Novem Job time : 1478.46 secs

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                                                    CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATGCAACA 180
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                  1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
                           1 (bases 1 to 345)
Wylle, D.E., Lopez, O., Murray, P., Joseph, and Goebel, P.
Lead binding polypeptides and nucleotides coding therefore
Patent: uS 6111079-A 35 29-AUG-2000;
Location/Qualifiers
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Best Local Similarity 89.7%; Pred. No. 3.6e-79;
Matches 331; Conservative 0; Mismatches 14
Mismatches
                                                                                                                                                                                                                            345 bp
Sequence 35 from patent US 6j11079.
AR108686.1 GI:12824173
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75 c 87 g
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Matches 293; Conservative
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369
1 GAAGTGATGCTGGTGGAGTC......CCTCACTCACGTCTCCTCA 369
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                             2185239 seqs, 1125999159 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | 3B1 heavy chain va | 3B1 single chain a | Anti-Her2neu singl | Lead binding MAb 2 | Lead binding MAb 6 | H. pylori 26 kDa p | Murine antibody 1D | Humanised murine a | 2G3 hvhridoma VH d |
|-----------|-----------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| | | | | | • | | | | | |
| | | | | | | | | | | |
| IES | | | | | | | | | | |
| SUMMARIES | ۰. | AAT15725 | AAT15733 | AAZ51115 | AAT58267 | AAT58261 | AAA40202 | AAD13178 | AAD13179 | AAA38896 |
| | B ID | | 17 | 21 | | 18 | 21 | | 22 | |
| | Query re Match Length DB | 357 | 1797 | 1079 | | | | | 357 | |
| æ | Ouery Match 1 | 81.4 | 81.4 | 9.62 | 78.2 | 77.1 | 76.9 | 73.0 | 67.5 | 61.6 |
| | Score | 300.4 | 300.4 | 293.8 | 288.6 | 284.4 | 283.8 | 269.2 | 249.2 | 227.2 |
| | Result No. | П | 7 | m | 4 | Ŋ | 9 | 7 | 89 | ð |

| Human secreted exp Plasmid preRMsc2H1 DNA encoding anti-Insulin/insulin-11 Lead binding MAD 2 5 single chain 3B10x5P-2 bispecif DNA encoding mouse Insulin/insulin-11 Nucleic acid encod Human HIV-1 monocid WM1 222-5 antibody Human autoantibody WM1 222-5 antibody Human autoantibody Sequence encoding CC49 VL / 217 / 4-DNA encoding a proban encoding bival DNA encoding bival DNA encoding bival DNA encoding bival DNA (SEQ ID NO:22) Antibody CC49/anti Sequence encoding DNA encoding a proban encoding antibody CC49/antibody |
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| AAA44338 AAX179533 AAX1795315 AAX1727139 AAX1727139 AAX17276 AAX271376 AAX271376 AAX2737139 AAX1729053 AAX1729053 AAX1729053 AAX1729053 AAX1729033 AAX172933 AAX172933 AAX172933 AAX172933 AAX172933 AAX172933 AAX172933 AAX1729 |
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ALIGNMENTS

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delta endotoxin; Bacillus thuringiensis; western corn rootworm; WCRW; maize; pesticide; brush border membrane vesicle; monoclonal;
                                                                     3B1 heavy chain variable region DNA from pCIB4613
                AAT15725 standard; cDNA; 357 BP
                                                                                                                                                                                                94US-0267641.
                                                                                                                                                                              95WO-IB00497
                                                  25-JUN-1996 (first entry)
                                                                                                                                                                                                                                     Carozzi NB, Koziel MG;
                                                                                                                                                                                                                  (CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                                     WPI; 1996-077494/08.
P-PSDB; AAR90829.
                                                                                                                                                                              20-JUN-1995;
                                                                                                                                                                                                28-JUN-1994;
                                                                                                        antibody; ss
                                                                                                                                           WO9600783-A1
                                                                                                                                                             11-JAN-1996.
                                                                                                                          Insecta sp.
                                 AAT15725;
RESULT 1
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New monoclonal antibodies which bind insect gut proteins - used

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20-JUN-1995;
                                                                                            Carozzi NB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ51115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302
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                                                                                                                                                                                                                                                                                                                 1;
                                                            ARTIS725-35 are DNA mols. encoding a monoclonal antibody or a binding fragment. MAbs were produced by using insect guts, partic, insect bursh border membranes (BBMS), esp. corn roctworm, as antigen; insultigen a donor animal with the antigen; isolating immunocompetent B cells from the immunised animal; fusing B cells with a tumour cell line; isolating the fused cells, culturing them and cloning positive hybrid cells; and screening the hybrid cells for prodn. of the required MAbs. The MAbs bind to the gut of a target insect but do not bind to mammalian BBMs. The DNA sequence can be operably linked to a toxin molety, esp. selected from e.g. Bacillus toxins, pseudomonas exotoxin and phytolaccin, etc. The Abs are useful for control of insect pests, e.g. Coleoptera, Diptera, Hymenoptera and Lepidoptera. The pesticidal compsn. is pref.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 CATGTGCAGCCTCTGGATTCACCTTCAATAACTTCGCCATGAACTGGGTCCGCCAGGCTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                               300 ------GGTAGTATACGGTGCTATGGACTACTGGGGTCAAGGAACCTCAGTCACCG 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                 122 CAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATTATGCAACAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           302 GGGGGGCTTCAGGGATTGACTATGCTATGGACTACTGGGGTCAAGGAACCTCACTACCG 361
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                             62 CATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCTC 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 TCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAGAC 301
                                                                                                                                                                                                                                                                                                                                                       2 AGGTCAAACTGCAGGAGTCTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCT 61
                                                                                                                                                                                                                                                                                                                                          2 AAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCT 61
partic. with toxin moieties for the control of insect pests, partic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WCRW; maize; pesticide; brush border membrane vesicle; monoclonal; antibody; ss.
                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       delta endotoxin; Bacillus thuringiensis; western corn rootworm;
                                                                                                                                                                                                                                                                                  Query Match
81.4%; Score 300.4; DB 17; Length 357;
Best Local Similarity 91.0%; Pred. No. 3.9e-80;
Matches 335; Conservative 0; Mismatches 21; Indels 12;
                                                                                                                                                                                                                                                        Sequence 357 BP; 102 A; 76 C; 91 G; 88 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3Bl single chain antibody DNA from pCIB4631.
                                       Claim 8; Page 50-51; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT15733 standard; cDNA; 1797 BP.
                                                                                                                                                                                                                                 applied to a plant, e.g. maize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 362 TCTCCTCA 369
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AAT15733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT15725-35 are DNA mols. encoding a monoclonal antibody or a binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         644 CTTATGGCGATTCAGTGAAAGACAGGTTCACCTCCCAGAGATGATTCACAAAGCATGT 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 CAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAAAAGTTATGCAACAT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                     New monoclonal antibodies which bind insect gut proteins - used partic. With toxin moieties for the control of insect pests, partic. in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 TCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 TTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGA'GATTCACAAAGCATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       524 CATGTGCAGCCTCTGGATTCACCTTCAATAACTTCGCCATGAACTGGGTCCGCCAGGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 AAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 300.4; DB 17; Length 1797;
Pred. No. 6.8e-80;
0; Mismatches 21; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1797 BP; 455 A; 488 C; 452 G; 402 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 68-72; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
AAZ51115
ID AAZ51115 standard; DNA; 1079 BP.
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91.0%;
                                                          94US-0267641.
95WO-IB00497
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Best Local Similarity 91.0°
Matches 335; Conservative
                                                                                                                                                                                    Koziel MG;
                                                                                                                       (CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                              WPI; 1996-077494/08.
P-PSDB; AAR90837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 TCTCCTCA 369
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                                                          28-JUN-1994;
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241 CTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGAGA 300
     623 TATTATGTCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 682
                                                                                                                            743 TCTTACTATGATTACGACAGGTCCTGTTTGCTTACTGGGGCCAAGGGACCACGGTCAC
                                                         Sequence 345 BP; 100 A; 75 C; 87 G; 83 T; 0 other;
                                                                                                                                                                                361 GTCTCCTCA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heavy metal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-OCT-1995;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9639518-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JUN-1996;
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AAT58267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The patent discloses a novel retroviral vector, particularly Spleen
Necrosis Virus (SNV) vector, having target cell specificity. The vector
has a targetting envelope which is a chimeric protein consisting of an
antigen binding site of an antibody (e.g. anti-DNP-scFv) or another
carboxy terminal part of the retroviral envelope protein, fused to the
carboxy terminal part of the retroviral envelope protein. The presence
of the wild type envelope protein serves as a helper molecule to
improve or supplement a functional membrane fusion domain. The
carboxinal vector is used for cell specific gene transfer,
carboxinal vector is used for cell specific gene transfer,
cspecially in gene therapy. The invention overcomes the restricted host
range limitation of retroviral vectors. The present sequence is a gene
cencoding anti-Herzneu single chain antibody (scA). This sequence was used
in the construction of plasmid pAJ7 which contains a tagetting vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           563 CCAGGAAAGGGTTTGGAATGGATTGTTCGCATAAGAAGTAAAAGTAATAATTATGCAACA 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cell specific gene transfer using retroviral vectors containing antibody-envelope fusion proteins and wild type envelope proteins
                                                                                       antibody-envelope fusion protein; retroviral envelope protein; gene therapy; antigen binding site; single chain antibody; human; Her2neu cell surface marker; cell specific gene transfer; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 1079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                  /*tag= a
/product= "Antl-Her2neu single chain antibody"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1079 BP; 303 A; 253 C; 255 G; 268 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SNV-Env(envelope)-TM(transmembrane) coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 293.8; DB 21;
Pred. No. 5.4e-78;
0; Mismatches 47;
                                                                        Retroviral vector; Spleen Necrosis Virus; SNV;
                                      Anti-Her2neu single chain antibody gene.
                                                                                                                                                                                                Location/Qualifiers
14..1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example; Fig 8; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               (UYJE-) UNIV JEFFERSON THOMAS.
                                                                                                                                                                                                                                                                                                                                                                                            98US-0135121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 79.6%;
Best Local Similarity 87.3%;
Matches 322; Conservative
                                                                                                                                                                                                                                                                                                                                                          99WO-US18141
05-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-224358/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAY70111
                                                                                                                                                                                                                                                                                      WO200009730-A2
                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                          10-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                            17-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dornburg RC;
                                                                                                                                                                                                                                                                                                                       24-FEB-2000
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NAMES OF COLOR OF STREET STREE

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monoclonal antibody (MAD) 284, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from hydridoma cells from mouse spleen cells. The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid; systems, in biological or environmental systems or in such compositions as perfumes, cosmetics, pharmaceuticals, health care products; skin treatment products, pesticides, herbicides, asolvents used in the production of semi-conductor and integrated circuit components and production materials
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cosmetic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy metals, such as lead cations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence encodes the heavy chain variable region for
                                                                                                                                                                                                                                                                                                                                                                                                       Lead binding MAb 2B4 heavy chain variable region encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Monoclonal antibody; Fd fragment; lead cation; perfume; pharmaceutical; health care; skin treatment; pesticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= a
/note= "no stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 88; 125pp; English.
                                                                                                                                                                                AAT58267 standard; cDNA; 345 BP
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95US-0462798.
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                                                                                                                                                                                                                                                                                                                              22-AUG-1997 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lopez O, Murray PJ,
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P-PSDB; AAW01593.
803 GTCTCTTCA 811
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us-09-893-615-86.rng

Wed Nov 27

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(CONN-) CONNEX GMBH
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                                                                                                                                                                                                                                                                                                                                                                     AAA40202;
                                                                                                                                Query Match
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                                                                                                                                            360
                                                                CAAGGAAAGGTTTGGAATGGTTGCTCGCATAAGAAGTAAAAGTAATAATATGCAACA 180
                                                                                                                       TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
                                                                                     CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATTATGCAACA 180
                                                                                                                 TITTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
               Gaps
                                   1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
                                                                                                                                                                        DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy metals, such as lead cations
               24;
                                                                                                                                                                                                                                                                                              Lead binding MAb 6F5 heavy chain variable region encoding cDNA
Length 345;
               Indels
                                                                                                                                                                                                                                                                                                            oody; Fd fragment; lead cation; perfume;
health care; skin treatment; pesticide;
DB 18;
               14;
Score 288.6; DB 1
Pred. No. 1.3e-76;
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..330
/*tag= a
/note= "no stop codon given"
              0; Mismatches
                                                                                                                                                                                                                                                     AAT58261 standard; cDNA; 330 BP.
78.2%;
89.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wylie
                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0541373
95US-0462798
                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US09258
                                                                                                                                                                                                                                                                                 (first entry)
              Matches 331; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BION-) BIONEBRASKA INC.
                                                                                                                                                                                                                                                                                                             Monoclonal antibody;
pharmaceutical; heal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murray PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-043140/04
                                                                                                                                                                                                             GTCTCCTCA 345
       Similarity
                                                                                                                                                                                                    361 GTCTCCTCA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAW01587.
                                                                                                                                                                                                                                                                                                                            heavy metal; ss.
                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                          WO9639518-A1
                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1996;
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05-JUN-1995;
                                                                                                                                                                                                                                                                                 22-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                        12-DEC-1996
                                                                                                                                                                                                                                                                   AAT58261;
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Query Match
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Acid-resistant microorganism; detection; faecal; intestine; infection; monoclonal antibody; heavy chain; ds.
                                                           The present sequence encodes the heavy chain variable region for monoclonal antibody (MAD) 6F5, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from hydridoma cells from mouse spleen cells. The protein can be used for bliding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in bological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, colvents used in the production of semi-conductor and integrated circuit components and production materials
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCTCCAGGAAAGGGTTTG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GGATTCACCTTCAATACCTACGCCATGAACTGGGTCCGCCAGGCCCCAGGAAGGGTTTG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAATGGGTTGCTCGCATAAGAAGTAAAAGTAATATATGCAACATTTTATGCCGATTCA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATTATGCAACATATTATGCCGATTCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 AACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAGACGGTTTGCTTACTGG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 GAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCTCATGTGCAGCCTCT 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H. pylori 26 kDa protein-binding antibody heavy chain encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GAGTCTGGTGGAGGATTGGTGCGCCTAAAGGGTCATTGAAACTCTCATGTGCAGCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATGCTCTATCTGCAAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 284.4; DB 18; Length 330;
Pred. No. 2.4e-75;
0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 330 BP; 93 A; 73 C; 82 G; 82 T; 0 other;
Claim 1; Page 76; 125pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA40202 standard; DNA; 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-EP08212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 GCCCAAGGGACTCTGGTC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          316 ATTGACTATGCTATGGAC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for electronic components.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 93.4 Matches 297; Conservative
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neuroprotective; immunosuppressive; human immunodeficiency virus; HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; asthma; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;

Murine antibody 109 heavy chain variable region encoding DNA

(first entry)

16-OCT-2001

AAD13178;

humanised antibody; CC-chemokine receptor 2;

fibrotic disease; angioplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neointimal hyperplasia; antibody 1D9 heavy chain variable region;

/transl_except= (pos:442..443, aa:Val)
/note= "CDS does not include start and stop codon"

/product- "Murine antibody 1D9 heavy

Location/Qualifiers

sp.

chain variable region"

CCR2; nephrotropic;

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This invention describes a novel method for the detection of a mammalian infection by an acid-resistant microorganism (A) by treating a faecal sample with at least two different monoclonal antibodies (MAb) (or their fragments or derivatives) or aptamers (collectively (I)) and detecting formation of a complex (C) between (I) and the corresponding antigen of formation of a complex (C) between (I) and the corresponding antigen of (A). The first and second (I) bind to epitopes of different antigens (Ag). These epitopes are present, after passage through the intestines, in at least some mammals, and have either: (I) their native structure; or (II) a structure against which an antibody is produced by an animal infected or immunized with (A), or its extract, lysate, derived protein cor fragment, or with a synthetic peptide. Practically all mammals display at least one of the specified epitopes. The method is used to detect infection by acid-fast bacteria, particularly of the genera Helicobacter, Mycobacterium and campylobacter, specifically H. Pytori, H. hepaticus, M. tuberculosis, C. jejuni and C. pylori. (I) may also be used therapeutically. The method is direct and non-invasive, and provides an inexpensive and easily standardizable diagnosis, despite possible sequence encodes the H. Pylori & Choms. Accesses the H. Pylori & Sequence encodes the H. Pylori & Choms. Accesses the H. Pylori & 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                       Detecting infection by acid-fast microbes for diagnosis of Helicobacter pylori, comprises reacting a faecal sample with two binding reagents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATAATGCAACATTTTA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCCAATTCAGTGAAAGACAGACTCACCATCTCCAGAGATGATTCACAAAACATGCTCTA 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATGCTCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.9%; Score 283.8; DB 21; Length 375; llarity 87.7%; Pred. No. 3.7e-75; Conservative 0; Mismatches 42; Indels 3;
Friedrichs U, Heppner P, Lakner M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 375 BP; 102 A; 86 C; 89 G; 98 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 3.7e-75;
0; Mismatches 42
                                                                                                                                                                                       antigens that survive intestinal passage
                                                                                                                                                                                                                                         Disclosure; Fig 4; 84pp; German.
Cullmann G,
                                                                 WPI; 2000-365747/31
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                                                                                               P-PSDB; AAB10022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Sim
Matches 322;
                         Ringeis A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoqiobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthitis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or disgnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'Keefe T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= e
/note= "Encodes a part of the constant region"
                                                                                                                                                                                                                                                                                                                                                                                  product= "Murine mature antibody 1D9 kappa
light chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'Brien S,
                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= d
/note= "Encodes variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jones ST,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 24; Fig 21; 183pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-FEB-2001; 2001WO-US03537.
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58..443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-488888/53.
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                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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                                                                                                                                                                                                                                                                                                                                     sig_peptide
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AAD13178 standard; DNA; 443 BP.

RESULT 7
AAD13178
ID AAD1
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Wed Nov 27

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09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neuroprotective; immunosuppressive; human immunodeficiency virus; neprotective; immunosuppressive; human immunodeficiency virus; inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock; multiple sclerosis; atherogenesis; atherosclerosis; restenosis; atherogenesis; atherosclerosis; allograft rejection; anaphylaxis; malignancy; inflammation; stenosis; allograft rejection; fibrotic disease; angloplasty; acquired immune deficiency syndrome; AIDS; inflammatory glomerulopathy; vascular intervention; neolintimal hyperplasia; antibody 1D9 heavy chain; 1D9RHA; ds.
             disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgE-mediated allergy. reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is a DNA encoding murine antibody ID9 heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                              TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITIATGCCGATICAGIGAAAGACAGGTICACCAICICCAGAGAIGAITCACAAAGCAIG 240
                                                                                                                                                                                                                                                                                                                                                              121 CCAGGAAAGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 CTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTAA 298
 the manufacture of a medicament for treating CCR-2 mediated
                                                                                                                                                                                                                                                                                                                                         GAAGTGATGCTGGTGGAGTGTGGAGGATTGGTGCAGCCTAAAAGGGTCATTGAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region, 1D9RHA"
/note= "CDS does not include start and stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Humanised murine antibody heavy chain
                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                        Length 443;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                  Sequence 443 BP; 117 A; 97 C; 108 G; 121 T; 0 other;
                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                                                                                                                                                  73.0%; Score 269.2; DB 22; 94.0%; Pred. No. 9.4e-71; ive 0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Humanised murine antibody heavy chain 1D9RHA DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD13179 standard; DNA; 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag≖ a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product=
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric - Mus sp.
Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /partial
                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                  variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157226-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001
                                                                                                                                                                                                                                                                                                       Matches 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD13179;
                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAD13179
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The patent discloses a humanised antibody or its antigen-binding (Tragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The ca cell expressing CCR2. They are useful for inhibiting or treating a cell expressing CCR2. They are useful for inhibiting or treating the interaction of a cell expressing CCR2. They are useful for inhibiting or treating correction. The proteins of the invention are useful for inhibiting in the manufacture of an edicament of the arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating allergy, anaphylaxis, and in the manufacture of a medicament for treating allergy, anaphylaxis, malignancy, chronic and acute inflammatory glomerate allergy, anaphylaxis, malignancy, chronic and acute inflammatory glomerate allergy reaction, shock, stenosis, allergy eff rejection, for including angioplasty and/or stent placement in a mammal. Inflammatory danger are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, preferably associated with vascular intervention. The present sequence ls a DNR encoding humanised murine antibody heavy chain region, 1DSRHA. 1DSRHA sequence consist of the complementarity contains antibody heavy chain region, 1DSRHA sequence consist of the complementarity contains the formal contains an intervention.
                                                                                                                                                                                                                                                                                                                                                                                                 Humanized immunoglobulin for treating a CC-chemokine receptor 2-mediated disorder in a patient, comprises a binding specificity for CCR2, and a non-human antigen binding region and human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                                                                                     O'Keefe T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inserted into the framework regions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCATGTGCAGCCTCTGGATTCACTTTCAGTGCCTACGCCATGAACTGGGTCCGCCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.5%; Score 249.2; DB 22; Length 357; 90.5%; Pred. No. 8.6e-65; Indels 0; Mismatches 28; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O'Brien S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 357 BP; 99 A; 79 C; 95 G; 84 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variable (VH) region genetically inserted int
(FRS) of the human 4B4'CL antibody VH region.
                                                                                                                                                                                                                     Jones ST,
                                                                                                                                                                                                                     Newman W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 64; Fig 23; 183pp; English.
                                                                                                                                             (MILL-) MILLENNIUM PHARM INC
02-FEB-2001; 2001WO-US03537.
                                                                    03-FEB-2000; 2000US-0497625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                     Horvath C,
                                                                                                                                                                                                                                                                                      WPI; 2001-488888/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                            P-PSDB; AAE07034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 266;
                                                                                                                                                                                                                     Larosa GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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299 -GGGAGGGACCTCTATTACTATACGACTACTGGGGTCAAGGAACCTCAGTCACA 357
                241 GTCTACCTGCAACTGAACAACTTAAGAGCTGAAGACACTGGCATTTATTACTGTGCCA---
                                                                                                                                                 358 GTATCCTC 365
                                                                                                                           361 GTCTCCTC 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200021991-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jacobs K, N
Merberg D,
                                                                                                                                                                                                                                                                        AAA44338;
                                                             301
                                                                                                                                                                                                          RESULT 10
                                                                                                                                                                                                                         AAA44338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a monoclonal antibody (MAb) (I) that binds to a human breast cancer antigen that is also bound by MAb 454C11 and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also described is a hybridoma that produces (I). (I) is useful in specific binding assays, affinity purification, drug or toxin targeting, imaging, and genetic or immunological therapeutics for various cancers. The present sequence encodes a VH domain derived from a 263 hybridoma, which is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Monoclonal antibody capable of binding to human breast cancer antigen useful for affinity purification, drug or toxin targeting, imaging, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAAATAATTATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CCAGAGAAGGGGCTTGAGTTGCTGAAATTAGATTGAAATCTAATAATTATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                        Antigen binding site; immunoglobulin; cancer antigen; immunological; antibody; tumour; human; mucin; cancer; cytostatic; hybridoma; specific binding assay; affinity purification; drug targeting; toxin targeting; imaging; genetic; therapeutic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GAAGTGAAGCTTGAGGAGTTGGAGGAGGCTTGGTGCAACCTGGAAGATCCATGAAACTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21; Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
61.6%; Score 227.2; DB 21; Length
Best Local Similarity 78.0%; Pred. No. 3.4e-58;
Matches 287; Conservative 0; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 366 BP; 103 A; 73 C; 95 G; 95 T; 0 other;
                                                                                                                          2G3 hybridoma VH domain encoding DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                  86US-0842476.
88US-0190778.
84US-0577976.
85US-0690750.
94US-0288981.
                            AAA38896 standard; DNA; 366
                                                                                                                                                                                                                                                                                                                                      95US-0483749
                                                                                        29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-338508/29.
P-PSDB; AAY90812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer
                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                      07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-1985;
11-AUG-1994;
                                                                                                                                                                                                                                                                      US6054561-A.
                                                                                                                                                                                                                                                                                                      25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                      21-MAR-1986
                                                                                                                                                                                                                                                                                                                                                                                     08-MAY-1988
                                                                                                                                                                                                                                                                                                                                                                                                     08-FEB-1984
                                                            AAA38896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ring DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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               AAA38896
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Human; mouse; chicken, rat; secreted expressed sequence tag; SEST;

wexpressed sequence tag; EST; probe; chemotactic; proliferative;
immunomodulatory; haematopoietic; chemotantic; anidgesic; haemostatic;
whinomoolytic; antinflammatory; cytostatic; anidgesic; haemostatic;
whinomoolytic; antinflammatory; cytostatic; anidgesic; haemostatic;
whinilice; osteopathic; neuroprotective; nootropic; antiparkinsonian;
wantiulcer; osteopathic; neuroprotective; nootropic; antiparkinsonian;
wantiulcer; autoimmune disorder; multiple sclerosis; allergic condition;
winsulin dependent diabetes; asthms; myeloid cell deficiency; ulcer;
winsulin dependent diabetes; asthms; osteoporosis; osteoarthritis;
central nervous system disorder; Alzheimer's disease; stroke;
watkinson's disease; Huntington's disease; coagulation disorder;
whemophila; thrombosis; inflammatory disorder; Crohn's disease;
wheumour; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA43426 to AAA45925 represent specifically claimed secreted expressed sequence tags (sESTs), isolated from human, mouse, chicken and rat tissue sources. The sESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotractic; proliferative; immunomodulatory; haematopolatic; enhances chemotractic; antibacterial; antibugal; antiviral; antibabatic; antibacterial; antilingal; antiviral; antidiabetic; antibacterial; antilingal; antiviral; antidiabetic; antipartiparkinsonlan; antipartiatic; cerebroprotective; anticonyulsant; and antidepressant. The sESTs can be used for gene therapy and in vaccines. The sESTs are useful as probes for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comprising secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Evans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collins-Racie LA,
                                                                                                                                                                                                                                                                                                 Human secreted expressed sequence tag SEQ ID NO:913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polynucleotides, and encoded proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 437-438; 803pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LaVallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bowman MR;
AAA44338 standard; cDNA; 359 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0104436
                                                                                                                                                                                                 21-AUG-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MCCOY JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-317938/27.
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             molecules which correspond to the SESTS. Proteins encoded by the SESTS are useful in assays for determining biological activity and raising antibodies. They may be useful for treatment of autoimnume disorders (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coaquiation disorders (haemophilla, thrombosis), inflammatory disorders (Crohn's disease, tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA45926 to AAA4591 represent linker variants which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                      1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identification of interacting polypeptide encoding nucleic acid sequences - e.g. to identify protein-protein interactions, which play an important role in biological processes
identification and isolation of full-length cDNAs and genomic DNA
                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                       Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein-protein interaction; interacting polypeptide; polyphage principle; plasmid pTERMsc2H10myc3sCAM; vector; Escherichia coli display; peptide library; ds.
                                                                                                                                                                                                                                                                        12; Indels
                                                                                                                                                                                                          Sequence 359 BP; 91 A; 66 C; 93 G; 109 T; 0 other;
                                                                                                                                                                                                                                         DB 21;
                                                                                                                                                                                                                                                         Pred. No. 8.8e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                         Score 225.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                         61.2%;
95.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT79537 standard; DNA; 5227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pTERMsc2H10myc3sCAM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                        Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-448687/41.
                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 CTCTA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354 CTCGA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L, Ilag V;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAT79537;
                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                           Local
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for identifying nucleic acid sequences (NAS), which encode for identifying nucleic acid sequences (NAS), which encode for identifying nucleic acid sequences (NAS), which encode polypeptides capable of interacting with at least 1 of their fellow polypeptides. This comprises: (a) providing a lst library of recombinant vectors containing genetically diverse NAS comprising a recombinant vectors containing genetically diverse NAS comprising a variety of NAS encoding polypeptides capable of interacting with carriety of NAS encoding polypeptides capable of interacting with carriety of NAS encoding polypeptides capable of interacting with carriety of NAS encoding polypeptides capable of interacting with carriety of NAS encoding polypeptides capable of interacting with carriety of NAS encoding polypeptides of and/or recombinant vectors and/or recombinant inserts used in steps (a) and (b), upon the interaction of a polypeptide from the librarie a displayed by the vectors and/or recombinant inserts used in steps (a) and (b), upon the interaction of a polypeptide from the libraries of the libraries of recombinant vectors or nucleic acid sequences of (a) and (b). In sectable property; (c) expressing members of the libraries of appropriate host cells so that at least 1 interaction is established; and (d) selecting for the generation of the screenable or selectable property representing the interaction of the interaction of the screenable or selectable property representing the interaction of the interaction of the interaction of the server of the interaction of the interaction of the screenable or selectable property representing the interaction of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1890 TCCTGTGTTGCCTCTGGAATCACTTTCAGTAATTACCGGATGAACTGGGTCGCCCAGTCT 1949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1830 GAAGTTAAACTGGTCGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTC 1889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2123 -----TAGAGGGGTTTCATATACTATAGACTACTGGGGTCAAGGAACCTCAGTCACA 2174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAAATAATTATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 CTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding anti-adipocyte monoclonal antibody heavy chain, FAT 103.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 215.4; DB 18; Length 5227;
Pred. No. 2.9e-54;
0; Mismatches 71; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGTTGGTGCAGCCTAAAGGGTCATTGAAACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5227 BP; 1232 A; 1265 C; 1355 G; 1375 T; 0 other;
                        Example 8; Fig 25; 105pp; English.
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Best Local Similarity 76.7
Matches 283; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2175 GTCTCCTCA 2183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Panel of specific binding members of antibody molecules which bind to whole adipocytes is used in the treatment of obesity and obesity related diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      300
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Pred. No. 2e-54;
0; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 369 BP; 81 A; 90 C; 122 G; 76 T; 0 other;
                                                                                                                                                                                                                                                                                                 (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 164; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                          Vaughan TJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 58.2%;
Best Local Similarity 74.2%;
Matches 271; Conservative
                                                                                                                                                                           11-OCT-2000; 2000WO-GB03900.
                                                                                                                                                                                                                                                                                                                                                          Main SH,
                                                                                                                                                                                                                                                                                                                                                                                                                  2001-282031/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAU02615
                                                        WO200127279-A1.
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Homo sapiens.
                                                                                                                                                                                                                                      12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                             Edwards BM,
                                                                                                                   19-APR-2001
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The invention relates to a method of modulating insulin activity in mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin agonist are useful for trating diabetes. Also, peptides that are antagonists of the insulin-like growth factor (IGF-1) receptor are useful for treating insulin-like growth factor (IGF-1) receptor are useful for treating insulin-like growth factor (IGF-1) receptor are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful in screening for compounds that bind to IR or IGF-1 receptor, potential therapeutics and research reagents. ABK47246-ABK47277 represent IR and/or IGF-1 receptor DNA sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumours, comprises using peptides that bind to insulin or insulin-like growth factor receptors '-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCTCCAG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pillutla R, Brandt J;
Ostergaard S, Mandecki WS;
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                                                                                                                                                                         Cytostatic; antidiabetic; neuroprotective; cerebroprotective; ophthalmological; insulin; receptor; gene therapy; diabetes; insulin-like growth factor-1: IGF-1; tumour; prostate; breast; diabetic retinopathy; neurological diseases; stroke; diabetic neuropathy; gene; ss.
                                                                                                                                          Insulin/insulin-like growth factor receptor, DNA sequence #25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94; Indels
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74.2%; Pred. No. 2.6e-54;
ive 0; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Figure 19; 390pp; English
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R, Spetzler J, Cheng W,
Ravera M, Hsiao K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DGIB-) DGI BIOTECHNOLOGIES LLC (NOVO ) NOVO NORDISK AS.
                                    ABK47271 standard; DNA; 761 BP.
                                                                                                                                                                                                                                                                                                                                                                                     29-MAR-2000; 2000WO-US08528
                                                                                                                                                                                                                                                                                                                                                                                                                      9-MAR-2000; 2000WO-US08528
                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                  WO200172771-A2.
                                                                                                       18-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beasley J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hansen PH,
                                                                                                                                                                                                                                                                                 Synthetic.
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Best Local S
                                                                       ABK47271;
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RESULT 13
ABK47271
ID ABK47
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125 GAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAGTAATAATTATGCAACATTTT 184

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conductor and integrated circuit components and production materials
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence encodes the heavy chain variable region for monoclonal antibody (MAb) 2E7, which immunoreacts with a lead cation. The sequence was derived from RNA isolated from hydridoma cells from mouse spleen cells. The protein can be used for binding heavy metals, such as lead cations. It can be used for detecting, removing, adding or neutralising the heavy metals in biological and inanimate systems. It can be used in e.g. aqueous liquid systems, in biological or environmental systems or in such compositions as perfumes, cosmetics, pharmaceuticals, health care products, skin treatment products, pesticides, herbicides, solvents used in the production of semi-
203 ACGCTGCACCCGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCAAAAAACACGCTGT 262
                                                                                                             304
                                                                                                                                                                          cosmetic;
herbicide;
                                               ATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATGCTCT
                                                                                                            245 ATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAGACGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding heavy metal binding polypeptide sequences - used for detecting, removing, adding or neutralising heavy metals, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                            Lead binding MAb 2E7 heavy chain variable region encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Monoclonal antibody; Fd fragment; lead cation; perfume; pharmaceutical; health care; skin treatment; pesticide; heavy metal; ss.
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/*tag= a
/note= "no stop codon given"
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                                                                                                                                                                                                                                                                                                                                                 AAT58268 standard; cDNA; 372 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wylie DE;
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95US-0462798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-043140/04.
P-PSDB; AAW01594.
                                                                                                                                                                                                                                      365 CCTCA 369
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05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                AAT58268;
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Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancreas; lung; larynx; breust; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; rescoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; ds; paleminth; cytostatic; antimicrobial; immunomodulatory; p4-2; p4-3; p4-14; p4-15; p5-2; p5-3; p5-9; p5-10; p5-11; p5-23; 3Bl0xP4-3; 3Bl0xP4-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GAGTACAGTGCATCTGTGAAGGGTGGTTCACCATCTCCAGAGATAATTCCCAAAGCATC 240
                                                                                                                                                                                                                                                                                                          180
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                                                                                                                                       Gaps
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                                                                                                                                                                                                               1 GAGGTGAAGCTGGTGGAGTCTGGAGGAGGCTTGGTACAGCCTGGGGGTTCTCTGAGACTC
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                                                                                           Length 372;
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                                                                                           DB 18;
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                                         95 T; 0 other
                                                                                                                 Pred. No. 4e-54;
0; Mismatches
                                                                                        Score 213.6;
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                                                                                        Query Match 57.9%;
Best Local Similarity 75.3%;
Matches 280; Conservative
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Hofmeister R;
                                         Sequence 372 BP; 95 A; 87
for electronic components.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200171005-A2.
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Mayer M,
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The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellular group of the NKG2D receptor complex and a second domain which functions as a receptor or ligand. The polypeptide and its associated composition for the treatment of cancer, infections and/or autolimune conditions. The cancer may be a tumour of the head and neck, stomach, largin, therest, oversy, uterus, cervix, prostate, kindrey, testis, thyroid, bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma. The infectious diseases can be caused by viruses, bacteria, fungi, protozoa or helminths. The autolimune diseases include multiple sclerosis, Grave's disease, ankylosing spondylitis, acute anterior uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent autolimune hepatitis. The sequences represent DNA encoding the polypeptides of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                 Multifunctional polypeptides comprising binding sites that specifically recognise extracellular groups of the NKG2D receptor complex and domains which function as receptors or ligands, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 AAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATTATGCAACATTTTA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 GAAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAAATTTATATGCAACACATTA 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 TCTGCAAATGAACAACTTGAAAACTGAGGACACCAGCCATGTATTACTGTGTGAGACGGGG 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 CCTGCAAATGAACAACTTAAGAGCTGAAGACACTGGCATTTATTACTGTACCAGGC---- 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24; Length 768;
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                                                                                                                                       Example 7; Fig 16; 114pp; English
                                                                                                 cancers and infectious diseases
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Mus musculus
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Eukaryota; Metazoa; Chordata; Craniata; Verrebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mus.
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E 2 (bases 1 to 865)
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BF135929 932 bp mRNA linear EST 24-OCT-2000 601781259F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4009334 5',
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                   /note-"Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo Clibrary constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

229 c 209 g 214 t
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                                                                                                                                                                                                                                                                                                                                                110 GAGGTGCAGCTTGTTGAGACTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 169
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                                                                                                                                                                                                                                                            DB 13; Length 865;
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Pred. No. 6.3e-72;
                                                                                                                                                                                                                                                                                              0; Mismatches
/organism="Mus musculus"
              /strain="CZECH II
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89.28;
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BF135929
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/strain="CZECH II"
/db.xref="taxon:10090"
/clone_lib="NoI_CZECP_Lu30"
/clone_lib="NoI_CZECP_Lu30"
/tissue_type="tumor, metastatic to mammary"
/lab_host="burding"
/note="organ: lung; Vector: pCMV-SPORT6; Site_l: NoII;
/note="organ: lung; Vector: pCMV-SPORT6; Site_l: NoII;
/note="organ: lung; Vector: pCMV-SPORT6; Site_l: NoII;
/note="organ: lung; Vector pCONT6]
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 700)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nlh.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Pred. No. 3.3e-56;
0; Mismatches 36;
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High quality sequence stop: 6
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 62.4%;
Best Local Similarity 85.1%;
Matches 286; Conservative
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lissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                         263
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                                                                                                                                                                                     source
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ORIGIN
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AW401500
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KEYWORDS
SOURCE
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                                                                                                                                         /tissue_rype="primary" B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1039)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 GAGGTGCAGCTGGTGGAGGTTGGGGGAGGCTTGGTCCTGGGGGGGTCCCTGAAACTC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TCATGIGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 TCCTGTGCAGCCTCTGGGTTCACCCTCAATGGCTCTACTATGCACTGGGTCCGCCAGCCT 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATTATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 TCCGGGGAAGGGCTGGAGTGGGTTGGCCGCATTAGAACCAAAACTAAAATTACGCGACA 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            283 GAATATATTGCGTCGGTGAAAGGCAGGTTCACCATCTCCAGAGATGATTCAAAAAACACG 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 GCGTTTCTGCAAATGGATAGCCTGGAAACCGAGGACGACGGCCGTGTATTACTGTGTAAGA 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403 GGGGGTCACGAGGGGTATTATTACGGTATGGACGTCTGGGGCCCAAGGGACCACGGTCACC 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGENCOURT_8952769 NCI_CGAP_CO24 Mus musculus cDNA clone INAGE:6474993 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                          DB 12; Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 229.8; DB 12;
Pred. No. 4.4e-56;
0; Mismatches 87;
                                                                     /organism-"Homo sapiens"
row: h column:
               High quality sequence stop: 696.
Location/Qualiflers
1. 700
                                                                                                          /clone="IMAGE:4855363"
/clone_lib="NIH_MGC_48"
                                                                                          /db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                      62.3%;
ilarity 76.4%;
Conservative (
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Matches 282; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GTCTCCTCA 369
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AUTHORS
TITLE
JOURNAL
COMMENT
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KEYWORDS
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BQ937972
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AW401500 522 bp mRNA linear EST 16-FEB-2000 UI-HF-BKO-aau-b-08-0-UI.rl NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3055046 5', mRNA sequence.
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                                                                                                                                                                                                                                                                       /strain="FVB/N"
/db_xref="taxon:10090"
/dclone="lmAGE:6474993"
/clone=lib="NuAGE:6474993"
/lab_host="DH10B (Tl phage-resistant)"
/lab_host="DH10B (Tl phage-resistant)"
/note="Organ: colon; Vector: pCMV:SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 263 c 257 g 242 t 14 others
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Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 522)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             356 GTCTACCTGCAAATGAACAACTTAAGAGCTGAAGACACTGGCATTTATTACTGTACCAGG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATTATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               236 CCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGATTGAGATCTAATAATTATGCAACA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Apencourt Bioscience Corporation
Clone distribution: MGC clone. distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
blate: LLAMA4013 row: a column: 10
High quality sequence stop: 612.
Location/Qualifiers
1. 1039
/organism="Muss musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 220.2; DB 14; Length 1039; Pred. No. 3.1e-53;
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74.88;
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Best Local Similarity 74.8
Matches 276; Conservative
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AW401500.1
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476 GTCTCCTCA 484
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TITLE
JOURNAL
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Email: Szhaoetigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 119 row: P column: 2
Seq primer: SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_"CH230-119P2"
/clone_lb="CHORI-230 Segment 1"
/sex="remale"
/cell_type="Brain"
/cell_type="Brain"
/coll_type="Brain"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
Pieter de Jong 1
10 c 116 g 161 t
                                                          Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., O'Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)
Other_GSSs: CH230-119P2.TVB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAA1TGGGTCCGCCAGGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 TCATGTGCAGCCTCTGGATTCACCTTCAGTACCTATACCGTGAGAVAGGACCACAAGGCT 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                             Contact: Shaying Zhao
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 212.8; DB 17;
Pred. No. 3.6e-51; 0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualiflers
1. .552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 57.7%;
Best Local Similarity 81.2%;
Matches 247; Conservative 0
                                             (bases 1 to 552)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: BAC ends.
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BB843560
LOCUS
DEFINITION
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                                                                 AUTHORS
                                             REFERENCE
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                                                                                                                                                                                                                                                                                                                                     /clone_lib="https://www.nih.mgc_36"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_type="germinal center B cells"
/cell_type="germinal center B cells"
/cell_type="germinal center B cells"
/cell_type="mod86"
/lab_host="mod86"
/lab_host="hot08 (rII)"
/note="vector: pT713-Pac; Site_1: NotI; Site_2: Eco RI;
/note="vector: pT713-Pac; Site_1: NotI; Site_2: Eco RI;
/ocstructed from size fractionated cytophasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
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               Email: cgapbs-remail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CINA Library Preparation: M.B. Soares Lab

CDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MCC clone distribution information can be count through the I.M.A.G.E. Consortium/LLNL at:

Www-blo.linl.gov/bbrp/image/image.html

Seq primer: MI3 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 522;
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Pred. No. 8.2e-53;
0; Mismatches 86; Indels
                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                        Location/Qualifiers
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ilarity 76.1%;
Conservative
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/dev_stage="6 days neonate"
/dev_stage="6 days neonate"
/dev_stage="6 days neonate"
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embryo cDNA libraries (including preimplantation stage
embryos from unfertilized egg to blastocyst, embryonic
part of E7.5 embryos, extraembryonic part of E7.5 embryos,
, and E12.5 female mesonephros/gonad) and one newborn
ovary cDNA library. Average insert size 1.5 kb. All
source libraries are cloned undidrectionally with Oligo(dT
)-Not primers. References include: (1) Genome wide
expression profiling of mid-gestation placenta and embryo
using a 15,000 mouse developmental cDNA microarray, 2000,
Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)
Large-scale cDNA analysis reveals phased gene expression
patterns during preimplantation mouse development, 2000,
                                                                                                                                                                                                                                                                                                                     Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatau, N., Hiramcto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Salto, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Taqawa, A., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y. Riken Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y. Computer-based methods for the mouse full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: genome-resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y. Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
Fre Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia, Sclurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Location/Qualifiers
                                                                             BB843560.1 GI:17081927
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Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7: 5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
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/lab.host="DH10B (phage-resistant)"
/note="Corgan: B-cells; vector: poTB7; Site_1: XhOI;
Site_2: ECORI, cDNA made by oilgo-dT priming.
Directionally cloned into EcoRI/Xh is lites using the following 5' adaptor: GGCAGGAG(G): Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Garalfornia, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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NIH-WGC http://mgc.nci.nih.gov/.
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone: distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

Hitp://mage.llnl.gov
Plate: LLCML693 row: 1 column: 17

High quality sequence stop: 711.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
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Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM1702 row: o column: 21
High quality sequence stop: 854.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/organism="Homo sapiens"
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AUTHORS
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BG754897
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COMMENT
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                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="InvaGE: 4219447"
/clone_lib="NoI_CGAP_CO34"
/dlob_nost="DH10B" (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (bases 1 to 560)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I. M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9801 row: h column: 08
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                                                                                                                                                                                                                                                                                                                                                         181 TITIATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                                                                                                                                                                                                                                          260 GAATACGCCGCGTCTGTGAAAGGCAGATTCACCATCTCAAGAGATGATGATGCAAAAGCATC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
                                                                                                                                                                                                                                                                               121 CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATTATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 CGGGGGCTTCAGG---GATTGACTATGCTATGGACTACTGGGGTCAAGGAACCTCACTC 357
                                                                                           Gaps
                                                                                                                              1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
                                                                                           3;
                                                      Length 711;
 2 others
                                                                                           Indels
                                                                                             96;
                                                      Score 203; DB 12;
Pred. No. 2.8e-48;
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                                                                                           0; Mismatches
 145
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Location/Qualifiers
1. 560
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 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BF581663
BF581663.1 GI:11655375
                                                    Query Match
Best Local Similarity 73.4%;
Matches 273; Conservative
   O
 209
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BF581663
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602714288F1 NIH_MGC_48 Homo sapiens cDNA linear EST 15-MAY-2001
mRNA sequence.
BG754897
EG754897.1 GI:14065550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              409
                                                                                                                                                                                                                                                                                   CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAAGT\\\"AATTATGCAACA 180
                                                                                                                                                                                                                    117 GAAGTGAAGCTTGAGGAGTCTGGAGGAGG-TTGGTGCAACCTGGAGGATCCATGAAACTC 175
                                                                                                                                                                                                                                                              TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 CATTATGCGGAGTCTGTGATAGGGAGGTTCACCATCTCAAGAGATGATTCCAAAAGTAGT
                                                                                                                                      7;
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
128 c 133 g 147 t
                                                                                                  DB 12; Length 560;
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                                                                                                                                                                                                   83;
                                                                                              Score 202.2; DB 1
Pred. No. 4.3e-48;
0; Mismatches 83
                                                                                                Query Match
Best Local Similarity 75.6%;
Matches 279; Conservative
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/organism="Homo sapiens"
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Best Local Simi
Matches 239;
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E. (bases 1 to 966)

NIH-MGC http://mgc.nci.nlh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Emall: cgapba-refmail.nih.gov
Tissue Procurement: Dr. Mark Watson
CONA Library Preparation: Rubin Laboratory
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
            Site_2: Ecori; cDNA made by oligo-dr priming.

Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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AGENCOURT_8487710 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6300705
5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                            242
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                                                                                                                                                                                                                                                                                                                                                                                                                              CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATTATGCAACA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         243 CCAGGGAAGGGGCTGGAGTGGCCGTTTAAAAGCAAAACTGATGGTGGGACAACA 302
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                   1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TITIATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG
                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                DB 12; Length 861;
                                                                                                                                                                                                             Score 201.4; DB 12; Length
Pred. No. 8.6e-48;
0; Mismatches 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM2515 row: g column: 10
High quality sequence stop: 561.
Location/Qualifiers
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                                                                                                                                                                                                               Query Match 54.6%;
Best Local Similarity 73.7%;
Matches 272; Conservative
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AUTHORS
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JOURNAL
COMMENT
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/db_xref="taxon:9606"
/clone="IMAGE:6300705"
/clone="IMAGE:6300705"
/clone="IMAGE:1300705"
/clone="IMAGE:1300705"
/clone="IMAGE:1300705"
/clone="IMAGE:1300705"
/lost=="Organ: spleen: Vector: pOTB7: Site_1: XhoI; Site_2:
/note="Organ: Spleen: Vector: Site_2: XhoI; Site_2: Adaptor:
/note="Organ: Spleen: Vector: Spleen: Site_2: XhoI; Site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCCAGAGATGATTCACAAAGCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 201.2; DB 14; Length 966; Pred. No. 1e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.5%;
ilarity 79.1%;
Conservative
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/strain="STBL/G"
/db_xref="Laxon:1000"
/db_xref="Laxon:1000"
/clone="IMAGE:3992829"
/clone=Lib="RoI="CGAP_mam5"
/tissue_type="T months"
/dev_stage="7 months"
/dab_host="DH10B"
/note="Organ: mammary; Vector: pCNV-SPORT6; Site_1: SalI: Site_2: NOTI; cloned unidirectionally. Primer: Oligo dT. Site_2: NOTI; cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGENCOURT_8351705 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6282330 5', mRNA sequence.
BQ706843.1 GI:21845742
EST.
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Primates; Catarrhini; Hominidae; Homo.
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lefound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMM208 row: e column: 22
High quality sequence stop: 539.
Location/Qualifiers
1...548
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Pred. No. 2.8e-47
0; Mismatches 66
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Email: cgapbs-rêmail.nih.gov
Tissue Procurement: Dr. Mark Watson
                                                                                                                                                                                                       /organism="Mus musculus"
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Best Local Similarity 78.4%;
Matches 239; Conservative (
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                                                                                /ub_Arel Laxun:39vv
/clone_lib="IMAGE:4764440"
/clone_lib="IMAGE:4764440"
/clone_lib="NIH_MGE_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/tlab_host="blul0b (phage=resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GCACGAGG(G). Size-selected >50bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callfornia, Berkeley) using 2AP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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54.4%; Score 200.8; DB 12; Length 693;
Best Local Similarity 74.6%; Pred. No. 1.2e-47;
Matches 282; Conservative 0; Mismatches 87; Indels 9;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Rob
CDNA Library Preparation: Life Technologies, Inc.
                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
           Location/Qualifiers
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/clone="image:6128330"
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BQ712530
BQ712530.1 GI:21851429
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.iln.gov.
Plate: LLCMA10 row: i column: 19
High quality sequence stop: 653.
Location/Qualifiers
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Pred. No. 7.5e-47;
0; Mismatches 93;
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NIH-MGC http://mgc.nc1.nih.gov/.
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274 c 25
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Best Local Similarity 73.2%;
Matches 270; Conservative (
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/organism="Homo sapiens"
/db.xref="taxon:9606"
/clone="IMAGE:628145"
/clone_lib="NiE_MGC_l13"
/clone_lib="NiE_MGC_l13"
/clone_lib="NiE_MGC_l13"
/clone_lib="NiE_MGC_l13"
/clone_lib="NiE_MGC_l13"
/clone_"Organ: spleen; Vector: pOTB7; Site_l: XhoI; Site_2: GOSI; cDNA made by Oilgo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                     Email: cgabbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can ifound through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCMA473 row: p column: 18
High quality sequence stop: 597.
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Pred. No. 7.6e
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                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Sequence 1, Application US/08442542

Patent No. 5686600
GENERAL INFORMATION:
APPLICANT: Carcial, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
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MEDIUM TYPE: FIDOPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BATEMIN SYSTEM:
CONFRANT SYSTEM:
SOFTWARE: PATEMIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 16-MAY-1995
CLASSIFICATION NUMBER: US/08/267,641
FILING DATE: 16-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAMME: SPULIAL, WMSTRAY
REGISTRENCE/DOCKET NUMBER: GC 1750:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8619
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
US-09-140-084-21
US-09-724-297-20
US-09-132-238A-14
US-09-166-093-14
US-09-166-093-14
US-09-166-094-14
US-08-138A-16
US-09-166-094-16
US-09-166-093-16
US-09-172-019-16
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US-09-166-093-16
US-09-166-094-16
US-09-166-093-16
US-09-166-093-16
US-09-172-019-18
US-09-149-287-3
US-08-449-287-3
US-08-138-9708-33
US-08-138-9708-33
US-08-138-9708-33
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COUNTRY:
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         (without alignments)
2736.194 Million cell updates/sec
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                                                                                                                                                                                                       November 27, 2002, 03:35:53; Search time 41.3581 Seconds
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Sequence 17,
Sequence 35,
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                                 GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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US-09-166-093-22
US-09-172-019-22
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US-08-926-789-13
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US-08-392-338A-12
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Maximum Match 100% :
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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/note= "3B1 heavy chain variable region from pCIB4613"

CTHER INFORMATION: , COTHER INFORMATION: , COTHER INFORMATION: I US-08-442-542-1

MOLECULE TYPE: CDNA

NAME/KEY: CDS

Sequence 3 Sequence 3 Sequence 3

Sequence.

Sequence Sequence Sequence

US-09-130-783-2

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Gaps

12;

Indels

Length 357;

DB 3;

241

361

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242 TCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAG-- 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/08442542
Patent No. 5686600
GENERAL INFORMATION:
APPLICANT: Carozi, Nadine B.
APPLICANT: Acazia, Natibodies which Bind to Insect Gut TITLE OF INVENTION: Proteins and their Use NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
                                                                                                                                /note= "3B1 heavy chain variable region from pCIB4613"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,542
FILING DATE: 16-MAY-1995
                                                                                                                                                                                                                     Query Match 81.4%; Score 300.4; DB 3 Best Local Similarity 91.0%; Pred. No. 3.1e-89; Matches 335; Conservative 0; Mismatches 21
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APPLICATION NUMBER: US 08/267,641
FILING DATE: 28-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 28-JUN-1994
ATTORNEY/AGENT INFORMATION:
    STRANDEDNESS: single
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                                                                                                           LOCATION: 1.357
OTHER INFORMATION:
OTHER INFORMATION:
                         TOPOLOGY: linear MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 7 Skyline
CITY: Hawthorne
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                       NAME/KEY:
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                                                                                                                                                                              62 CATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCTC 121
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                                                                                                              2 AGGTCAAACTGCAGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATGAAACTCT 61
                                                                                         2 AAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 GGGGGGCTTCAGGGATTGACTATGCTATGGACTACTGGGGTCAAGGAACCTCACCG
                                                12;
    DB 1; Length 357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTE: IBM PC COMPUTE: TO COMPUTE: TO COMPUTE: COMPUTE: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/765,469
FILIG DATE:
                      .1e-89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Carozzi, Nadine B.
APPLICANT: Carozzi, Michael G.
TITLE OF INVENTION: Antibodies which Bind t
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
Score 300.4; I
Pred. No. 3.1e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGC 1750
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APPLICATION NUMBER: 08/267,641
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08765469 Patent No. 6069301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION:
TELEPHONE: 919-541-8615
    81.4%;
91.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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nucleic acid
                                                Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    919-541-8689
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                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hawthorne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 TCTCCTCA 369
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US-08-765-469-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
      Query Match
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242 TCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTA&TGTGTGTGAGAC 301
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from pcIB4631"
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Patent No. 611079
GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: GOBBEL, PETER JOSEPH
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
     OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PATENTIN Release #1.0, N
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,469
                                                                                                             PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/267,641
                                                                                                                                             FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC I
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEPHONE: 919-541-8689
                                                                                                                                                                                                                                                                           TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 91,0
Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1.1797
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA
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CLASSIFICATION:
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US-08-767-128-35
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APPLICANT: Koziel, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SOUTENES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                           LOCATION: 1.1797
COTHER INFORMATION: /note= "3B1 single chain antibody
COTHER INFORMATION: from pCIB4631"
US-08-442-542-17
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                                                                                                                                                                                                                                                                                                                                                              Query Match 81.4%; Score 300.4; DB 1; Best Local Similarity 91.0%; Pred. No. 6.1e-89; Matches 335; Conservative 0; Mismatches 21;
NAME: Sprull, W. Murray
REGISSRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: CGC 1750
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTER STICS:
LENGTH: 1797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Ciba-Geigy Corporation
7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/08765469; Patent No. 6069301; GENERAL INFORMATION:
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ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA
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CITY: Hawthorne
STATE: NY
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APPLICANT: LOPEZ, OSVALDO
APPLICANT: LOPEZ, OSVALDO
APPLICANT: GOBBEL, PETER JOSEPH
APPLICANT: GOBBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
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APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-CCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/41,373
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: CATTER CARTES G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOGTWARE: FASTESO Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8648.49USF1
                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-08-767-128-23
Sequence 23, Application US/08767128
Patent No. 6111079
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 86
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/331-5278
TELEFAX: 612/332-9081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: Genomic DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Carter, Charles G. REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 330 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 424
                                                                                                                                                                                                                                                     361 GTCTCCTCA 369
                                                                                                                                                                                                                                                                                 337 GTCTCCTCA 345
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                                                                                                                                                                                                         301 CGG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATTATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TITIATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
                              ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STRRET: 3100 No. 6111079west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3; Length 345;
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TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE NUMBER OF SEQUENCES: 46 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.2e-85;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION 14.4
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION NUMBER:
FILING DATE: 05-JUN 1996
CLASSIFICATION NUMBER:
APPLICATION NUMBER: 08/41,373
FILING DATE: 05-JUN 1996
FILING DATE: 06-JUN 1996
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: 08/41,373
FILING DATE: 10-OCT-1995
FILING DATE: 08-JUN 1996
FILING DATE: 05-JUN 1995
FILING DATE: 05-JUN 1995
FILING DATE: 05-JUN 1995
FILING DATE: 05-JUN 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REPERNCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ VERSION 1.5
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: Genomic DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 345 base pairs
TYPE: nucleic acid
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COMPUTER READABLE FORM:
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ORIGINAL SOURCE:
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Diskette
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COMPUTER READABLE FORM:
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   nucleic acid
TYPE: nucleic acic
STRANDEDNESS: sing
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Minneapolis STATE: MN
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                                                             NAME/KEY:
                                                                           LOCATION:
                                                                                        US-08-483-749A-1
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                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                    GTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATGCTCTATCTGCAAATG 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAGACGGGGGGCTTCAGGG 315
                                                                                                                                                                     Gaps
                                                                                                                                                                                                75
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                                                                                                                                                                                               16 GAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTCTCATGCAGCCTCT
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                                                                                                                                      Length 330;
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TITLE OF INVENTION: AWTIGEN BINDING SITES OF ANTIBODY
TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
WUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CHIRON CORPORATION
STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
CITY: EMERYVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-JUN-1995
                                                                                                                                   Score 284.4; DB 3;
Pred. No. 5.2e-84;
0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 0508.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2285
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08483749A Patent No. 6054561 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: SAVEREIDE, PAUL B.
REGISTRATION NUMBER: 36,914
                                                         NAME/KEY: Coding Sequence LOCATION: LOCATION: 1...330
OTHER INFORMATION:
US-08-767-128-23
                                                                                                                                   77.1%;
ilarity 93.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 ATTGACTATGCTATGGAC 333
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                                                                                                                                                  Best_Local Similarity
Matches 297; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
            FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
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ANTI-SENSE:
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STATE:
                                                                                                                                     Query Match
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241 GTCTACCTGCAACTGAACAACTTAAGAGCTGAAGACACTGGCATTTATTACTGTGCCA-- 298
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                                                                                                                                                                                                                       TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 CTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 -GGGAGGGACCTCTATTACTATACTATGGACTACTGGGGTCAAGGAACCTCAGTCACA 357
                                                                                                                                                                                                                                                                                                   CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAAATAATTATGCAACA 180
                                                 Gaps
                                                                                                                                    1 GAAGTGAAGCTTGAGGAGTCTGGAGGCTTGGTGCAACCTGGAAGATCCATGAAACTC 60
                                                                                                1 GAAGTGATGCTGGTGGAGTCTGGTGGAGTTGGTGCAGCCTAAAAGGGTCATTGAAACTC
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3100 No. 6111079west Center, 90 South Seventh St
  Length 366;
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND TITLE OF INVENTION: NUCLEOFIDES CODING THEREFORE NUMBER OF SEQUENCES: 46 CORRESPONDENCE ADDRESS:
                  , 2e-65;
nes 78;
Score 227.2; DB 3;
                                                 0; Mismatches
                            Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FASLEGO VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37, Application US/08767128
Patent No. 6111079
GENERAL INFORMATION:
APPLICANT: WYLLE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GOEBEL, PETER
61.68;
78.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
                            Best Local Similarity 78.0
Matches 287; Conservative
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CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATTATGCAACA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ITTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
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                 APPLICANT: Barclay, George R.
APPLICANT: POXLON, Ian R.
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AGAINST LPS CORE NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 205; DB 2; Length 361;
Pred. No. 6e-58;
0; Mismatches 85; Indels
                                                                                                                                                                                                 ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Ralease #1.0, Version #1.25
CURRENT APPLICATION NATR:
APPLICATION NUMBER: US/08/647,144
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 105 08/119,046...
FILING DATE: 10-SEP-193
APPLICATION NUMBER: EP 92/00380.
FILING DATE: 22-FEB-192
ATOONEY/AGENT INFORMATION.
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFENCE/DOCKET NUMBER: 1749-114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140.
                                                                                                               E: Kenneth D. Sibley
Post Office Drawer 34009
                                                                                                                                 STREET: Post Office Drawer 340
CITY: Charlotte
STATE: No. 5858728th Carolina
COUNTRY: U.S.A.
Di Padova, Franco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (919) 881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 361 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 74.5'
Matches 275; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 575102
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                               ADDRESSEE:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 CTCTATCTTCAAATGAACACCCTGAGAGCTGAGACAGTGCCACTTATTACTGTGCAAGA 300
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Pred. No. 9.2e-61;
0; Mismatches 89; Indels
             APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY-AGENT INFORMATION:
NAME: CALTER, CHAILES 35,093
REGISTRATION NUMBER: 35,093
REGISTRATION NUMBER: 35,093
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 612/311-5278
                                                                                                                                                                                                                               8648.49USF1
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; Sequence 1, Application US/08647144
; Patent No. 5858728
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Coding Sequence;
LOCATION: 1...372
OTHER INFORMATION:
US-08-767-128-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.9%;
75.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: Genomic DNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.3
Matches 280; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gram, Hermann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
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  556 TATTATTCAGATTCTGTGAAAGGCAGATTCACCATCTCAAGAGATGATTCCAAAAGTAGT 615
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                                                            15;
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wood, James F.
APPLICANT: Hardman, Karl
APPLICANT: Hardman, Karl
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Filpula, David
APPLICANT: Filpula, David
APPLICANT: Filpula, David
APPLICANT: ANVENTION: Milivalent Antigen-Binding Proteins
CORRESPONDENCES: 23
CORRESPONDENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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1100 New York Avenue, NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/392,338A
FILING DATE: 22-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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Pred. No. 1.5e-57;
0; Mismatches 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION 432
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     Sequence 22, Application US/08392338A Patent No. 5869620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Goldstein, Jorge A. REGISTRATION NUMBER: 29,021 REFERENCE/DOCKET NUMBER: 09 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 55.3%;
Best Local Similarity 74.8%;
Matches 276; Conservative
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                 Whitlow, Marc
Wood, James F.
Hardman, Karl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 738 base pairs
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EDNESS: both
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                                                                                                                                                                                                                                 721 GTCTCCTAA 729
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APPLICANT: Whitlo
                                                                                                                                                                                                          361 GICTCCICA 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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US-08-392-338A-22
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301 CAG------GGACGGGCTATACTTTGGACTATTGGGGTCAAGGAACCTCAGTCACC
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                                                                                                                                                                         Sequence 13, Application US/08224591
Patent No. 5856456
GENERAL INFORMATION:
APPLICANT: Whillow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sterne, Kessler, Goldstein & Fox STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 204.2; DB
Pred. No. 1.5e-57
0; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REGISTRATION NUMBER: 29,021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2500
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/002,845
FILING DATE: 15-JAN-1993
APPLICATION UNDBER: US 07/980,529
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/224,591
FILING DATE: Herewith
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Best Local Similarity 74.8%;
Matches 276; Conservative
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join(1..726)
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20005
                                                              352 GTCTCCTCA 360
                                      361 GTCTCCTCA 369
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; LOCATION:
US-08-224-591-13
                                                                                                                                           RESULT 10
US-08-224-591-13
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                                                                                             CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATTATGCAACA 180
                                                                                                                                                             TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
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                                                                                                                                                                                                                                                                                        376 GAAGTTAAACTGGATGAACTGGAGGAGGCTTGGTGCAACCTGGGAGGCCCATGAAACTC 435
                                                                                                                                                                                                                                            Sequence 13, Application US/08926789
Patent No. 5990275
GENERAL INFORMATION:
APPLICANT: Whitlow, Marc
APPLICANT: Filpula, David
TITLE OF INVENTION: Linker For Linked Fusion Polypeptides
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Goldstein, Jorge A.
REGIGYRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.1920002/JAG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFRAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Sterne, Kessler, Goldstein & 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/002,845
FILING DATE: 15-JAN-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 07/980,529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 738 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                      361 GTCTCCTCA 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-926-789-13
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CITY: Wa
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APPLICANT: Bird, Robert
APPLICANT: Bird, Robert
APPLICANT: Filpula, David
APPLICANT: Filpula, David
APPLICANT: Filpula, Bridelle
TITLE OF INVENTION: Methods for Producing Multivalent Antigen-Binding
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                    121 CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATTATGCAACA 180
                                                                                                                                                                                                                                                                                                                      TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                                                                                                                                                                                                                                                                  241 CTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
                                                                                                                                                1 GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
                                                                         Length 738;
                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sterne, Kessler, Goldstein & Fox P.L.L.C
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                                                                     Score 204.2; DB 2;
Pred. No. 1.5e-57:
0; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION DATA: US 07/989,846
APPLICATION NUMBER: US 07/989,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/166,75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/09166750 Patent No. 6025165 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
                                                                       Query Match 55.3%;
Best Local Similarity 74.8%;
Matches 276; Conservative
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Wood, James F
CDS
join(1..726)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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20005
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721 GTCTCCTAA 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361 GTCTCCTCA 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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NAME/KEY:
                 ; LOCATION:
US-08-926-789-13
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US-09-166-750-22
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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121 CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAAGTAA'AATTATGCAACA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT 120
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                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rclease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55.3%; Score 204.2; DB 3; 74.8%; Pred. No. 1.5e-57; iive 0; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                        PULICATION DATA:
APPLICATION NUMBER: US 08/392,338
FILING DATE: 22-FEB-1995
PFILING DATE: 22-FEB-1995
PFILING DATE: 22-FEB-1995
PPLICATION NUMBER: US 07/989,846
FFILING DATE: 00 NOV-1992
PFILING DATE: 00 NOV-1992
PFILING DATE: 00 NOV-1993
PPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY AGENT INFORMATION:
NAME: Goldstein, Jorge A. REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000B
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/166,093 FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity 74.8
Matches 276; Conservative
                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: CDS
; LOCATION: 1..726
US-09-166-093-22
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US-09-172-019-22
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Patent No. 6027725
GENERAL INFORMATION:
APPLICANT: Wood, James F.
APPLICANT: Wood, James F.
APPLICANT: BIJULA, RAIL
APPLICANT: Filpula, Bavid
APPLICANT: Filpula, David
APPLICANT: Filpula, David
APPLICANT: Filpula, David
APPLICANT: Filpula, David
APPLICANT: Rollence, Michelle
ATITE OF INVENTION: Multivalent Antigen-Binding Proteins
NUMBER OF SEQUENCES: 23
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STREET: 1100 New York Avenue, NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
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Best Local Similarity 74.8%; Pred. No. 1.5e-57.
Matches 276; Conservative 0; Mismatches 78
PRICK DATE: 20-NOV-1992
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000C
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDENNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Ke
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; LOCATION: 1..7
US-09-166-750-22
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Sequence 22, Application US/09172019
Patent No. 6103889
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Mittlow, Marc
APPLICANT: Hardman, Karl
APPLICANT: Highla, David
TITLE OF INVENTION: Nucleic Acid Molecules Encoding Single-Chain
TITLE OF INVENTION: Antigen-Binding Proteins (As Amended)
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
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                                                                                                                                                            JOINTESSE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, NW
CITY: Washington
STATE: D.C.
COUNTRY: U.S.
2.TP.
                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/172,019
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 55.3%; Score 204.2; DB 3; Best Local Similarity 74.8%; Pred. No: 1.5e-57; Matches 276; Conservative 0; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Goldstein, Jorge A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0977.003000D
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNBER:
APPLICATION UNBER: US 08/392,338
FILING DATE: 22-FEB-1995
PRIOR APPLICATION UNBER: US 07/989,846
FILING DATE: 20-NOV-1992
PRIOR APPLICATION DATA: US 07/96,936
FILING DATE: 25-NOV-1991
APPLICATION UNBER: US 07/796,936
FILING DATE: 25-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 738 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                        RY: U.S.A.
20005
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US-09-172-019-22
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November 27, 2002, 03:46:58; Search time 42.4323 Seconds: (without alignments) 3349.042 Million cell updates/sec
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369
1 GAAGTGATGCTGGTGGAGTC.......CCTCACTCACCGTCTCCTCA 369
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/cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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                                Compugen Ltd.
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        341543 seqs, 192557720 residues
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Listing first 45 summaries
                                                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                          IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                        Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database
                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

/cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USI0_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USI0_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

| Description | 5-86 Sequence 86, App. | Sequence 15, | Sequence 96, | | Sequence 97, 1 | 3 Sequence 103, | | 9-130 Sequence 130, App | 1A-4 Sequence 4, Appl | Seguence 4, | -4 Sequence 4, | 1A-4 Sequence 4, Appli | Sequence 4, | Sequence 4, | Sequence 4, | Sequence 62, | S | 3 | Sequence 6, 1 |
|--------------------------|------------------------|------------------|--------------|--------------|------------------|-----------------|-----------------|-------------------------|-----------------------|-----------------|----------------|------------------------|-----------------|----------------|-----------------|------------------|-----------------|----------------|-----------------|
| DI | US-09-893-615-86 | US-09-881-823-15 | US-09-840-45 | US-09-840-45 | US-09-840-459-97 | US-09-840-459 | US-09-286-240-3 | US-09-910-029- | US-09-756-301A-4 | US-09-927-703-4 | US-09-766-535A | US-09-756-161A-4 | US-10-010-229-4 | US-10-043-450- | US-10-044-534-4 | US-09-730-857-62 | US-10-124-905-7 | US-09-883-758- | US-09-883-758-6 |
| DB | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 12 | 12 | 12 | 10 | 6 | 10 | 10 |
| Query Match Length DB | 369 | 466 | 443 | 443 | 357 | 357 | 420 | 1446 | 357 | 357 | 357 | 357 | 357 | 357 | 357 | 424 | 1437 | 856 | 856 |
| Query | 100.0 | 75.7 | 73.0 | 73.0 | 67.5 | 67.5 | 54.6 | 53.7 | 52.1 | 52.1 | 52.1 | 52.1 | 52.1 | 52.1 | 52.1 | 51.9 | 51.6 | 51.5 | 51.5 |
| Score | 369 | 279.4 | 269.2 | 269.2 | 249.2 | 249.2 | 201.4 | 198.2 | 192.4 | 192.4 | 192.4 | 192.4 | 192.4 | 192.4 | 192.4 | 191.4 | 190.4 | 190 | 190 |
| Result No. | 1 | 7 | m | ი 4 | ហ | o o | 7 | 80 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | c 19 |

| Sequence 50, Appl Sequence 64, Appl Sequence 44, Appl Sequence 54, Appl Sequence 54, Appl Sequence 11, Appl Sequence 18, Appl Sequence 14, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 17, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl | Sequence 3, Appli Sequence 3, Appli Sequence 14, Appl Sequence 25, Appl |
|--|---|
| 10 US-09-730-857-50 10 US-09-730-857-64 10 US-09-730-857-44 11 US-09-730-857-48 12 US-09-730-857-54 13 US-09-730-857-58 14 US-09-730-857-28 15 US-09-730-857-28 16 US-09-730-857-28 17 US-09-730-857-40 18 US-09-884-684-14 19 US-09-884-811-14 10 US-09-884-811-14 10 US-09-884-811-14 10 US-09-834-758-1 10 US-09-837-758-1 10 US-09-837-758-1 | 12 US-10-006-773-3 7 US-08-779-784-3 7 US-08-779-784-14 9 US-09-187-693-25 |
| 24444444444444444444444444444444444444 | 504 423 364 532 |
| 11111111111111111111111111111111111111 | 48.5 48.4 47.9 47.8 |
| 1899.8 1889.8 1888.2 1888.2 1888.2 1883.6 183.6 183.6 183.6 183.6 183.6 183.6 183.6 183.6 183.6 183.6 | 179 178.6 176.8 176.4 |
| 0 10 10 10 10 10 10 10 10 10 10 10 10 10 | 4 4 4 4 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 |

ALIGNMENTS

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SCILULION, WONG, Hing Wong, Hing Stinson, Jeffrey L. Stinson, Jeffrey L. TITLE OF INVENTION: OPSONIC AND PROFECTIVE MONOCLONAL AND CHIMERIC ANTIBODIES SPECIFIC FOR LIPOTEICHOIC ACID OF GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/893,615
FILING DATE: 29-Jun-2001
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudi, Carrol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 04995.0041-00000
TELEPHONE: 202-408-4400
INFORMATION FOR SEQ ID NO: 86:
                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                               STREET: 1300 I Street, NW
                  Sequence 86, Application US/09893615; Patent No. US2002008235Al
GENERAL INFORMATION: APPLICANT: Fischer, Gerald W. Schuman, Richard F.
                                                                                                                                                                                                                                                                                                                                                                                         COUNTY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 369 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                               DUNNER, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                         CITY: Washington STATE: DC
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US-09-893-615-86
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CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAGTAATAATTATGCAACA 180
                                                                                                                                                            TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                                                                                                   TATTATGCCGATTCAGTGGAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 310
                                                                                                                                                                                                                                                                                          CTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAGA 300
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                                                           TCATGTGCAGCCTCTGGATTCACCTTCAATAACTACGCCATGAATTGGGTCCGCCAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Largeas, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Horvath, Christopher
APPLICANT: Nowman, Walter
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Refe, Thereas
APPLICANT: O'Refe, Thereas
APPLICANT: O'Refe, Thereas
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED OF USE THEREFOR
FILLE REFERENCE: 1855,1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1998-07-23
PRIOR PLICATION NUMBER: 09/121,781
PRIOR PLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
PRIOR FILING DATE: 1998-07-23
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 269.2; DB 10;
Pred. No. 8.5e-73;
0; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/09840459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.0%;
Best Local Similarity 94.0%;
Matches 280; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 96, Application UE; Patent No. US20020150576A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mus musculus US-09-840-459-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||||| ||| ||| GTCTCTTCA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                361 GTCTCCTCA 369
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APPLICANT: ANDERSON, MAXWELL
APPLICANT: ANDERSON, MAXWELL
APPLICANT: MORRISON, SHERIE
APPLICANT: TRINH, RYAN
APPLICANT: TRINH, RYAN
APPLICANT: CHEN, LI
TILE OF INVENTION: Wethod for the Treatment and Prevention of Dental Caries
FILE REFERENCE: 22851-032
CURRENT APPLICATION NUMBER: US/09/881,823
CURRENT FILING DATE: 2001-06-15
PRIOR PRILING DATE: 1999-08-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.0
SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                             Gaps
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                                                                                                                                    Length 369;
                                                                                                                                                                             Indels
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                                                                                                                                Query Match 100.0%; Score 369; DB 10; Best Local Similarity 100.0%; Pred. No. 2.9e-103; Matches 369; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
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Pred. No. 6.8e-76;
0; Mismatches 46;
                     ) NAME/KEY: CDS
) LOCATION: 1.369
) SEQUENCE DESCRIPTION: SEQ ID NO: 86:
US-09-893-615-86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 15, Application US/09881823
; Patent No. US20020068066A1
; GENERAL INFORMATION:
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86.78;
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Best Local Similarity 86.73
Matches 320; Conservative
MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : LOCATION: (14)..(442)
US-09-881-823-15
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ORGANISM: Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-881-823-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 466
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAACTAAAAATAATAATATGCAACA 207
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                   CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAACTAAAAATAATAATATGCAACA 237
                                                                      326 TCATGTGCAGCCTCTGGATTCAGCTTCAATGCCTACGCCATGAACTGGGTCCGCCAGGCT 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAGTGATGCTGGTGGAGTCTGGTGGAGGATTGGTGCAGCCTAAAGGGTCATTGAAACTC 60
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                                                                                                                          241 CTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGA 298
                                                                                                                                             CTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGA 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 443;
                                                                                                                                                                                                                                                                                                                  APPLICANT: Larosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: Jones, S. Tarran
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE OF INVENTION: METHODS OF USE THEREFOR
FILE OF INVENTION: WUMBER: US/09/840,459
CURRENT APPLICATION NUMBER: 001-02-02
CURRENT APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 1999-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE FEALENCY OF WINDOWS VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 269.2; DB 10;
Pred. No. 8.5e-73;
0; Mismatches 18; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 97, Application US/09840459 Patent No. US20020150576A1
                                                                                                                                                                                                                                                       ; Sequence 99, Application US/09840459
; Patent No. US20020150576A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.0%;
94.0%;
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
PPPLICANT: LaRosa, Gregory J.
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US-09-840-459-99
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                                                                                                                                                                                                                    RESULT 4
US-09-840-459-99/c
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Best Local Simi
Matches 280;
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181 TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
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APPLICANT: LARGAS, Gregory J.
APPLICANT: LARGAS, Gregory J.
APPLICANT: Newman, Walter
APPLICANT: Newman, Walter
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Refe, Theresa
APPLICANT: O'Refe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HETHODS OF USE THEREFOR
TITLE OF INVENTION: METHODS OF USE THEREFOR
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-03
PRIOR FILING DATE: 2000-02-03
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-22
PRIOR FILING DATE: 1999-07-23
PRIOR FILING DATE: 1999-07-25
PRIOR FILING DATE: 1999-07-23
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APPLICANT: Horvath, Christopher
APPLICANT: Nowman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
TITLE OF INVENTION: HUMANIZED OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 249.2; DB 10;
Pred. No. 9.8e-67;
0; Mismatches 28;
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CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Humanized heavy chain US-09-840-459-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 103, Application US/09840459
Patent No. US20020150576A1
GENERAL INFORMATION:
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ilarity 90.5%;
Conservative
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266; Conserv
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us-09-893-615-86.rnpb

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Matches 270;
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Best Local S
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Patent No. US20020010320A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TILLE OF INVENTION: Chimeric and Humanized Antibodies to Anglogenin
FILE REFERENCE: 10498/74073
CURRENT APPLICATION NUMBER: US/09/286,240
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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Pred. No. 3.9e-52;
0; Mismatches 91; Indels
                                                                                                                                                                                                                    Query Match 67.5%; Score 249.2; DB 10; Best Local Similarity 90.5%; Pred. No. 9.8e-67; Matches 266; Conservative 0; Mismatches 28;
                                                                                                                                                                                                                                                0; Mismatches
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1990-07-22
PRIOR PLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: FastsEQ for Windows Version 3.0
SEQ ID NO 103
LENGTH: 357
                                                                                                                                                                             OTHER INFORMATION: Humanized heavy chain
                                                                                                                                                      ORGANISM: Artificial Sequence
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; LOCATION: (1)..(420)
US-09-286-240-3
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Matches 272; Conserv
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                                                                                                                                          TYPE: DNA
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FGRUERAL INFORMATION:

APPLICANT: Copley, Clive G
APPLICANT: Edge, Michael Derk
APPLICANT: Edge, Michael Derk
APPLICANT: Edge, Michael Derk
APPLICANT: Edge, Michael Derk
APPLICANT: Enery, Stephen Charles
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
TITLE OF INVENTION: Their Therapeutic use in an Adept System
FILE REFERENCE: 1991-209
CURRENT APPLICATION NUMBER: US/09/910,059
CURRENT FILING DATE: 1998-10-29
PRIOR FILING DATE: 1998-04-29
PRIOR PELLING DATE: 1997-04-29
PRIOR FILING DATE: 1997-04-29
PRIOR FILING DATE: 1997-04-29
PRIOR FILING DATE: 1997-02-14
PRIOR FILING DATE: 1996-05-04
NUMBER: GB9609405.7
PRIOR PELLING DATE: 1998-06-06-04
NUMBER OF SEQ ID NOWS: 131
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                                                                                                 TTTTATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
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                                                                                                                                                                                                                             CTHER INFORMATION: full-length human B7.1-murine ASB7 Fd fusion MAME/KEY: CDS
COATION: (16)..(1434)
CSPHER INFORMATION:
US-09-910-059-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 1446;
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Pred. No. 6.2e-51;
0; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 130, Application US/09910059 Patent No. US20020142359A1
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ilarity 73.2%;
Conservative (
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241 CTCTATCTGCAAATGAACAACTTGAAAACTGAGGACACAGCCATGTATTACTGTGTGAGA 300
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                                                                                                                                                                                                                                                                                                                                                                                                    121 CCAGGAAAGGGTTTGGAATGGGTTGCTCGCATAAGAAGTAAAAAGTAATAATTATGCAACA 180
                                                                                                                                                                                                    181 TITIATGCCGATTCAGTGAAAGACAGGTTCACCATCTCCAGAGATGATTCACAAAGCATG 240
                                                                                                                                                                                                                                 APPLICANY: Siegel, Scott TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of TITLE OF INVENTION: Auti-TNF Antibodies and Peptides of TITLE OF INVENTION: Human Tumor Necrosis Factor CURRENT FILLS 0975.1005-013
CURRENT FILLNG DATE: 2001-08-10
PRIOR APPLICATION NUMBER: U.S. 09/756,398
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1995-10.11
PRIOR APPLICATION NUMBER: U.S. 08/192,409
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/192,093
PRIOR PILING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/192,093
PRIOR PILING DATE: 1994-02-04
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR PILING DATE: 1993-00-02
PRIOR PILING DATE: 1993-00-02
PRIOR APPLICATION NUMBER: U.S. 08/013,413
PRIOR PILING DATE: 1993-00-11
PRIOR PILING DATE: 1993-00-11
PRIOR PILING DATE: 1993-09-11
PRIOR PILING DATE: 1993-03-18
PRIOR PILING DATE: 1992-09-11
PRIOR APPLICATION NUMBER: U.S. 07/843,606
PRIOR PILING DATE: 1992-09-11
PRIOR APPLICATION NUMBER: U.S. 07/853,606
PRIOR APPLICATION NUMBER: U.S. 08/010,406
PRIOR PILING DATE: 1993-03-18
PRIOR PILING DATE: 1993-03-18
PRIOR APPLICATION NUMBER: U.S. 07/853,606
PRIOR APPLICATION NUMBER: U.S. 07/803,606
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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Patent No. US20020002720A1
GENERAL INFORMATION:
APPLICANT: Le, Junming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Knight, David M.
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Vilcek, Jan
Daddona, Peter
Ghrayeb, John
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ORGANISM: Mus Balb/c
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knight, David M.
APPLICANT: Slegel, Scott
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
TITLE OF INVENTION: Human Tumor Necrosis Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Human Tumor Necrosis Factor FILE REFERENCE: 0975.1005-008
CURRENT APPLICATION NUMBER: US/09/756,301A
CURRENT APPLICATION NUMBER: US/09/756,301A
CURRENT APPLICATION NUMBER: US/09/756,301A
PRIOR FILING DATE: 1998-0812
PRIOR FILING DATE: 1998-0812
PRIOR FILING DATE: 1998-0812
PRIOR APPLICATION NUMBER: U.S. 08/570,674
PRIOR APPLICATION NUMBER: U.S. 08/724,799
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1994-01-29
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-03
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-03
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PRIOR FILING DATE: 1992-03-18
PRIOR APPLICATION NUMBER: U.S.07/670,827
PRIOR FILING DATE: 1991-03-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 357
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Patent No. US20010027249A1
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GENERAL INFORMATION:
APPLICANT: Le, Junming
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; LOCATION: (1)...(357)
US-09-756-301A-4
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US-09-756-301A-4
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APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: Vilcek, Jan
APPLICANT: Vilcek, Jan
APPLICANT: Stegel, Scott
TITLE OF INVENTION: AALT-THE Antibodies and Peptides of
TITLE OF INVENTION: AALT-THE Antibodies and Peptides of
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILE REFERENCE: 0975.1005.007
CURRENT APPLICATION NUMBER: US.09/756,161A
CURRENT APPLICATION NUMBER: US. 09/133,119
PRIOR PELING DATE: 1998-08-12
PRIOR FILING DATE: 1998-08-12
PRIOR PELING DATE: 1995-12-11
PRIOR PELICATION NUMBER: U.S. 08/324,799
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-10-18
PRIOR PELICATION NUMBER: U.S. 08/32,102
PRIOR APPLICATION NUMBER: U.S. 08/32,102
PRIOR APPLICATION NUMBER: U.S. 08/192,861
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0; Mismatches
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PRIOR FILING DATE: 1991-03-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICATION NUMBER: U.S. 08/192,093
FILING DATE: 1994-02-04
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72.7%;
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Best Local Similarity 72.7'
Matches 266; Conservative
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                                                                                                   TYPE: DNA
ORGANISM: Mus Balb/c
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LOCATION: (1)
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US-09-756-161A-4
                                                           SEQ ID NO 4
LENGTH: 357
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                                                             Length 357;
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APPLICANT: Use, Juniury
APPLICANT: Use, Juniury
APPLICANT: Daddona, Peter
APPLICANT: Ghrayeb, John
APPLICANT: Khight, David M.
APPLICANT: Kiegel, Scott
TITLE OF INVENTION: Human Tumor Necrosis Factor
FILE REFERENCE: 0975.1005-010
CURRENT APPLICATION NUMBER: U.S. 09/133.119
PRIOR FILING DATE: 1998-08.12
PRIOR FILING DATE: 1998-08.12
PRIOR FILING DATE: 1998-12.11
PRIOR APPLICATION NUMBER: U.S. 08/570,674
PRIOR APPLICATION NUMBER: U.S. 08/192,102
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-02-04
PRIOR FILING DATE: 1993-02-04
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-01-29
PRIOR PRILCATION NUMBER: U.S. 08/192,093
PRIOR FILING DATE: 1993-01-29
PRIOR PRILCATION NUMBER: U.S. 08/010,406
PRIOR APPLICATION NUMBER: U.S. 08/010,406
PRIOR APPLICATION NUMBER: U.S. 08/010,406
PRIOR APPLICATION NUMBER: U.S. 08/010,406
PRIOR PILING DATE: 1993-01-29
PRIOR APPLICATION NUMBER: U.S. 07/943,852
PRIOR APPLICATION NUMBER: U.S. 07/943,852
                                                         Score 192.4; DB 10; Length
Pred. No. 2e-49;
0; Mismatches 91; Indels
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APPLICATION NUMBER: U.S. 07/670,827
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                                                         Query Match 52.1%;
Best Local Similarity 72.7%;
Matches 266; Conservative
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APPLICANT: Le, Junming
APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter
; LOCATION: (1)...(357)
US-09-927-703-4
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US-09-766-535A-4
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GENERAL INFORMATION
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| Patent No. US20020114805A1
| GENERAL INFORMATION:
| APPLICANT: Le, Junming
| APPLICANT: Le, Junming
| APPLICANT: Vilcek, Jan
| APPLICANT: Daddona, Peter
| APPLICANT: Grayeb, John
| APPLICANT: Siegel, Scott
| TITLE OF INVENTION: Anti-TYF Antibodies and Peptides of
| TITLE OF INVENTION: Human Tumor Necrosis Factor
| FILE REFERENCE: 0975.1005-013
| CURRENT APPLICATION NUMBER: US/10/010,229
| CURRENT FILING DATE: 2001-12-07
| PRIOR FILING DATE: 2001-12-07
| PRIOR FILING DATE: 2001-08-10
| NUMBER OF SEQ ID NOS: 19
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PRIOR APPLICATION NUMBER: U.S. 08/010,406
PRIOR FILING DATE: 1993-01-29
PRIOR PELLING DATE: 1993-01-29
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1992-09-11
PRIOR PELLING DATE: 1992-09-11
PRIOR PELLING DATE: 1992-09-11
PRIOR PELLING DATE: 1992-09-11
PRIOR FILING DATE: 1992-03-18
PRIOR FILING DATE: 1992-03-18
PRIOR FILING DATE: 1991-03-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FEALESEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 72.7
Matches 266; Conservative
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; LOCATION: (1)...(357)
US-09-756-161A-4
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ORGANISM: Mus Balb/c
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US-10-010-229-4
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CURRENT APPLICATION NUMBER: US./10/043,450
CURRENT FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: 0.5. 09/756,398
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 1001-01-08
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: U.S. 09/133,119
PRIOR FILING DATE: 1998-08-12
PRIOR FILING DATE: 1998-10-18
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-10-18
PRIOR APPLICATION NUMBER: U.S. 08/324,799
PRIOR APPLICATION NUMBER: U.S. 08/192,861
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Pred. No. 2e-49;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 357
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72.7%;
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APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter
APPLICANT: Ghrayeb, John
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott
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Best Local Similarity 72.77
Matches 266; Conservative
                                                                                                                                                          NAME/KEY: CDS
LOCATION: (1)...(357)
                                                                                 TYPE: DNA
ORGANISM: Mus Balb/c
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APPLICANT: Lo. Junming
APPLICANT: Vilcek, Jan
APPLICANT: Daddona, Peter
APPLICANT: Grayeb, John
APPLICANT: Knight, David M.
APPLICANT: Slegel, Scott
TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
CURRENT APPLICATION: Human Tunnor Necrosis Factor
CURRENT APPLICATION: Human Tunnor Necrosis Factor
CURRENT PELING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: 09/927,703
PRIOR APPLICATION NUMBER: U.S. 08/192,093
PRIOR FILING DATE: 1994-02-04
PRIOR PILING DATE: 1994-02-04
PRIOR FILING DATE: 1993-01-29
PRIOR FILING DATE: 1993-01-29
PRIOR PILING DATE: 1993-02-02
PRIOR PILING DATE: 1993-02-02
PRIOR PILING DATE: 1993-09-11
PRIOR PILING DATE: 1992-09-11
PRIOR PILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-09-11
PRIOR FILING DATE: 1992-03-18
PRIOR FILING DATE: 1991-03-18
PRIOR FILING DATE: 1991-03-18
PRIOR FILING DATE: 1991-03-18
PRIOR FILING DATE: 1991-03-18
SOFTWARE: FRASEEQ for Windows Version 4.0
SEQ ID NO 4.
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Matches 266; Conservative
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; LOCATION: (1)...(357)
US-10-043-450-4
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352 GTCTCC 357
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US-10-044-534-4
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Pred. No. 2e-49;
0; Mismatches 91;
PRIOR APPLICATION NUMBER: U.S. 09/756,398
PRIOR FILING DATE: 2001-01-08
PRIOR PELING DATE: 1998-08-12
PRIOR PELING DATE: 1998-08-12
PRIOR PILING DATE: 1998-08-12
PRIOR FILING DATE: 1995-12-11
PRIOR FILING DATE: 1995-12-11
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-10-18
PRIOR FILING DATE: 1994-02-04
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PRIOR FILING DATE: 1993-01-29
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Best Local Similarity 72.7
Matches 266; Conservative
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US-10-044-534-4
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